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Jose, CA 95117 (US). **DRMANAC, Radeje, T.** [YU/US];
850 East Greenwich Place, Palo Alto, CA 94303 (US).

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(74) Agents: **ELRIFI, Ivor, R.** et al.; Mintz, Levin, Cohn,
Ferris, Glovsky and Popeo, P.C., One Financial Center,
Boston, MA 02111 (US).

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(71) Applicant (*for all designated States except US*): **HYSEQ,
INC.** [US/US]; 670 Almanor Avenue, Sunnyvale, CA
94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **TANG, Y., Tom**
[US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US).
LIU, Chenghua [CN/US]; 1125 Ranchero Way #14, San

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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and
uses thereof.

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NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases.

The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NOS: 1-13901. The polypeptides sequences are designated SEQ ID NOS: 13902-27802. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-13901 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NOS: 1-13901. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-13901 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-13901. The sequence information can be a segment of any one of SEQ ID NO: 1-13901 that uniquely identifies or represents the sequence information of SEQ ID NOS: 1-13901.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-13901 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-13901 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-13901; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NOS: 1-13901; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NOS: 1-13901. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-13901; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (e.g., SEQ ID NOS: 13902-27802); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-13901; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOS: 1-13901.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NOS: 1-13901. The sequence information can be a segment of any one of SEQ ID NO: 1-13901 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NOS: 1-13901. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1+4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-13901; a polynucleotide encoding any one of the peptide sequences of SEQ ID NOS: 13902-27802; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NOS: 13902-27802. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-13901; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NOS: 13902-27802. Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in receptor-like polypeptides include ligand-binding,

extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-13901 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-13901 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-13901 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-13901, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that

are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO: 1-13901, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-13901 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-13901 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altschul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-13901, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, *e.g.*, plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-13901 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-13901 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and

promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTtrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-13901, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NOS: 13902-27802 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-13901 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-13901), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxycarboxymethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -nucleic acid molecule. An α -nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -nucleic acids, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-O-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-13901). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-1124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element.

Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultschi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NOS: 13902-27802 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-13901 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-13901 or

(b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NOS: 13902-27802 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NOS: 13902-27802 or the corresponding full length or mature protein; and "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NOS: 13902-27802.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NOS: 13902-27802.

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., *Nucleic Acids Res.* vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., *J. Comp. Biol.*, Vol. 6; pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, *ISMB-97*, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., *Nucleic Acids Res.*, Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (*J. Mol Biol.*, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappell; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultschi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No. 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., *Cell* 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3,

4 MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci. U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias, or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue
4 to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

8 A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

12 Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

16 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

20 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described
24 herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells
28 and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses,
32 herpes viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by *in vivo* animal models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial

immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1.3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bowman et al., *J. Virology* 61:1992-1998; Bertagnoli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

- 4 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J. J. and Brunswick, M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

- Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnoli et al., *J. Immunol.* 149:3778-3783, 1992.

- Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

- Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et al., *Cellular Immunology* 155:111-122, 1994; Galy et al., *Blood* 85:2770-2778, 1995; Toki et al., *Proc. Nat. Acad. Sci. USA* 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells.

Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy.

- 4 Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation,

- 8 inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic
12 cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal
16 cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle,
20 kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma,
24 hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically
28 effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

- 32 The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine.

Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepe, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguanzone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltzenberg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dörner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligand(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of

therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, e.g.,

choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or

- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);

effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or

absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*, by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoshitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth

factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other

hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers

comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, e.g., by means of conventional mixing,

dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral

administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other

sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically

acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired

patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 1351), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will

indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety.

Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (*The Scientist*, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for

example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (*Bio/Technology* 10, 779-783 (1992)); Lonberg et al. (*Nature* 368 856-859 (1994)); Morrison (*Nature* 368, 812-13 (1994)); Fishwild et al. (*Nature Biotechnology* 14, 845-51 (1996)); Neuberger (*Nature Biotechnology* 14, 825 (1996)); and Lonberg and Huszar (*Intern. Rev. Immunol.* 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

4 An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the
8 locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

12 A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another
16 mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds
20 immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

24 According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of
28 monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)2} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated
32 by reducing the disulfide bridges of an F_{(ab)2} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) Fv fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, *Science* 229:81 (1985) describe a procedure

wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab' -TNB derivatives is then reconverted to the Fab' -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab' -TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., *J. Immunol.* 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on

a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc R), such as Fc RI (CD64), Fc RII (CD32) and Fc RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention.

Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, *J. Exp. Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, *Anti-Cancer Drug Design*, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of

bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolacca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-13901 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-13901 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored

therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,

amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection).

See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-13901, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

(a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems.

Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NOS: 1-13901. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-13901 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-Melm₇), is then added to a final concentration of 10 mM 1-Melm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-Melm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor et al. (1991) *Science* 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness et al. (1991) *Nucleic Acids Res.* 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) *Anal. Biochem.* 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *CviJI* normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*CviJI***), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI*** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems

(ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-13901 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 3 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-13901) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 1-13901. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-13901 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and Geneseq database release 200101 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest

homologue for SEQ ID NOS: 1-13901. The nearest neighbor results for SEQ ID NO: 1-13901 are shown in Table 2 below.

Tables 1, 2 and 3 follow. Table 1 shows the various tissue sources of SEQ ID NOS: 1-

- 4 13901. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homolog with an identifiable function for each assemblage. Table 3 contains the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 3 also provides a correlation between the amino acid sequences set forth
- 8 in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO. in USSN 09/515,126

TABLE 1

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	83 544 597-598 600-607 616 841 1004 1148 1346 1493 1974 2138 2141 2143 2161 2266 2345 2363 2511 2569 2876 2880 3001 3099-3101 3105-3106 3110-3111 3115-3117 3199 3272 3282 3284 3356 3425 3537 3634 3689 3709 3797 3810 3839 3899 4006 4021-4022 4025 4043 4194 4201 4253 4277 4297 4388 4399 4410 4667 4671 4722 4747-4748 4750 4755 4767 4845 4865 4940 5037 5075 5093 5118 5163 5171-5172 5268 5481 5523 5553 5656 5724 5894 5902 5938 6052 6170-6173 6176 6214 6307 6336 6369 6374 6793 6894-6897 6979 7058 7169 7455 7492-7493 7495-7499 7501 7504 7577 7586 7761 7792 7864 7870 8035 8065 8085 8110 8120 8140 8224 8226 8298 8372 8427 8452 8456 8535 8648 8672 8674-8679 8681- 8684 8816 8838-8839 8870 8898 9012 9041 9079 9128 9257 9264 9304 9317 9460 9503 9517 9567 9623 9734 9781 9792- 9798 9929 9964 9999 10296 10330 10469-10470 10578 10679 10778 10786 10895 10984-10986 11032 11052 11069 11130 11145 11239 11289 11402 11818 11862 11870-11876 11878- 11881 12017 12037 12127 12160 12294 12363 12375 12405 12424 12438 12467 12539 12570 12590 12615-12616 12618 12685 12688 12712 12739 12748 12830 12913 12916 12948- 12950 13002 13064 13073 13083 13141 13150 13153 13164- 13166 13257 13391 13456 13479 13489 13492 13494 13499 13501 13503 13560 13595-13596 13627 13645 13679 13782 13795 13861 13866 13869 13882
adult brain	GIBCO	ABD003	67 83 142 443 587 598 608-609 611 613-624 633 731 734 737- 742 760 799-800 809 1148 1152 1167-1184 1193 1346 1433- 1516 1552 1575 1671 1756 1774 1833 1974 2138 2145 2176- 2178 2237 2266 2299-2301 2303-2306 2343 2363 2412 2444 2449 2511 2516 2555 2569 2576 2614 2716 2809 2876 2911 2926 3001 3093 3114 3119 3121-3124 3126 3128-3130 3234 3254-3256 3258-3263 3265-3267 3270-3274 3276-3277 3280- 3281 3284 3286 3348 3356 3378 3435 3459 3484 3537 3548 3595 3605 3625 3627 3634 3686-3697 3700 3702 3709 3711 3720 3722 3737 3757 3797 3804 3810 3839 3856 4006 4019 4025 4040 4055 4057-4058 4060 4078 4194 4201 4246 4253 4277 4282 4390 4405 4412 4431 4620 4622 4641 4689 4751- 4764 4791 4808 4837 4845 4847-4849 4852-4858 4860-4862 4864-4869 4940 4957 4962 4972 4998 5021 5031 5037-5038 5040 5076 5093 5108 5118 5167 5169 5171-5172 5251-5261 5263-5265 5270 5364 5401 5481 5492 5521 5523 5535 5656 5674 5693 5766 5788 5817 5906-5909 5938 6005 6027 6057 6064 6147 6178 6180-6182 6189 6214 6229-6233 6254 6272 6369 6371 6421-6426 6555 6595 6598 6601 6799 6803 6825 6836 6886 6894 6913 6972 6995 7058 7104 7130 7133 7148 7164 7169 7339 7347 7386 7426 7455 7494 7502 7507 7509 7511-7512 7516 7520 7584-7587 7590-7596 7598-7601 7603- 7604 7608 7632 7677 7743 7748 7761 7768 7792 7797 7807 7815 7839 7849-7861 7864 7870 7930 7937 8035 8065 8067 8080 8087 8095 8110 8120 8139-8140 8209 8224 8226 8235 8246 8262 8285 8298 8320 8323 8336 8354 8361 8365 8370 8375 8387 8452 8456 8535 8556 8576-8577 8603 8630 8648 8674 8685-8686 8688-8690 8693 8695 8702 8712 8742 8760- 8761 8763-8764 8766-8769 8813 8815-8816 8830 8834 8838- 8839 8848 8863 8870 8898 8921 8943-8944 8951 8989 9010 9041 9050-9056 9058-9064 9076 9079 9092 9097 9128 9144- 9145 9257 9264 9271 9278-9279 9304 9315 9317 9455 9466 9472 9475 9480 9503 9511 9517 9525 9539 9689 9734 9773 9781 9791 9799-9802 9847 9852 9873 9928-9929 9964 9999-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			10001 10003-10004 10053 10175 10267 10276 10330 10349 10434 10449 10466 10471-10474 10492 10496 10509 10566 10578 10597-10599 10645 10679 10788 10891 10948 10988- 10990 11032 11039 11041-11043 11052 11065 11069 11105 11108 11130 11145 11167 11196 11203-11207 11209 11239 11399 11401-11402 11406 11459 11470 11604 11606 11642 11761 11818 11862 11877 11882-11884 11886 11889-11893 11944-11946 11981 11988 12016 12019 12022 12037 12083 12127 12143 12164-12165 12168-12171 12178 12195 12236 12265 12305 12327 12363 12375 12405 12423-12424 12430 12438 12546 12570 12590 12594 12612 12615-12618 12630 12670 12674 12685-12688 12693 12704 12706-12707 12748 12772 12830 12885 12904 12913 12916 12923 12933 12951 12956 12993 13001 13020-13021 13038 13047 13064 13072- 13073 13084-13085 13092 13117 13142 13167-13171 13191 13254 13257 13260 13295 13390-13391 13394 13456 13479 13483 13489 13497 13501 13503 13505-13507 13512 13516 13546 13551 13555 13575 13590 13592 13597 13613-13614 13645 13649 13659 13711 13782 13795 13838 13861 13869 13875 13882 13884-13885 13888 13892 13896
adult brain	Clontech	ABR001	142 858 1542 2174 2407 2485 2652 3272 3287 3460 3492 3535 3595 3737 3839 4005 4060 4282 4434 4791 4972 5040 5293 5523 5530 5535 5788 5906 6082 6601 6799 6980 7373 7577 7587 7759 7788 7851 8081-8082 8110 9167 9455 9466 9781 9928 10422 10774 10791 11069 11401 11406 11459 11604 11607 11791 11818 11865 11961 11979 12022 12122 12160 12327 12442 12594 12615 12640 12670 12705 12935 12957 12985 13047 13197 13257 13456 13511-13512 13546 13554 13646 13793 13885 13889 13893
adult brain	Clontech	ABR006	6 67 1004 1908 3272 3286 3548 4011 4282 4998 5923 5928 6374 6730 6815 6867 6890 7067 8365 9264 9729 9780 10776 11587 11618 12596 12601 12605 12704 12749 12754 12951 13047 13051 13090 13479 13488 13498-13499 13503 13512 13575 13882
adult brain	Clontech	ABR008	6 11 21 41 51 88 142 364 376 579 598 651 736 800 1050 1148 1184 1251-1265 1291 1346 1404 1479 1529 1543 1671-1674 1697 1699-1710 1820 1830 1832-1838 1840 1848-1849 1908 1914 1919 1927 1957 1964 1974 1976 1978-1979 2005-2006 2050 2081 2090 2110-2111 2129 2150 2174 2200 2310 2327 2342 2408-2410 2420 2444 2449 2461-2467 2484 2490 2499- 2506 2511 2553 2574 2576 2611 2652 2809 2827 2866 2894 3032 3207 3535 3591 3610 3634 3715 3722 3737 3766-3770 3819 4006-4007 4011 4025 4032 4060 4078 4095 4109 4128 4143-4155 4182 4194 4247-4257 4277 4282 4294 4296 4310 4330 4348 4355 4360 4381 4395 4399 4411 4431 4543 4641 4662 4694 4698 4767 4781 4791 4808 4833 4837 4985 5001 5022 5040 5075 5094 5108 5163 5303-5306 5308-5314 5320 5380 5523 5553 5615 5625-5626 5634 5638-5644 5701 5706 5711 5727-5742 5766 5772 5775 5783 5801 5814 5817 5820- 5821 5829 5837 5851 5855 5858 5864 5867 5874 5885 5890 5897 5901 5906 5923 6057 6125 6214 6223 6288 6302 6456- 6464 6545 6598 6601-6602 6624 6676-6685 6699 6726 6728 6746-6749 6765 6799 6805 6854 6860 6893-6894 7004-7007 7049 7076 7078 7081-7083 7105 7117 7119 7133 7153 7166 7431 7579 7708 7768 7849 7900-7905 8018 8083-8084 8095 8110 8196-8208 8262 8288 8312 8320 8331 8336 8356 8375 8452 8482 8633 8681 8710 8739 8777 8815 8817 8830 8839 8963 8965 8983 9010 9097 9100 9102-9108 9111 9128 9142 9257 9264 9313 9364 9378-9384 9401 9454-9455 9458 9460- 9464 9503 9509 9511 9515-9516 9522 9528-9529 9533 9539 9542 9544 9573 9577 9646 9773 9780 9924 10000 10025-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			10029 10097 10148 10209 10218-10223 10225-10229 10267 10275-10276 10284 10292 10296 10303 10313 10326 10329- 10331 10333-10334 10343 10346 10393 10430 10494 10496 10513 10542 10557 10613-10616 10679 10688 10691 10719- 10721 10729 10743 10758 10760 10776 10782 10786 10795 10895 11100 11114 11132 11195 11240 11242-11254 11401 11406 11437 11454 11459 11462 11466-11473 11475-11476 11519 11532-11535 11550 11553 11555-11556 11559 11588- 11589 11606 11615 11618 11621 11627-11628 11633 11761 11791 11807 11818 11932 11955 12006 12039 12041 12092 12212-12224 12231 12236 12305 12363 12368 12396-12399 12405 12424 12439 12442 12465-12466 12468 12477 12479- 12482 12490 12521 12546 12552-12553 12576-12577 12579 12582 12585 12590 12601 12609 12617-12618 12636 12658 12707 12725 12735-12736 12749 12754 12776-12779 12859 12868 12894 12905 12909 12940 12955 12959 12977 12980 12990 13002 13004-13005 13020 13035 13038 13042-13044 13047 13051-13052 13056 13062 13073 13082-13083 13196 13249 13280 13311-13312 13336 13387 13417 13421-13426 13436 13445 13456 13458 13479-13482 13488 13490 13494- 13495 13497-13500 13503 13507 13512 13516 13533 13546 13554-13555 13590 13613 13630 13649 13659 13670 13678 13713 13724 13769 13793-13794 13808 13827-13828 13838 13861 13867-13868 13875 13882 13884-13885 13888-13889 13893 13896 13898
adult brain	Clontech	ABR011	1006 1257 3797 4006 4025 5535 6057 7169 7870 8262 8937 8966 9257 10778 12736 13394 13679 13793 13861
adult brain	BioChain	ABR012	88 598 1007 1134 2597 3557 3590 3627 3797 4006 4192 4246 4282 4391 4940 5523 5535 6288 6338 7138 8110 8898 9076 9401 9455 9476 10772 11061 11114 12989 13394 13511 13866
adult brain	Invitrogen	ABR013	598 2614 3191 4355 4391 5525 5788 8085 8486 11513 12521 12989 13861
adult brain	Invitrogen	ABT004	40 51 598 1050-1057 1148 1777-1778 1947 1976 2270-2272 2327 2490 2617 3050 3600-3602 3722 3987 4390-4391 4434 4543 4689 5031 5157-5159 5167 5169 5466 5505 5682-5683 5701 5766 5778 5794 5902 6147 6367-6371 6459 6545 6709 6728 6783 6801 6971 7104 7175 7815 7839 7864 8139 8342 8345 8355 8363 8372 8452 8633 8963 8975-8976 9012 9133 9423-9424 9511 9515 9517 9528 9556 9827 9949 10260 10267 10275 10570-10571 10733 10767 11132 11159 11406 11459 11932 12009 12092 12109-12111 12127 12283 12428 12511 12579 12605 12725 12747 12830 12885-12886 12910 12913 12954 12987-12989 13051 13054 13062 13073 13090 13249- 13253 13438 13445 13456 13489 13500 13512 13516 13533 13546 13590 13622 13649 13683-13684 13713 13803 13838 13861 13866 13896
cultured preadipocytes	Stratagene	ADP001	1134 1346 2343 2614 3272 3426 3610 3720 3839 3885 4011 4277 4282 4297 4346 4388 4391 4405 4434 4641 4833 4940 4985 5018 5030 5040 5163 5167 5523 5581 5778 5788 5794 5895 5951 6082 6147 6272 6607 7067 7141 8093 8235 8285 8312 8363 8629 8648 8830 8839 9290 9401 9466 9503 9781 10346 10470 10776 10795 10971 11108 11170 11513 11818 12034 12037 12046 12093 12375 12387 12405 12424 12570 12636 12670 12674 12688 12735 12749 12913 12940 13126 13163 13295 13489 13494 13497 13499 13511 13516 13575 13652-13653 13866 13888-13889
adrenal gland	Clontech	ADR002	8 83 142 225 351 443 551 569 731 864 1134 1266-1271 1273- 1274 1276-1292 1294-1295 1381 1391 1544-1545 1658 1671 1908 1959 1983 2010 2023 2145 2175 2283 2310 2328-2334 2343 2444 2449 2510 2522 2576 3032 3069 3153 3166 3272

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			3378 3416 3548 3625 3709 3711 3771-3788 3790-3791 3797 3839 3870 3899 3985 4019 4054 4060 4109 4173 4192 4194 4201 4253 4277 4282 4389 4391 4395-4396 4431 4667 4687 4694 4783 4957 4966 4985 4998 5037 5108 5293 5316-5323 5325-5336 5481 5505 5527 5531-5533 5560 5628 5656 5701 5766 5865 5874 5902 5939 5979 6020 6052 6057 6227 6288 6354 6405 6449 6465-6482 6521 6603 6726 6894 6979 7008- 7011 7155-7156 7204 7604 7634 7845 7871 7906-7912 7915- 7918 7920-7930 8022 8067 8085-8086 8095 8110 8116 8224 8262 8363 8365 8412 8520 8535 8554 8699 8742 8831 8870 8950-8951 9002 9010 9012 9097 9109-9119 9121-9127 9190 9264 9280 9304 9317 9455 9457 9495 9503 9553 9556 9586 9709 9780-9781 9895 9927 10007 10030-10032 10034-10035 10037-10045 10119 10277 10284 10346 10595 10617-10620 10623-10627 10645 10675 10679 10760-10761 10766 10774 10782 11108 11194 11255 11258-11270 11289 11400 11406 11457 11519 11588 11600 11621 11626 11818 11952 12080 12159 12225 12227-12230 12232-12237 12239-12240 12242- 12249 12251 12305 12363 12375 12404-12405 12424 12439 12577 12599 12601 12630 12636 12657-12658 12663 12688 12693 12706 12713 12715 12735 12749 12754 12780-12787 12848 12863 12909 12913 12923 12957 12990 13006-13007 13020-13021 13064 13095 13104 13295 13313 13315 13388- 13389 13391 13456 13473 13494 13507 13515 13546 13613 13631 13679 13725-13733 13858 13866 13872 13883-13884 13888-13889
adult heart	GIBCO	AHR001	51 83 88 94 221 239 360 366-367 404 410-411 413 415 458- 459 461 465-468 471 473-478 486 545-546 559 567 616 625- 630 743-744 799 802-806 808 810-835 837-842 959 1004 1066- 1085 1134 1178 1184-1193 1346 1512 1516 1546-1547 1556 1575 1671 1727 1774 1829 1959 1976-1977 2090 2096 2108 2110 2128 2138 2145-2147 2161 2179 2195-2198 2257 2276 2278-2281 2302 2307-2309 2363 2398-2399 2409 2411-2412 2444 2449 2497 2516 2529 2563 2569 2575-2576 2597 2605 2614 2617 2762 2809 2816 2879-2880 2911-2924 2926 2961 2978-2980 2985-2986 2993 2995-3002 3032 3042 3051 3058 3069 3081 3091-3094 3109 3114 3132-3133 3135 3137-3138 3141 3191 3196 3199 3215 3263 3272 3282-3286 3317 3349- 3350 3353-3359 3361-3362 3364-3367 3370-3393 3396-3399 3403 3406 3425 3451 3465-3466 3479 3500 3503 3537-3538 3544 3548 3550 3555 3557 3590-3591 3595 3604 3606-3612 3614-3621 3623-3627 3634 3689 3697-3698 3701-3709 3711- 3713 3720 3722 3737 3757 3797 3839 3885 3898 3988-3989 3996 4005-4006 4008 4010-4011 4019 4021-4022 4025 4040 4043 4054-4055 4058-4060 4078 4183 4192 4194 4201 4246 4253 4269 4277 4282 4341 4351 4391 4403 4405 4434 4517 4543 4553 4590 4615 4622 4631 4633-4634 4641 4654 4664 4666-4667 4672-4675 4688-4689 4693-4694 4738 4740 4755 4783 4828 4870-4871 4905-4906 4909-4915 4917-4919 4921- 4924 4926-4927 4940 4957 4972 4985 4991 4998 5001 5030 5037-5038 5040 5076 5118 5163 5171-5175 5177-5178 5180- 5182 5266-5268 5380 5422 5481 5490 5492 5506-5507 5523 5534-5535 5581 5656 5682 5711 5740 5766 5788 5895 5908 5923-5924 5938 6047 6057 6083 6085 6104 6110-6111 6117 6147 6184-6185 6189 6195 6215 6255-6257 6259-6266 6268 6272 6288 6307 6336 6375-6379 6382 6427-6429 6458 6555 6588 6595 6607 6629 6665 6689 6765 6767 6799 6815 6871- 6873 6879 6881-6882 6898 6926-6928 6975-6978 6987 7058 7090 7148 7313-7314 7341 7343-7344 7346-7347 7350 7354 7359 7362 7373 7380 7394 7402 7407-7408 7410 7413 7415- 7416 7418-7419 7426 7431 7468 7473 7480 7494 7505 7513-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			7516 7520 7544 7561 7584 7587 7599 7601-7604 7635 7638- 7643 7645-7649 7651-7655 7657 7659-7662 7733 7735 7743 7748 7783-7796 7815 7852 7857 7862-7863 7865-7870 7930 7933 7983 8062-8065 8067 8087-8088 8093 8095 8110 8116 8120 8139-8140 8224 8226 8235 8262 8298 8336 8344-8345 8354 8356 8363 8368 8372 8378 8387 8410 8427 8452 8456 8531-8532 8534-8535 8563-8569 8572 8576-8577 8592-8593 8597 8603 8606 8610 8613-8614 8616-8617 8646 8648 8670 8681 8691 8698-8699 8702 8712 8742 8756 8760 8763 8795 8807-8809 8811-8814 8816-8819 8821-8833 8835-8839 8858 8863 8870 8898 8921 8927 8936 8939 8943 8946 8950-8951 8966 8988-8992 8994-8995 9010 9049 9059 9065-9067 9070- 9072 9076 9097-9098 9167 9190 9257-9260 9262 9269 9281 9287 9301 9304 9315 9317 9401 9454-9455 9466 9476 9480 9484 9556 9577 9612 9689 9698 9720-9721 9734 9741-9743 9747-9750 9758 9781 9791 9804 9871-9882 9884-9885 9928 9939 9942 9954-9960 9999-10000 10005 10175 10179 10275 10284 10292 10296 10329-10331 10346 10400 10422 10430- 10431 10437 10442 10444-10447 10475 10511-10512 10514- 10521 10557 10576-10577 10616 10645 10679 10691 10729 10742 10744 10772 10774 10777-10778 10782 10788 10839 10891 10894-10895 10902 10917-10920 10937 10942 10946 10948 10969-10970 10992 11032 11044-11045 11061 11066- 11074 11108 11114 11132 11145 11153 11165-11170 11173 11205 11208 11210-11215 11283 11289 11386 11388 11401- 11402 11406 11462 11559 11565 11576 11596 11606 11615 11620 11744 11788-11789 11793 11818 11823-11825 11831- 11832 11869 11894 11947 11961 11982-11989 12000 12006 12009 12011 12019-12020 12028 12037 12044 12078 12081 12093 12119-12122 12143 12160 12166 12172-12175 12177- 12179 12197 12305 12335 12363 12375-12376 12383 12387 12400 12402 12405 12424 12428 12438 12479 12521 12523 12546 12560 12564 12570 12590 12599 12601 12605 12609 12611 12616-12618 12653 12662-12663 12670 12674 12688 12717-12720 12734 12752 12754 12772 12905 12907 12914 12916-12917 12923 12925 12940 12961 12963-12965 12989 12991 12993 13020-13021 13033 13035 13072-13073 13082- 13083 13104 13117 13126 13132 13136 13141-13142 13148 13169 13203-13210 13212 13260-13261 13293 13295 13326 13377 13394 13413 13442 13456 13477 13480 13488 13490 13494-13496 13501-13503 13506-13507 13511 13516 13533 13568 13570-13571 13575 13582 13592 13613 13624-13630 13632 13644 13646 13659-13660 13678-13679 13689 13701 13711-13713 13775 13782 13795 13797 13866-13869 13872 13882 13884-13885 13893
adult kidney	GIBCO	AKD001	49 67 83-84 142 354 405-407 415-429 431-432 445 460 462 479-484 486 488 492-493 524 548-549 598 616 631-638 744 787 809 841 1004 1068 1086 1160 1163-1166 1171 1184 1193 1346 1359 1449 1479 1516 1552 1556 1671 1724 1727 1774 1826 1858 1914 1974 1976 1978-1979 2081 2097-2099 2111- 2113 2117-2118 2129-2130 2138 2145 2148-2150 2161 2186 2218 2266 2268 2302 2310 2327 2343 2363 2409 2412 2444 2449 2468 2483 2523 2569 2576 2614 2617 2827 2845 2876 2910 2915 2926-2931 2933-2934 2938-2943 2945-2947 2955- 2956 2976 2981 2983-2984 3001-3016 3018 3053 3109 3114 3140 3142-3146 3149-3150 3199 3254 3265 3272 3283-3284 3286 3333 3350 3356 3378 3406 3435 3445 3460 3492 3503 3535 3537 3544 3548 3590-3591 3598 3625 3627 3634 3676- 3677 3679-3685 3689 3697 3709 3711 3720 3722 3737 3757 3797 3808 3810 3839 3885 3989 4005-4006 4011 4019 4022 4025 4040 4043 4054-4055 4060 4078 4109 4192 4194 4201

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			4246 4253 4269 4277 4341 4354 4387-4388 4390 4398 4402 4405 4410 4434 4473 4540 4543 4583 4591-4592 4607 4637 4640-4641 4649 4654 4665 4668 4676-4677 4680-4685 4688- 4689 4711-4712 4751 4758 4766-4768 4783 4808 4833 4836- 4837 4845 4874 4904 4940 4957 4962-4963 4972 4983 4991 4998 5022 5037 5040 5076 5093 5118 5143 5163 5171-5172 5246-5249 5281 5362 5364 5380 5422 5481 5521 5523 5526- 5527 5535 5656 5693 5726 5740 5766 5769 5778 5788 5794 5894 5902 5908 5911 5916-5917 5923 5928 5938 5990 6005 6049-6051 6057 6078 6082 6086 6088 6105-6107 6112-6117 6120-6122 6147 6159 6186-6189 6215 6257 6272 6288 6369 6418 6423 6430 6555 6595 6598 6738 6743 6765 6767 6793 6799 6805 6815 6836 6857 6867-6870 6872-6873 6878 6884 6886 6893 6899-6900 6931 6947 6976 6979 6988 7024 7045 7058 7104 7118 7155 7275 7281 7306 7312 7338 7347-7348 7351-7352 7355 7357 7359-7363 7366 7369 7371-7373 7381 7383 7386 7400 7402 7404-7406 7408 7420 7422 7424 7426- 7428 7430-7431 7433-7435 7439 7455 7465-7468 7494 7502 7506 7517-7521 7579 7587 7604 7634 7639 7642 7733 7735 7743 7748 7792 7797 7839 7842-7846 7848 7852 7857 7862 7864 7870 7930 7933 8065 8077 8084 8087 8093 8095 8105 8110 8116 8120 8139-8140 8156 8224 8226 8235 8262 8320 8336 8345 8351 8354 8359 8364 8368 8370 8372 8375 8377 8387 8427 8452 8456 8461 8486 8518 8520 8527 8535 8563- 8564 8566 8572-8573 8575-8577 8580-8583 8585 8588-8589 8597 8603 8618-8621 8623 8625-8626 8628 8630 8634 8647- 8650 8664 8674 8677-8678 8691 8694 8701-8704 8706 8711 8722 8740 8742 8763 8792 8798 8806 8812-8813 8816 8830 8838-8839 8848 8853 8863 8876 8898 8921 8935 8943-8944 8948 8951 8966 8989 9012 9041 9047-9049 9076 9092 9128 9137 9167 9218 9244 9249 9257 9264 9287 9304 9315 9317 9424 9455-9457 9466 9472 9475 9484 9503 9511 9517 9529 9536 9542 9544 9558 9612 9683 9699 9703 9722-9723 9725 9734 9744 9752-9755 9758 9772-9773 9780-9781 9805-9807 9841 9843 9927-9929 9939 9942 9969 9998-10000 10007 10175 10275 10284 10287 10292 10319 10346 10376 10423- 10424 10431 10442 10446 10448 10450 10475 10480 10496 10542 10557 10645 10679 10774 10778 10782 10788 10895 10921-10928 10947 10949-10953 10986 10994-10996 11032 11052 11061 11069 11114 11130 11132 11143 11145 11197- 11202 11205 11208 11212 11239 11289 11401-11402 11406 11459 11513 11586 11596 11604 11607 11618 11620 11695 11711 11759 11761 11790-11791 11793-11794 11818 11820- 11822 11834-11836 11857 11865 11869 11895-11899 11950 11970 12006 12022 12041 12078 12143 12159-12160 12178 12195 12197 12256 12265 12305 12327 12359 12363 12375 12387 12405 12424 12428 12438 12442 12467 12511 12521 12523 12535 12539 12546 12564 12570 12590 12599 12601 12609-12611 12616 12618 12630 12653 12656 12664 12666- 12667 12670 12674 12688-12689 12691 12739 12754 12830 12834 12904 12913-12914 12916-12917 12923 12940-12941 12951-12952 12956 12972 12976-12977 12993 12999 13002 13052 13062 13064 13066 13072-13073 13082-13083 13095 13104 13127 13131 13133 13136 13141 13143-13146 13148 13154-13155 13169 13172 13184 13195-13196 13249 13254 13260 13263 13280 13295 13307 13319 13394 13442 13456 13477 13479-13480 13488-13490 13492 13494-13495 13497- 13503 13506-13507 13512 13515-13516 13546 13551 13554- 13556 13572-13574 13590 13592 13613 13627 13631 13644- 13645 13656 13659-13660 13665 13670 13710 13713 13776 13782 13795 13859-13860 13864 13866-13868 13872 13882-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
adult kidney	Invitrogen	AKT002	13885 13888 13891-13892
			67 142 550-552 598 639-641 1004 1015 1493 1516 1947 2215 2299 2343 2363 2449 2618 3054-3055 3152-3153 3155-3157 3434 3535 3590 3709 3797 3808 3839 3885 4011 4022 4025 4040 4253 4277 4391 4405 4671 4759 4767 4769 4837 4949 4972 5001 5035 5037 5052 5108 5526 5581 5615 5726 5788 5895 6062 6139 6190-6191 6803 6900 6947 6975 7468-7469 7473 7733 8095 8110 8139 8262 8323 8361 8363 8375 8520 8539 8648 8711 8798 8912 8950 8966 8983 9076 9264 9368 9510 9517 9665 9703 9734 10175 10476 10791 10989 10997 11132 11618 11745 11900 12006 12039 12160 12363 12375 12405 12424 12685 12702 12707 12904 13035 13060 13104 13136 13295 13394 13456 13488 13495 13501 13512 13533 13554 13583 13644 13670 13679 13696 13713 13795 13866 13888 13891
adult lung	GIBCO	ALG001	83-84 553 598 642-644 650 747 975 1004 1009 1015-1022 1449 1516 1816 2161 2186 2215 2343 2444 2968 3056 3158 3160-3162 3345 3466 3503 3519 3566 3568-3573 3595 3709 3797 3810 3839 3885 4025 4039 4059 4194 4405 4622 4755 4767 4770 4797 4865 4940 4949 4963 4972 4987 4991 4998 5001 5117-5129 5171-5172 5233 5401 5481 5581 5724 5788 5938 5960 6123 6125 6140 6215 6322 6336 6343-6348 6371 6886 6966-6967 7024 7143 7275 7441 7444 7502 7522-7523 7749-7752 8093 8110 8140 8336 8345 8375 8378 8449 8535 8612 8622 8635 8648 8651 8674 8702 8707-8708 8838-8839 8898 8941-8942 8944 8948 8951 9076 9128 9457 9466 9475 9497 9503 9544 9567 9703 9756 9758 9808-9810 9843 9873 9926 9999 10161 10175 10275 10329 10344 10400 10458 10554-10555 10796 10998 11032 11046 11069 11132 11144- 11145 11483 11627 11818 11837 11901 12006 12028 12039 12041 12087-12092 12146 12363 12375 12424 12438 12539 12570 12601 12617 12661 12670 12674 12688 12738 12749 12754 12904 12940 12974 13062 13173 13195 13232 13234 13260 13295 13307 13456 13472 13477 13490 13494 13497- 13498 13569 13584 13592 13660 13663-13666 13670 13743 13776 13882 13885 13889 13891
lymph node	Clontech	ALN001	83 142 364 487 495-497 554 629 645-646 648-650 716 938-951 953-962 1134 1516 1549 1671 1774 1976 2138 2225-2232 2234-2235 2340 2879 3019-3020 3057 3103 3163-3165 3272 3356 3498-3505 3507-3513 3515-3516 3538 3548 3628 3697 4194 4201 4253 4405 4641 4687-4688 4771-4772 4783 4808 4845 4963 4972 4987 4998 5042-5065 5076 5163 5504 5523 5835 5895 5917 6027 6142 6192 6272 6288 6308-6311 6313- 6314 6765 6805 6871 6949-6951 7700-7705 7707-7709 8085 8088 8091 8110 8235 8375 8387 8432 8629 8631 8633 8648 8677 8709 8713-8715 8830 8863 8887-8889 8891-8896 8943- 8944 8966 9010 9076 9111 9128 9142 9222 9455 9472 9520 9544 9734 9774 9780 9811 9905-9907 9928 9939 9999 10027 10129 10296 10439 10452 10501 10543-10545 10679 10777- 10778 10788 10891 10999-11000 11111-11113 11115 11130 11145 11344 11406 11513 11584 11885 12006 12028 12050- 12056 12143 12256 12363 12405 12442 12570 12674 12690 12913 12917 12940 12968-12970 13173 13220-13221 13394 13400 13492 13503 13511 13533 13630 13642 13645 13713 13868 13885 13889 13891
young liver	GIBCO	ALV001	211 498 598 651-653 1008-1014 1193 1264 1575 1976-1977 2131 2161 2254-2255 2269 2363 2568 2617 2627 2633 2636 2961 3021 3059 3093 3166 3215 3272 3356 3378 3426 3479 3559-3565 3590 3597 3627 3634 3673 3709 3797 3810 3885 3993 4006 4011 4019 4025 4194 4246 4253 4277 4422 4426 4431 4434 4437-4438 4634 4654 4687 4714 4722 4755 4773-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			4774 4808 4957 5001 5037 5052 5113-5115 5163 5167 5171 5508 5510 5526 5581 5616 5693 5726 5757 5772 5788 5928 6125 6141-6142 6193 6288 6340-6342 6589 6765 6815 6886 6901 7024 7118 7141 7442 7524 7735 7747-7748 7792 7852 7870 7924 7930 8066 8110 8120 8262 8375 8378 8518 8520 8648 8652 8691 8702 8716-8718 8816 8838-8839 8938-8940 9097 9119 9263-9264 9301 9317 9424 9454-9455 9544 9689 9703 9734 9758 9775 9925 9947 10393 10477 10769 10774 11001 11132 11140-11142 11173 11208 11318 11406 11587- 11588 11725 11804 11902 12081-12086 12118 12160 12178 12375 12377 12405 12424 12479 12511 12570 12599 12601 12618 12670 12674 12688 12737 12830 12913 12916 12933 12953 12977 12993 13047 13062 13073 13126 13169 13174 13230-13231 13295 13488-13489 13494 13498-13499 13502 13506-13507 13575 13592 13646 13660-13662 13670 13866 13868-13869 13882 13888 13901
adult liver	Invitrogen	ALV002	6 25 60 142 598 1004 1213 1296-1301 1381 1493 1513-1514 1977 2139 2161 2269 2310 2335 2342 2400 2413 2449 2458 2497 2568-2569 2576 2636 2809 2827 2880 2926 3471 3484 3503 3597 3722 3792-3796 3885 3994-3995 4025 4060 4201 4326 4422 4426 4618 4689 4767 4786 4985 4998 5093 5163 5337-5339 5511 5526 5581 5693 5701 5724 5726 5757 5895 5922-5923 5979 6020 6027 6083 6125 6192 6195 6253 6333 6346 6483-6485 6716 6765 6797 6975 7169 7422 7468 7614 7642 7807 7932 8089 8110 8140 8262 8323 8378 8633 8677 8711 8740 8759 8786 8834 8839 8944 9002 9128-9129 9264- 9265 9282 9466 9484-9485 9517 9677 9700 9773 10007 10046- 10047 10135 10616 10669 10777 11032 11114 11132 11142 11194 11271 11389 11462 11502 11560 11587 11602 11818 11980 11989 12086 12160 12195 12253-12254 12316 12327 12363 12378-12379 12411 12424 12511 12570 12630 12693 12706 12788-12789 12840 12863 12913-12914 13047 13062 13072-13073 13090 13242 13256 13378-13379 13389 13479 13487 13489 13497 13555 13734-13738 13859 13864 13889
adult liver	Clontech	ALV003	346 2529 3548 3797 3885 4438 4940 5101 5801 5902 9597 10769 10778 11587 11927 12086
adult ovary	Invitrogen	AOV001	6 13 40 67 83 88 142 196 444 522 555-560 577 579 598 609 654-657 659-665 667-668 708 740 745-749 751-754 756-761 806 841 871 1004 1023 1028-1034 1036-1039 1041-1047 1055 1087-1115 1119 1151-1162 1298 1346 1359 1456 1493 1507 1516 1658 1697 1752 1774 1812 1826 1848 1914 1974 1976- 1977 1979 1983 2099 2111 2138 2153-2155 2161 2175 2180- 2181 2186 2258-2267 2284-2286 2288-2290 2298-2299 2342- 2343 2449 2483 2523 2529 2555 2569 2576 2591 2597 2618 2708 2750 2783 2818 2839 2926 2961-2962 2988 3007 3022 3031 3060-3061 3063 3069 3166-3172 3174-3175 3177-3189 3226 3272 3286 3288-3289 3291-3293 3295-3299 3435 3450 3460 3479 3486 3503 3535 3577-3589 3612 3627 3629 3631- 3643 3673 3675 3720 3722 3737 3797 3806 3810 3812-3813 3839 3885 3985 4006 4012-4014 4023 4025 4040 4043 4060 4078 4133 4192 4194 4201 4246 4269 4277 4282 4341 4362 4381 4383 4385 4388 4390-4391 4396 4399 4402 4405 4410 4434 4465 4473 4515 4543 4582 4610 4654 4689 4694 4715- 4717 4722 4759 4767 4775-4782 4836-4837 4873-4878 4880 4940 4944 4957 4960 4962-4964 4972 4975 4981 4985 4998 5001-5002 5018 5030 5037 5040 5045 5075-5076 5093 5108 5135-5136 5138-5146 5148 5163 5191-5209 5213 5238-5245 5262 5374 5380 5451 5455 5490 5503 5505 5521 5523 5527 5560 5581 5674 5701 5724 5757 5778 5783 5788 5794 5817 5874 5894-5895 5902 5906 5908-5909 5916-5917 5923 5952 5938 5979 5989-5990 6005 6027 6048 6054 6057 6061 6078

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			6082 6086 6125 6140 6143-6144 6165 6171 6192 6194-6200 6215 6235-6239 6241 6270 6288 6307 6333 6336 6354-6360 6362-6364 6374 6385-6392 6410 6412 6415-6417 6458 6461 6508 6555 6583 6595 6598 6604 6607 6624 6626 6629 6708 6765 6767 6793 6797 6799 6801 6805 6825 6860 6870-6871 6873 6886 6888 6900 6902-6904 6915-6917 6947 6969-6970 6975 6980-6987 6998 7054 7058 7104 7109 7118 7133 7137 7141 7155 7166 7169 7171 7191 7204 7281 7386 7408 7431 7443 7468 7471-7472 7494 7507 7525-7528 7604-7609 7614 7642 7687 7716 7729 7762-7763 7765-7767 7769-7771 7773- 7775 7788 7802-7818 7829-7835 7838-7841 7864 7905 7937 7977 8007 8035 8077 8088 8093 8095 8110 8120 8134 8139- 8140 8143 8156 8235 8246 8262 8292 8320 8336 8345 8355 8358 8363 8365 8368 8370 8372 8375 8387 8444 8452 8456 8486 8520 8593 8610 8633-8634 8653 8719-8724 8773-8777 8779 8781-8782 8792 8798 8813 8830 8839 8853 8863 8870 8876 8898 8928 8944 8950 8956-8961 8963-8971 8989 9004- 9007 9009-9019 9042-9046 9055 9076 9097 9128 9134 9185 9264 9283-9284 9291 9313 9358 9424 9445 9454-9455 9457 9460 9466 9471-9472 9475 9480 9511 9517 9533 9539 9542 9544 9553 9565 9577 9586 9612 9626 9677 9694 9703 9722 9734 9757-9758 9773 9776-9778 9791 9812-9819 9827 9838 9843 9848-9853 9922 9927-9940 9942 9962-9970 9989-9992 9994-9997 10007 10027 10097 10149-10152 10249 10252 10275 10298 10333-10334 10346 10349 10351 10383 10386 10417 10438-10439 10452 10459 10470 10478-10480 10493- 10498 10557-10562 10564-10565 10580-10586 10594-10596 10645 10658 10676 10679 10767 10772 10774 10778 10782 10788 10791 10954 10971-10972 11002-11004 11032 11047- 11052 11061 11069 11083 11108 11130 11132 11151-11153 11155 11157-11158 11167 11170 11172-11176 11193-11196 11274 11343 11369 11406 11411 11431 11588 11596 11600 11604 11606-11607 11618 11620-11621 11629 11668 11814 11860 11865 11876 11903-11909 11932 11949-11954 11980 11985 12000 12006 12017 12022 12033 12039 12080 12083 12092-12093 12095-12104 12127-12129 12131-12142 12146 12159-12160 12162-12163 12178 12213 12216 12236 12256 12260 12305 12327 12363 12368 12371 12375 12379 12387 12401-12402 12405 12424 12430 12467 12520 12522 12546 12570 12576 12590 12594 12599 12605 12609 12611 12615 12617-12618 12630 12636 12643 12657-12658 12663 12670 12674 12685 12688 12691 12693 12702 12705-12707 12713 12724 12729 12735 12740-12745 12749 12754-12760 12765- 12770 12777 12842 12848 12875 12904 12906 12910 12913 12916-12917 12935 12940 12955 12957 12963 12972 12977- 12980 12982-12984 12992-12994 12997-13000 13020 13034 13047 13051 13054 13056 13060 13062 13066 13070 13072- 13073 13075 13082 13090 13092-13093 13104 13126 13136 13141 13175-13177 13179-13180 13193-13194 13196-13197 13202 13236-13241 13243 13245 13249 13254 13263-13275 13277 13286-13292 13295 13319 13351 13377 13389-13391 13394 13420 13436 13456 13477 13479 13488 13492 13494- 13495 13497-13499 13502-13503 13506 13512 13516 13533 13546 13549 13554-13555 13575 13590 13597 13600-13601 13613 13616-13620 13627 13631 13644-13645 13649 13659- 13660 13670 13674-13679 13693-13699 13707-13709 13713 13782 13803 13864 13866 13868-13869 13872 13875 13882- 13885 13888-13889 13892
adult placenta	Clontech	APL001	669-671 1006 1134 1184 1551 2053 2090 2156-2158 2342 2490 2716 3001 3064-3065 3190 3272 3625 3670 4019 4055 4194 4201 4246 4641 4718 4720-4721 4783-4786 4957 5523

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			5536 5581 5788 5895 6145-6146 6201-6202 6358 6803 7049 7204 7529 8367 8375 8609 8611 8630 8725-8727 9097 9480 9734 9820 10319 10460 10579 10795 10895 11519 11723 11737 11776 11827-11828 11959 12403 12546 12570 12663 12848 12875 12913 13051 13394 13782 13869 13889
placenta	Invitrogen	APL002	142 561 1023 1551 1976 2449 2569 2614 3191 3340 3592 3668 4060 4346 4767 4787-4789 4892 4985 5536 5674 5693 5757 5772 5794 5906 6147 6203 6215 6598 6788 6799 6979 7158 7530-7531 8139 8361 8611 8863 9457 9484 9517 9563 9703 9758 9821 9927 9939 9942 10481 10557 10778 10802 10973 11006-11011 11723 11731 11737 11776 11807 11866 11910- 11916 11959 12379 12403 12590 12685 13020 13054 13392 13489 13533 13554-13555 13867 13882 13888 13891
adult spleen	GIBCO	ASP001	463 499 562-563 598 672 990-993 995 1004 1020 1346 1515- 1516 1556 1774 1877 1914 1977 2159 2161 2215 2248 2257 2363 2529 2569 2614 2617 2812 2827 3093 3192 3195 3199 3272 3286 3350 3356 3434 3470 3503 3537 3544-3546 3548 3604 3634 3689 3709 3720 3722 3796-3798 3812 3839 3885 4006 4011 4022 4025 4043 4194 4201 4246 4253 4277 4388 4391 4396 4405 4434 4641 4689-4690 4781 4957 4987 4998 5001 5017 5030 5037 5052 5076 5118 5512-5513 5523 5526 5701 5740 5778 5788 5796 5801 5895 5938 6005 6064 6125 6140 6147 6192 6204 6272 6329 6458 6551 6590 6607 6873 6886 6931 6958 7018 7058 7109 7118 7133 7171 7233 7506 7532-7533 7561 7586 7733 7736 7807 7842 7845 7933 8065 8085 8093 8095 8110 8116 8139-8140 8226 8235 8262 8323 8359 8363 8365 8368 8372 8456 8535 8648 8702 8792 8816 8838-8839 8858 8863 8865 8876 8923-8928 8943 8950-8951 9128 9257 9264 9317 9455 9457 9466 9474 9544 9560 9773 9781 9919-9920 9927 9939 9942 10000 10048-10049 10155 10175 10267 10275 10296 10331 10549 10566 10774 10777 10828 10944 11032 11061 11108 11113 11132 11173 11272 11401 11406 11620-11621 11804 11818 11861 11917 12006 12039 12041 12073-12074 12078 12118 12127 12236 12327 12375 12387 12402 12405 12424 12426 12511 12546 12560 12570 12601 12617-12618 12670 12674 12734-12735 12749 12772 12790 12913 12916-12917 12972 12977 13002 13021 13066 13082 13084-13085 13169 13228-13229 13256 13260 13295 13316-13317 13394 13456 13488-13489 13494 13497 13512 13516 13546 13645 13649 13651 13659 13679 13739 13776 13864 13866-13867 13888
testis	GIBCO	ATS001	50 142 500-502 564-565 598 673-678 963-968 1193 1346 1556 1671 1826 1968 1977 2160-2161 2236-2237 2555 2590 2597 3024 3093 3196-3202 3284 3378 3517-3522 3524 3720 3797 3839 3885 4006 4025 4055 4109 4253 4354 4377 4388 4405 4434 4473 4480 4543 4688 4792 4940 4957 4962 4964 4975 5001 5018 5030 5037 5067-5072 5076 5118 5171 5481 5525 5535 5740 5757 5788 5907 5924 6125 6147 6257 6316-6322 6324 6607 6886 6952 7058 7141 7288 7445 7484 7534-7540 7677 7710-7711 7713-7717 7735 7792 7815 8087 8110 8120 8262 8368 8370 8375 8535 8577 8648 8655 8702 8729 8838- 8839 8848 8898-8906 8936 8939 8966 9076 9087 9244 9264 9304 9455 9466 9485 9542 9567 9703 9758 9822-9825 9908- 9910 9928 10462 10475 10478 10482 10551 10583 10679 10772 10778 10795 10955 10974 11108 11113 11116 11118- 11120 11132 11173 11239 11425 11606 11620 11629 11695 11807 11862 11918-11919 12000 12006 12017 12033 12057- 12061 12375 12405 12424 12570 12577 12599 12601 12605 12609 12668 12692 12730-12731 12748 12904 12917 12923 12929 12935 12940 12956 12971 13047 13051 13073 13090 13169 13222-13225 13249 13394 13442 13456 13479 13494

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			13497 13502-13503 13506 13512 13515 13533 13549 13555 13575 13613 13616 13627 13644-13646 13660 13866 13875 13882 13889
Genomic DNA from BAC 63118	Research Genetics (CITE BAC Library)	BAC001	8711
adult bladder	Invitrogen	BLD001	731 1710 1779-1791 2076 2367 2479-2481 4067 4208-4214 4681 4767 4775 5163 5169 5553 5560 5581 5674 5684-5688 5794 6082 6244 6716 6718-6721 6799 6931 7045 7094-7097 7967 8110 8226 8249-8258 8364 8648 8737 9012 9097 9425- 9428 9430 9626 9703 9928 10007 10261 10557 10734-10735 11459 11504-11506 12000 12212 12512-12513 12515-12517 12670 12735 12914 13085 13439 13512 13687 13838-13841 13866
bone marrow	Clontech	BMD001	11 70 83 85 142 150 162-184 186-198 200-210 230-243 245- 277 279-281 306 370 373-387 389 433-435 438-440 457 483 503-510 566 568-569 595-596 598 609 616 679-683 740 770 843-857 859 861 864 867-876 880-884 886-890 892-893 896 900 902-920 1000 1004 1116-1120 1122-1126 1128-1134 1184 1211 1346 1359 1516 1552-1554 1575 1583 1671 1724 1774 1877 1894 1927 1974 1976 1983 2012-2024 2031 2033-2038 2040 2043-2044 2084-2088 2111 2120-2121 2132-2133 2137- 2138 2161 2163-2164 2186 2189 2199-2200 2202-2203 2205- 2210 2213-2218 2266 2291-2295 2342-2343 2414-2416 2444 2529 2555 2566 2569 2575-2576 2591 2597 2652 2681-2709 2711-2716 2735-2738 2740-2744 2746-2748 2750-2756 2758- 2759 2761-2764 2766-2768 2770 2772-2781 2783-2787 2806 2812-2813 2816 2873 2875 2880-2881 2883-2885 2887-2897 2899 2901 2926 2948 2954 2958 2977 2984 3026-3029 3032 3068-3069 3071 3081 3093 3096-3097 3139 3203-3205 3207 3238 3257 3272 3282-3283 3286 3317 3345 3356 3404-3418 3422-3434 3437-3438 3440 3442 3447 3449-3450 3456-3459 3461-3464 3466-3473 3483 3497 3535 3538 3548 3557 3572 3588 3593 3600 3604-3605 3610 3612 3625-3627 3634 3644- 3647 3649-3651 3653-3657 3709 3711 3722 3725 3727 3737 3797 3804 3808 3810 3839 3899 4005-4006 4011 4015-4019 4023 4025 4040 4043 4058 4060 4129 4132 4192 4194 4201 4246 4253 4277 4282 4367 4403 4466-4472 4474-4477 4479- 4484 4486-4490 4492-4497 4509 4512-4540 4582 4595 4597- 4606 4608-4615 4622 4642 4648 4650 4654 4667 4691-4695 4723 4741-4742 4759 4767 4783 4794-4796 4808 4836 4928- 4929 4931-4934 4938 4940 4942 4944-4948 4950-4953 4955- 4960 4962-4964 4967-4971 4973 4976-4979 4985-4987 4992- 4998 5000 5004-5016 5030 5037 5052 5075-5076 5093 5143 5149-5151 5163 5169 5210-5215 5217-5226 5262 5317 5357 5503 5523 5535 5537-5540 5560 5604 5695 5740 5748 5766 5788 5796 5801 5862 5874 5895 5906 5908 5938 5965-5967 5969-5979 5991-5994 5996-6005 6007-6009 6027 6047 6057 6065 6067-6068 6071-6072 6082 6086 6089-6091 6112 6125- 6127 6148-6152 6195 6214 6233 6257 6269-6276 6278-6280 6282-6283 6285-6289 6292-6300 6321 6374 6393-6403 6508 6555 6605 6607 6722 6730 6788 6815-6822 6826-6832 6836 6859-6861 6867 6870-6871 6873-6874 6905 6915 6929 6933- 6937 6940-6942 6944-6945 6988-6992 7051 7126 7155 7166 7169 7199-7210 7212-7219 7226 7233-7253 7256-7264 7275 7317-7318 7320 7322-7326 7347 7349 7373-7374 7379 7382 7446-7448 7473-7474 7491 7502 7542 7544 7569 7577 7579 7663-7671 7674 7677-7678 7680-7684 7686 7689-7696 7742 7768 7791 7815 7819-7824 7847 7864 7930 7995 8065 8085

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			8088 8090-8093 8095 8110 8120 8134 8139 8224 8226 8235 8241 8246 8262 8336 8354 8359 8363 8365 8368 8375 8421- 8427 8429-8440 8444 8452 8456-8460 8463-8465 8467-8476 8478-8489 8538-8539 8542-8551 8563 8566 8577 8593-8595 8597 8603 8633 8635-8637 8648 8656-8657 8671 8677 8679 8701 8792 8796 8817 8830 8840-8845 8847-8849 8852 8855- 8860 8863-8868 8870 8873 8875 8879-8881 8898 8935 8944 8963 8965 8995 9010 9012 9020-9031 9049 9051 9066 9076 9092 9097-9098 9128 9257 9264 9285-9288 9304 9317 9339 9381 9399 9401 9454-9455 9466 9471-9472 9474-9476 9516- 9517 9519 9529 9544 9622 9630-9643 9646 9650-9665 9689 9705-9712 9730 9734 9740 9758 9779-9781 9826 9885-9889 9892-9902 9928-9929 9939 9942 9972-9976 9978-9982 9999- 10000 10068 10153 10175 10249 10275 10277 10284 10287 10296 10319 10321 10343-10344 10346 10364-10374 10379- 10382 10385-10394 10414 10416 10426 10429 10439 10447 10452 10467-10468 10475 10483 10520 10522-10526 10528- 10529 10531-10535 10587-10590 10595 10616 10677-10679 10691 10750 10760 10767 10772 10778 10788 10794-10795 10828 10831-10837 10846-10847 10849-10851 10853-10858 10891 10895 10897 10899-10903 10905-10907 10931-10933 10956-10959 10975-10976 11012 11032 11046 11057 11059 11061 11077-11082 11085-11086 11088-11098 11108 11113 11132 11145 11177-11181 11194 11208 11289 11344 11401- 11402 11513 11618 11620 11631 11673-11675 11677-11690 11695 11697-11704 11706 11708-11715 11736 11742 11762- 11772 11774 11795-11796 11802-11804 11817-11818 11829 11839-11842 11863 11920 11946 11992-12002 12004-12008 12010 12012-12013 12015-12019 12022-12029 12033 12041 12081 12142-12149 12160 12178 12195 12200 12231 12236 12283 12305 12308 12316 12327 12363 12368 12404-12405 12424 12426 12430 12439 12527 12546 12570 12576 12590 12608 12610 12616 12634-12636 12641-12645 12654-12655 12657-12659 12669-12670 12674 12721-12724 12754 12761 12834 12840 12842 12904-12905 12910-12911 12913 12916- 12917 12922-12923 12925-12928 12933 12938 12956 12966 12977 12989-12990 12993 12995 13020 13033 13047 13060 13062 13064 13066 13095 13098 13103-13105 13107 13111- 13113 13129 13135 13137 13141 13150 13163 13173 13181 13213-13217 13234 13276-13278 13280 13391 13394 13400 13456 13472 13477 13490 13492 13494 13498 13501-13502 13506-13507 13511 13516 13528 13530-13534 13538 13540 13546 13551-13552 13554-13555 13560 13585-13586 13594 13613 13630 13633-13639 13644-13646 13649 13659-13660 13670 13673 13679 13713 13775 13795 13866 13872 13875 13882-13885 13889 13891 13893
bone marrow	Clontech	BMD002	51 242 442 654 1004 1134 1841-1904 1908 1927 2023 2107 2215 2342 2408 2507-2529 2576 2597 2806 2866 3286 3434 3722 3736-3737 3817 3823 3839 4060 4246 4258-4290 4389 4396 4411 4618 4641 4828 4836 4957 4987 5030 5037 5052 5108 5163 5526 5711 5743-5772 5774-5804 5813 5895 5939 6131 6236 6266 6287 6306-6307 6333 6655 6675 6728 6730 6750-6762 6764-6769 6788 7049 7106-7117 7137 7156 7738 8068 8085 8134 8156 8290-8297 8299-8305 8307-8312 8323 8368 8482 8499 8858 8863 8865 8928 8935 9076 9111 9128 9465-9502 9626 9700 9703 9923 9928-9929 9942 10277-10280 10282-10284 10286-10297 10396 10434 10515 10551 10645 10675 10691 10744-10753 10772 10778 11057 11098 11108 11132 11232 11252 11519 11536-11553 11606 11620 12033 12039 12146 12260 12305 12387 12402 12405 12500 12554- 12578 12594 12599 12608 12674 12754 12777 12839 12895-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12904 12916 12923 13020-13021 13043 13057-13064 13169 13249 13446-13454 13479 13492 13494 13513 13533 13555 13659 13713 13775 13803 13863-13875 13877-13887 13889 13891
bone marrow	Clontech	BMD004	2249 2529 3286 3494 3548 3551 3797 3839 4025 4058 4201 4277 4282 5052 5108 6545 6961 8262 8898 9474 10000 11098 11818 13021 13893
bone marrow	Clontech	BMD007	8539 9780 9927 13021
adult colon	Invitrogen	CLN001	319 346 487 731 799 1792 1848 2050 2161 2449 2482-2483 3431 3901 4215-4217 4940 4957 4987 5163 5239 5560 5689-5695 5865 5911 5923 6722 6765 7098 7815 7864 7880 8110 8259-8262 8486 8597 8951 9484 9529 9542 9556 10376 11507-11508 11617 11869 12127 12236 12424 12518-12523 12601 12610 12777 12976 13062 13073 13367 13440 13507 13512 13630 13713 13843-13844 13864 13868-13869 13888
Mixture of 16 tissues - mRNAs*	Various Vendors*	CTL016	6815 10776 12977 13064 13512
Mixture of 16 tissues - mRNAs*	Various Vendors*	CTL021	1671 6738 8432 8648 8863 8944 9511 10769 13021 13062 13064
adult cervix	BioChain	CVX001	50 67 142 158 308 332 346 475 598 654 895 1004 1086 1286 1449 1516 1671 1698 1701 1711-1756 1758-1776 1828 1848 1959 2134 2186 2257 2267 2343 2408 2414 2468-2474 2476-2478 2608 2716 3002 3136 3166 3191 3199 3529 3535 3554 3572 3627 3722 3737 3777 3797 3839 3985 4158-4176 4178-4195 4197 4199-4207 4246 4277 4391 4396 4434 4641 4667 4759 4783 4828 4885 4940 4957 4963 4987 4998 5001 5038 5075 5108 5163 5293-5294 5455 5481 5523 5552 5581 5646-5652 5654-5659 5661-5671 5673-5681 5687 5701 5711 5723 5740 5788 5794 5848 5902 5908 5925-5924 5964 6020 6052 6057 6062 6091 6106 6112 6125 6129 6181 6350 6371 6374 6410 6446 6458 6504 6508 6512 6551 6598 6686-6687 6689-6705 6707-6715 6788 6873 6893 6917 6998 7008 7045 7078 7084-7093 7095 7130 7141 7148 7169 7204 7507 7579 7608 7675 7733 7768 7815 7871 7880 7893 8078 8138 8209-8215 8217-8236 8238-8242 8244-8248 8298 8345 8370 8444 8456 8486 8499 8535 8558 8592 8633 8635 8648 8669 8679 8742 8853 8863 8870 8898 8921 8939 8948 9012 9061 9098 9107 9128 9137 9153 9304 9308 9317-9318 9355 9385-9391 9393-9403 9405-9406 9408-9418 9420-9422 9457 9466 9475 9510 9539 9612 9734 9773 9927-9928 9939 9947 9960 10110 10175 10230-10256 10258-10259 10267 10274 10319 10329 10344 10491 10496 10540 10616 10660 10691 10722-10732 10778 10782 11055 11145 11217 11376 11462 11477-11489 11491-11503 11519 11584 11604 11695 11853 11869 11891 11980 12006 12066 12081 12127 12160 12195 12216 12240 12266 12308 12363 12379 12402 12405 12424 12438 12483-12494 12496-12510 12579 12605 12610-12611 12617-12618 12643 12653 12670 12674 12688 12691 12703 12707 12735 12740 12754 12830 12840 12866 12870-12881 12883-12884 12905

* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12913-12914 12917 12923 12951 12955 12957 12965 12989-12990 12993 13002 13020 13035 13045-13050 13062 13064 13072 13092 13136 13141 13174 13197 13254 13283 13307 13391 13428 13430-13437 13442 13473 13479 13492 13494-13495 13497-13498 13502 13532 13554-13555 13575 13590 13597 13613 13616 13627 13644 13679 13713 13775 13829-13837 13866 13868-13869 13872 13884 13888 13891
diaphragm	BioChain	DIA002	731 1346 3548 3711 3885 4282 4654 5895 6875 8120 8931 8936 9455 11132 11818 12405 12609
endothelial cells	Strategene	EDT001	21 51 67 83 332 569 598 609 762 796 1004 1024-1026 1086 1561 1848 1928 1959 1976-1977 1983 2138 2161 2166 2257 2282-2283 2417 2483 2490 2555 2569 2614 2926 3042 3189 3191 3272 3300-3303 3426 3494 3503 3548 3574-3576 3605 3627-3628 3673 3709 3720 3722 3737 3797 3839 3885 4005 4011 4019 4055 4133 4192 4246 4269 4282 4340 4354 4365 4384 4388 4399 4405 4410-4411 4434 4545 4641 4654 4767 4797-4799 4802 4881-4882 4885-4886 4888 4940 4957 4964 4972 4985 4998 5002 5017 5030 5076 5103-5104 5132-5133 5163 5167 5183-5185 5187-5190 5380 5523 5527 5535 5541-5542 5544 5674 5684 5693 5724 5766 5778 5788 5794 5796 5874 5895 5916 5923 5928 5938 6005 6048 6057 6068 6082 6165 6205 6215 6240-6241 6307 6321-6322 6349-6353 6383 6458 6595 6598 6606-6607 6765 6799 6805 6815 6860 6871 6873 6890 6918 6968 6972 6976 6979-6980 6998 7058 7067 7104 7113 7116 7137 7139 7169 7275 7468 7613 7716 7755-7757 7759-7760 7797 7799-7801 7930 8077 8084 8093-8095 8120 8139 8235 8262 8320 8323 8335-8336 8345 8354 8358 8363-8364 8370 8372 8375 8387 8452 8592 8648 8786 8788 8792 8813 8863 8898 8944-8955 8965 8996-9001 9051 9076 9097 9128 9264 9289-9291 9304 9315 9414 9455-9456 9466 9472-9473 9475 9484 9504 9517 9529 9542 9563 9570 9626 9703 9780-9781 9843 9927 9939 9961 10000 10027 10154 10267 10285 10321 10330-10331 10342 10344 10349 10496 10500 10550 10556-10557 10579 10679 10772 10776 10778 10788 10795 10802 11013 11132 11136 11146-11149 11406 11483 11565 11588 11600 11606-11607 11615 11626 11807 11818 11932 11955 12006 12034 12037 12041 12044 12078 12092-12094 12123-12126 12150 12213 12375 12381 12387 12405 12411 12424 12426 12522 12570 12576 12590 12601 12610 12612 12615 12617-12618 12663 12670 12674 12707 12729 12739 12749 12753-12754 12777 12830 12842 12913-12914 12916 12918 12929 12940 12972 12975-12977 13002 13024 13047 13051 13054 13062 13064 13082-13084 13090 13092 13094 13123 13126 13136 13195 13235 13263 13380 13389 13392 13394 13400 13456 13479 13488-13489 13492 13494-13499 13502 13506-13507 13514 13516 13546 13555 13568 13575 13590 13592 13613 13616 13621 13630 13649 13659-13660 13667-13668 13670-13673 13678-13679 13690-13692 13713 13796-13797 13838 13866-13869 13872 13882 13884 13888 13893
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	150 2023 2327 2490 4109 4783 5503 5560 10267 10760 12017 12160 12557 12582 12923 13020 13514
Genomic clones from the short arm of chromosome	Genomic DNA from Genetic Research	EPM003	5560 12017 12146

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
8			
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM004	4783 4798 5560 10817 11926 12017 12160
esophagus	BioChain	ESO002	999-1000 2449 3272 3315 3548 3550 3634 3697 3796 4011 4025 4058 4201 4282 5106 5163 5553 6082 6873 7739 9304 10296 11133 11818 12033 12570 13869
fetal brain	Clontech	FBR001	51 142 1184 3664 4060 4109 4940 5021 5270 5523 5553 6112 6805 6908 7294 8558 9457 10376 11059 11985 12006 12122 12160 12754 13438 13507 13888
fetal brain	Clontech	FBR004	60 2704 3711 4025 4109 4783 5001 6082 7597 9010 9504 9949 11837 12033 12039 12363 12705 12905 13020 13503 13512 13891
fetal brain	Clontech	FBR006	6 60 67 598 800 932 1004 1170 1793-1794 1796-1797 1799-1805 1905-1914 1916-1958 1974 1976 1979 1983 2057 2129 2174 2221 2407 2444 2449 2484-2492 2530-2554 2556-2561 2563 2576 2857 3064 3207 3479 3556 3673 3709 3722 4060 4078 4157 4218-4221 4223-4224 4277 4291-4334 4338 4355 4364 4369 4431 4957 5001 5109 5270 5380 5553 5634 5696-5706 5711 5724 5766 5788 5794 5801 5805-5832 5834-5879 5882-5901 5936 5990 6057 6723-6732 6765 6770-6791 6797 6805 6894 7049-7050 7100-7102 7105 7118-7123 7125 7127 7169 7905 8263-8265 8267-8273 8294 8312-8333 8359 8361 8375 8452 8633 8664 8740 8757 8884 9010 9111 9432-9436 9503-9516 9518-9545 9547-9551 9556 9570 9577 9780 9895 9923-9924 9928 9942 10007 10027 10202 10263-10268 10276 10284 10298-10310 10329 10331 10496 10542 10595 10621 10736-10737 10755-10761 10772 10774 10795 11108 11132 11406 11483 11509-11523 11555-11582 11589-11590 11600 11606 11621 11713 11729 11807 11837 12006 12039 12044 12092 12113 12218 12231 12236 12327 12363 12398 12405 12465 12511 12524-12530 12576-12577 12579-12601 12729 12735 12754 12863 12869 12889 12906-12910 12914 12954 12973 13020-13021 13051-13052 13054 13065 13082-13083 13427 13445 13455-13470 13488 13490 13496 13498-13501 13507 13516 13560 13613 13630 13649 13708 13713 13769 13831 13845-13855 13868 13872 13882 13884 13888-13894 13896-13900
fetal brain	Clontech	FBRs03	1005 4405 5111 6337 6964 7742 13084 13864 13891
fetal brain	Invitrogen	FBT002	51 83 142 321 430 746 932 1054 1058-1065 1493 1833 1947 2273-2275 2299 2444 2449 2926 3479 3492 3885 4347 4354 4391 4405 4410 4434 4530 4804 4985 4998 5075 5160-5169 5380 5428 5466 5750 5788 5801 5895 6132 6215 6371-6374 6458 6598 6973-6974 7067 7096 7776-7778 7780-7782 7937 8143 8323 8361 8364 8372 8377 8452 8633 8977-8984 8986 9010 9142 9264 9332 9457 9474 9503 9511 9517 9539 9582 9827 9848 9927 9950-9953 10027 10161 10329 10430 10492 10573-10575 11014 11160-11164 11406 11628 11742 11814 11830 11985 12092 12112-12114 12116-12117 12127 12424 12511 12521 12570 12576 12643 12696 12735 12748-12751 12754 12830 12835 12913 12957 12977 12990 13002 13020 13062 13072 13083 13117 13254-13259 13377 13486 13489 13496 13499 13507 13590 13649 13685-13688 13713 13867 13888 13891 13893
fetal heart	Invitrogen	FHR001	1001 1004 2250 4025 6334 6765 7740 8933 8935 9457 9544 10000 11132 12599 12609 13021 13568 13656 13866
fetal kidney	Clontech	FKD001	142 346 364 511-517 570-572 574 598 685-690 969-970 972-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			981 983-987 1134 1346 2123 2167-2169 2238-2246 2342 2444 2483 2516 2555 2617 2728 2843 2876 3032 3049 3072 3206 3208 3282-3283 3525-3531 3533-3543 3548 3591 3709 3722 3797 3839 3878 4015 4019 4043 4246 4277 4367 4405 4696-4698 4725 4767 4805-4810 4940 4947 4957 4986 4998 5037 5056 5073-5080 5082-5091 5099-5100 5108 5258 5504 5523 5560 5923 6005 6207-6208 6225 6272 6288 6325-6332 6478 6603 6702 6793 6815 6906 6953-6959 7045 7058 7204 7355 7426 7449-7450 7520 7543-7546 7561 7587 7718-7732 7930 8077 8097 8262 8375 8387 8452 8520 8638 8658 8736-8737 8834 8863 8898 8907-8918 8922 8950 9010 9134 9257 9401 9457 9544 9597 9760 9781 9791 9828-9830 9912 9914-9918 10296 10440 10484 10546-10548 10772 11108 11121-11129 11131-11132 11170 11513 11638 11695 11923-11924 12006 12033 12062-12070 12072 12160 12405 12522 12570 12594 12599 12605 12626 12663 12670 12732-12733 12749 12848 12904 12914 12940-12941 12990 13020 13083 13188 13226-13227 13234 13263 13277 13280 13351 13391 13394 13491 13501 13512 13590 13644 13647-13650 13713 13782 13867-13868 13872 13875
fetal kidney	Clontech	FKD002	3286 5030 5037 5105 11108 12033 12490 12570 13494 13866
fetal kidney	Invitrogen	FKD007	3272 3806 4025 4253 4277 4654 5112 5535 5788 5801 8863 8935 9401 9466 10553 11628 11818 13494 13646 13866
fetal lung	Clontech	FLG001	79 2367 2395 3010 3460 3885 4828 4948 4962 5001 5723 5748 5902 5908 6186 6738 7051 7067 7677 7759 9264 9553 9700 10007 10478 11098 12017 12383 12417 12424 12749 12917 13020 13169 13472 13554 13644 13782 13835
fetal lung	Invitrogen	FLG003	142 319 364 629 1671 1806-1814 1816-1819 1877 2129 2161 2169 2367 2449 2493 2529 3191 3503 3610 4109 4225-4234 4367 4434 4957 5108 5380 5421 5581 5707-5710 5712 5714 5788 5801 6057 6733-6741 7034 7103 8274-8278 8365 8597 8948 9264 9327 9437-9442 9444 9466 9510 9525 9530 9539 9677 9773 9841 10007 10190 10198 10269-10271 10329 11519 11524-11527 11927 12531-12539 12848 12890 12904 13021 13072 13249 13445 13472 13489 13551 13575 13649 13670 13679 13856-13857
fetal lung	Clontech	FLG004	1003-1004 2597 5110 6963 9924 10552 11138-11139 12080 12990 13659
fetal liver-spleen	Columbia University	FLS001	-2,4-14 16-22 24 26 28-31 33-46 48-49 51-61 63-68 71-91 93-102 104-110 112-124 126-156 158-162 282-283 285-290 292-299 301-304 307-312 314-326 328-338 340-344 346-353 355-365 369 390-400 402 436 441 483 557 567 575-585 595 598 629 673 678 691-699 701-702 708 731 736 763-767 769-776 778-786 788-791 793-794 796 925 975 1004 1015 1023 1038 1068 1104 1134 1144 1184 1192 1216 1264 1298 1346 1482 1493 1516 1518-1521 1551 1556 1575 1583 1594 1636 1641 1707 1724 1774 1826-1829 1841 1858 1927 1959 1962-1965 1967-1972 1974-1979 1981-1998 2000-2009 2011 2045-2051 2053-2055 2057-2058 2060-2063 2065-2083 2089-2094 2100-2101 2161 2170 2174 2184-2194 2215 2222 2269 2290 2310 2342 2409 2411 2414 2444 2449 2458 2483 2490 2497-2498 2510 2516 2523 2529 2555 2562 2566-2576 2578-2586 2588-2591 2593-2601 2604 2607-2608 2611-2612 2614-2618 2620 2622-2642 2644 2646-2653 2655-2664 2666 2668 2670-2680 2696 2750 2788-2793 2795-2811 2814-2826 2828-2835 2837-2842 2844 2846-2848 2851-2858 2860 2862-2871 2876 2878 2893 2900-2905 2907-2909 2926 2929 2949 2952-2953 2959-2960 2984 2992 3032 3058 3069 3073-3076 3078-3080 3082 3093 3166 3194 3196 3207 3210-3211 3213-3214 3217-3225 3249 3257 3272 3282 3286-3287 3304-3307 3310-3311 3314-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			3317 3319 3321-3332 3334-3346 3356 3419 3426 3434 3446 3450 3455 3468 3470 3479 3484 3494 3503 3535 3537 3548 3552 3557 3572 3590 3594 3597 3604-3605 3610 3612 3625 3627 3634 3668 3670 3709 3711 3720 3722 3729 3737 3777 3797 3806 3808 3810 3813 3839 3885 3926 3990 3996-3997 4006 4009 4011 4019-4022 4025 4040 4043 4060 4078 4095 4109 4129 4192 4194 4201 4245-4246 4253 4261 4277 4282 4297 4335-4338 4340-4357 4359-4361 4364 4366-4367 4370- 4372 4374-4377 4379-4382 4384-4386 4388-4392 4395-4396 4398-4414 4417-4424 4426-4455 4457-4458 4460-4465 4542- 4543 4545 4547-4553 4555-4562 4565-4575 4577 4579 4581- 4582 4585-4588 4593 4596 4607 4616-4629 4644-4645 4647 4654 4671 4676 4687 4689 4694 4721 4726-4729 4759 4767 4775 4783-4784 4788 4790-4791 4811-4819 4830 4837 4845 4862 4874 4889-4902 4930 4940 4948-4949 4957 4962-4965 4972 4985 4998 5022 5029-5030 5037 5040 5075-5076 5092 5108 5132 5152 5163 5167 5171-5172 5335 5380 5398 5473 5503 5514 5516 5523 5526-5527 5535-5536 5553 5581 5598 5604 5616 5674 5684 5691 5693 5711 5715 5724 5726 5748 5750 5757 5778 5788 5794 5801 5817 5865 5874 5894-5895 5902-5914 5916-5919 5921-5928 5930-5949 5951-5954 5956- 5964 5966 5979 6005 6010 6013-6015 6017-6018 6020-6022 6024-6025 6028-6032 6034-6048 6052-6062 6064 6068 6073- 6081 6086 6092-6094 6104 6112 6125 6135 6140 6147 6149 6153-6157 6165 6186 6195 6209-6211 6240-6241 6243-6248 6250-6253 6272 6276 6287-6288 6307 6313 6338 6371 6374 6419 6430 6446 6451 6458 6478 6496 6508 6545 6579 6595 6598 6607 6611 6624 6629 6642 6658 6695 6726 6728 6730 6738 6745 6754 6765 6767 6788 6793-6797 6799-6808 6810- 6815 6833-6843 6845-6847 6850-6856 6858 6860 6862-6865 6870-6871 6875 6877 6891 6893-6894 6900 6907-6908 6917 6919-6925 6950 6979 7049 7058 7067 7077 7096 7109 7116 7118 7128-7131 7133-7135 7137-7141 7144-7147 7149-7150 7152-7153 7155-7179 7181-7192 7194-7198 7265-7271 7273- 7280 7282-7305 7307-7312 7316 7327-7336 7375-7376 7383 7386 7451 7455 7468 7473 7475-7477 7479 7484 7548-7553 7555-7558 7561 7608 7617-7618 7620-7631 7642 7675 7687 7695 7716 7768 7809 7811 7839 7842 7864 7883 7933 7977 8069 8093 8095 8105 8110 8116 8139 8224 8226 8235 8241 8262 8323 8334-8340 8342-8350 8352-8355 8357-8359 8361- 8408 8410-8411 8414-8419 8452 8456 8490-8498 8500-8502 8504-8526 8529-8530 8537 8540-8541 8553-8560 8563 8566 8568 8577 8592 8611 8639 8648 8659-8661 8664 8668-8669 8710 8738-8739 8741 8777 8792-8804 8830 8834 8839 8853 8858 8863 8865 8876 8898 8926 8935 8939 8950-8951 8957 8963 9010 9012 9076 9092 9097 9112 9119 9128 9257 9264 9266 9284 9291 9301 9304 9313 9318 9352 9375 9399 9414 9424 9445 9455 9457 9466 9473-9474 9476 9480 9484-9485 9511 9517 9528-9529 9536 9539 9542 9544 9552-9557 9559 9561-9564 9566-9572 9574-9577 9579-9630 9646 9655 9666- 9667 9669-9671 9673 9675-9697 9700-9701 9703-9704 9713- 9715 9718-9719 9722 9726-9729 9734 9752 9758 9761 9777 9780-9784 9813 9831 9854-9867 9869 9906 9927 9929 9939 9942-9943 9969 9983 10000 10007 10205 10267 10284 10296 10305 10311 10313-10316 10318-10325 10327 10329-10331 10333-10354 10356-10363 10395-10397 10400-10403 10405- 10410 10413 10417-10422 10427 10446-10447 10463 10470 10485 10496 10502-10507 10515 10542 10557 10565-10566 10645 10679 10688 10691 10729 10750 10760 10762 10764- 10769 10772-10774 10776-10782 10784 10786-10795 10797- 10815 10817-10830 10859 10861-10869 10871-10879 10881-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			10893 10908-10916 10929 10934 10943 10948 10968 10971 10975 10977-10983 11005 11009 11011 11015-11018 11028 11031 11054-11063 11094 11108 11114 11132 11136 11142 11194 11208 11213 11246 11390-11391 11401 11406 11411 11414 11459 11462 11483 11508 11513 11521 11534 11559- 11560 11565 11573 11585-11603 11606-11610 11612-11616 11618-11638 11640 11642-11657 11659-11667 11669-11670 11672 11699 11716-11718 11720-11722 11724-11741 11743- 11758 11760-11761 11775-11787 11797 11799-11801 11818 11830 11862 11864-11866 11869 11876 11889 11911 11925- 11928 11958-11961 11963-11976 11979-11980 12000 12006 12017 12019 12028 12033-12034 12041 12078 12086 12092 12122 12127 12159-12160 12178 12216 12218 12236 12245 12256 12260 12289 12303 12305 12308 12327 12330 12363 12375 12382 12387 12402-12405 12424 12426 12439 12442 12465 12470 12476 12511 12522-12523 12546 12551 12560 12570 12576 12590 12601-12602 12604-12619 12621-12633 12636 12639 12646-12653 12670-12671 12674 12682-12683 12688 12693 12696 12706 12709-12715 12735 12749-12750 12772 12790 12823 12830-12832 12835 12842 12849 12855 12863 12904-12905 12910-12911 12913-12916 12918-12924 12929 12931-12932 12934-12937 12939-12940 12954-12955 12965 12973 12976-12977 12989-12990 12993 12999 13020- 13021 13035 13051 13054-13055 13060 13062 13066-13067 13069-13087 13089-13095 13097-13102 13114-13117 13119- 13120 13122-13126 13134-13136 13141 13147 13156 13174 13193 13195-13196 13198-13201 13254 13260 13264 13277 13280 13295 13351 13368 13377 13391 13394 13400 13409 13412 13420 13456 13472-13477 13479-13484 13486-13492 13494-13496 13498-13499 13501-13510 13512-13516 13518- 13527 13533 13541-13544 13546-13551 13553-13555 13560 13575 13587-13589 13597 13603-13604 13613 13616 13622- 13623 13630-13631 13644-13646 13649 13659 13670 13679 13713 13743 13748 13769 13775 13782 13793 13803 13808 13818-13819 13858-13860 13864 13866-13869 13872 13882 13884 13888-13889 13891 13893 13901
fetal liver- spleen	Columbia University	FLS002	6 16 24 30-31 63 67 81 83 89 95 103 115 117 126 140 142 147 150-151 158 162 211 225 287 308 332 356 358 390-391 438- 439 483 551 556 641 654 694 701 708 731 788 997 1006 1012 1047 1082 1151 1154 1178 1184 1208 1212 1356 1480 1507 1551 1556 1623-1647 1649-1667 1669-1671 1675 1677-1698 1828-1829 1858 1877 1885 1889 1914 1927 1947 1961 1997 1999 2028 2057 2070 2092 2098 2138-2139 2154 2161 2174- 2175 2189 2191 2257 2282 2327 2342 2363 2399 2403 2409 2440-2441 2443-2450 2452-2459 2490 2498 2522-2523 2544 2555 2568 2575-2576 2592 2597 2605 2619 2623 2659 2806 2809 2812 2860 2869 2879 2903 2926 2932 2988 3031 3066 3075 3089 3188-3189 3286-3287 3319 3343-3344 3356 3426 3535 3548 3552 3554-3555 3583 3591 3610 3625 3634 3673 3709 3711 3720 3722 3839 3899 3926 3985 4005-4006 4011 4020 4025 4055 4058 4060 4078 4091-411 416 4118-4126 4128- 4142 4172 4194 4201 4253 4277 4282 4347 4350 4353-4355 4362 4367 4374 4379 4386 4391 4394 4396 4402 4426 4431 4435 4437-4439 4512 4553 4578 4586 4607 4622 4644 4654 4671 4758 4767 4783 4798 4836 4845 4899 4940 4948 4962- 4963 4985 4991 4998 5001 5037 5108 5167 5171 5177 5198 5237 5293-5294 5380 5400 5523 5535-5536 5581-5591 5593- 5599 5601-5613 5615-5624 5627-5637 5653 5674 5691 5693 5711 5724 5726 5733 5748 5757 5772 5778 5794 5817 5874 5894 5902 5904 5906-5907 5909 5911 5916-5919 5923-5924 5927 5929 5932 5938 5941 5948 5957 5959-5960 5962 5964

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			5979 6005 6020 6027 6037-6038 6052 6054 6057 6060-6062 6064 6068 6112 6140 6195 6225 6246 6287-6288 6306-6307 6336 6354 6371 6374 6423 6430 6451 6458 6461 6469 6478 6496 6508 6538 6545 6563 6580 6583 6595 6598 6607 6629 6638 6641-6643 6645-6675 6709 6726 6730 6765-6766 6788 6792-6793 6795 6797-6798 6800-6801 6808 6812 6836 6843 6850-6851 6855 6860 6864 6870 6875 6888 6908 6924 6950 6958 6968 6998 7003 7018 7045 7049 7056 7071-7079 7095- 7096 7109 7116 7118 7126 7133 7135 7137-7139 7155-7156 7166-7167 7169 7175 7178 7275 7291 7294 7329 7422 7426 7478 7608 7627 7687 7695 7716 7815 7839 7871 7893 7914 7937 7977 8022 8095 8120 8133-8134 8148-8149 8151-8167 8169-8182 8184 8186-8192 8194-8196 8241 8246 8276 8289 8298 8336 8339 8343 8345 8349 8355-8356 8361 8363 8365 8367-8368 8370 8373 8375-8378 8385 8388 8417 8496 8518 8520 8543 8558 8561 8563 8646 8667 8710 8738-8740 8786 8803 8813 8865 8926 8946 8948 8963 8970 9010 9049 9119 9128 9142 9164 9222 9264 9289 9296 9301 9317-9318 9320 9322 9335-9341 9343-9362 9365-9368 9370 9372-9373 9375- 9377 9399 9455 9457 9466 9472 9475 9480 9483 9495 9526 9533 9536 9553 9556 9558 9560 9563 9567 9570 9582 9597 9601 9630 9646 9655 9671 9683 9695 9700 9703 9715 9722 9729 9733 9752 9758 9783 9843 9848 9855 9880 9936 9942 9983 10007 10027 10103 10142 10186-10217 10274 10284 10287 10296 10313-10314 10329 10331 10349 10352 10354 10400 10405 10430 10439 10496 10500 10507 10542 10621 10709-10710 10712-10717 10750 10760 10776-10779 10782 10794 10809 10816 10837 10885 10891 10895 10913 10960 10971 10975 11057 11071 11098 11142-11143 11148 11194 11246 11401 11406 11430-11453 11455-11464 11483 11504 11508 11556 11560 11589 11596 11615 11618 11626 11631 11714 11729 11830 11833 11865 11988 12000 12006 12017 12019-12020 12041 12044 12081 12092 12178 12195 12245 12256 12277 12297 12327 12363 12383 12402-12403 12405 12426-12427 12444-12455 12457-12465 12467-12473 12475- 12476 12520 12546 12576 12599 12607 12611 12614-12615 12617-12618 12622 12627 12630-12632 12636 12647-12648 12650 12685 12688 12691 12693 12696 12703 12739-12740 12743 12763 12808 12830 12834 12842 12849-12858 12860- 12866 12885 12895 12906 12910 12913 12915 12917 12920 12922 12929 12933 12940-12941 12954-12955 12957 12965 12977 12990 12993 12999 13021 13039-13040 13047 13051 13054-13055 13060 13062 13072-13073 13077 13082-13083 13085 13092-13095 13098 13117 13123 13136 13173 13195- 13197 13202 13249 13254 13362 13377 13391 13394 13406- 13409 13411-13415 13417-13420 13456 13473-13474 13477 13480 13484 13486 13488-13489 13496-13498 13500 13502 13504 13506-13507 13511-13512 13515 13521 13546 13551 13554-13555 13560 13575 13590 13597 13613 13616-13617 13622 13630 13659-13660 13670 13678-13679 13695-13696 13701 13708 13713 13726 13748 13775 13795-13796 13815- 13826 13835 13838 13859-13860 13864 13867 13869 13872 13882-13885 13888-13889 13891 13893
fetal liver-spleen	Columbia University	FLS003	525 2269 2529 2627 2636 3552 3554-3555 3597 4201 4246 4253 4422 4426 4434 4438 5536 5801 8935 9536 11136 11142 11519 11626 11927 12028 12077-12079 12086 12305 12403 12424 13021 13472
fetal liver	Invitrogen	FLV001	40 51 60 598 731 1023 1048-1049 1820 1976 2111 2268-2269 2449 2483 2529 2568 2576 2614 2809 3207 3220 3468 3595- 3599 3885 4020 4346 4390 4422 4434 4543 4615 4767 4833 5092 5152-5155 5270 5505 5526 5553 5581 5715 5724 5726

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			5750 5766 5788 5794 5801 5902 6125 6147 6458 6598 6624 6645 6765 6799 6805 6862 7104 7856 8070 8156 8359 8361 8432 8740 8928 8935 8972-8974 9012 9041 9128 9264 9445 9474 9485 9511 9536 9593 9597 9703 9780 9927 9943 9945- 9946 9948 10007 10137 10275 10334 10529 10557 10566- 10569 10776 10828 11142 11560 11587 11618 11927 12070 12086 12105-12108 12127 12218 12236 12327 12424 12511 12541-12542 12605 12746 12916 12977 12985-12986 13020- 13021 13060 13064 13135 13246-13247 13472 13479 13488- 13489 13497 13533 13554 13590 13659 13680-13682 13859- 13860 13882 13888-13889
fetal liver	Clontech	FLV002	360 996 1134 3226 5102 9401
fetal liver	Clontech	FLV004	998 1927 2449 2627 4025 4043 4426 4438 4834 5030 5726 6730 9474 9942 10769 11142 11587 12590 12608 13889
fetal muscle	Invitrogen	FMS001	40 150 731 894 1264 1555 1613 1821-1822 1883 1959 2161 2343 2494-2496 2555 3203 4235-4237 4434 4671 4694 4783 4885 4940 4985 5037 5045 5481 5716-5718 5724 5788 5902 5932 6624 6742-6743 6825 7054 7104 7141 7632 7800 8279- 8281 8863 8935 9204 9264 9446-9449 9451 9474 9511 9536 9556 9722 9780-9781 10097 10273-10274 10330 10738-10739 10750 11098 11406 11528-11530 11560 12305 12544-12546 12590 12609 12618 12663 12670 12702 12735 12891-12892 12916 13051 13053 13195 13441-13442 13479 13613 13782
fetal muscle	Invitrogen	FMS002	3378 4348 4434 8932 11132 12033 12570 13782
fetal skin	Invitrogen	FSK001	60 142 235 319 641 683 800 1015 1050 1346 1774 1823-1825 2044 2099 2111 2161 2215 2223 2280 2367 2401 2408 2513 2516 2614 2812 2871 2926 3207 3356 3468 3490 3503 3548 3599 3720 3722 3885 4020 4032 4060 4109 4238 4240-4244 4246 4253 4277 4340 4353 4355 4388-4389 4391 4405 4434 4543 4562 4568 4654 4667 4671 4767 4940 4944 4947 5030 5037 5075 5163 5198 5296 5380 5481 5514 5581 5656 5674 5691 5719-5724 5748 5757 5801 5894 5902 5923 6057 6076 6078 6125 6147 6215 6336 6374 6409 6437-6438 6551 6563 6744 6783 6803 6805 6815 6873 6900 6908 6917 6985 6987 7037 7054 7058 7067 7075 7275 7355 7431 7484 7507 7587 7627 7642 7653 7687 7871 7977 8110 8134 8186 8226 8235 8251 8262 8282-8287 8298 8356 8365 8368 8452 8455-8456 8539 8597 8648 8679 8813 8863 8898 8921 8935 8939 8948 8951 8957 8983 9002 9041 9061 9122 9128 9257 9285 9414 9452-9453 9466 9474 9484 9503 9517 9529 9553 9563 9671 9677 9703 9714 9781 9841 9927 10007 10175 10296 10343 10491 10741-10742 10778 10795 10907 10948 11239 11513 11531 11573 11606 11626 11807 11869 11952 12000 12006 12160 12190 12218 12256 12327 12363 12371 12375 12378 12426 12438 12465 12470 12488 12549-12550 12570 12604 12615 12617 12663 12670 12735 12749 12754 12830 12893 12904 12910 12916-12917 12976-12977 13038 13084 13090 13116 13249 13254 13367 13389 13391 13443-13445 13456 13472 13479-13480 13494 13496 13499 13505 13512 13516 13551 13554-13555 13575 13590 13613 13630-13631 13644 13670 13713 13782 13784 13793 13803 13858 13866 13869 13882 13891
fetal skin	Invitrogen	FSK002	1004 3544 4834 5523 9922 9942 11134-11135 12570 13495 13499 13793 13884 13889
fetal spleen	BioChain	FSP001	997 5030 9466 11108 12033 12749 13590
umbilical cord	BioChain	FUC001	60 83 89 142 166 567 609 760 997 1302-1304 1306-1307 1309 1671 1697 1724 1848 1917 1978 2111 2154 2161 2207 2215 2315 2343 2444 2569 2576 2591 2597 2652 2866 2926 3468 3526 3599 3602 3625 3697 3722 3799-3805 3813 3839 3885 4025 4060 4173 4197 4246 4277 4340 4364 4387 4391 4395-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			4396 4405 4410 4434 4543 4589 4667 4694 4767 4834 4865 4940 4957 4963 4985 5030 5093 5096 5108 5163 5171 5213 5313 5340 5342-5344 5380 5481 5521 5526 5627 5656 5674 5714 5743 5750 5757 5801 5895 5902 5912 5938 6027 6061 6082 6125 6186 6195 6218 6241 6313 6321 6410 6458 6486- 6495 6595 6607-6608 6668 6745 6825 6860 6870 6979 7054 7141 7260-7261 7275 7329 7355 7373 7383 7444 7579 7586 7677 7716 7807 7930 7935-7936 7995 8077 8093 8226 8246 8262 8298 8343 8345 8358 8387 8452 8535 8563 8635 8669 8711 8819 8858 8863 8921 8935 8943-8944 8948 8963 9001- 9002 9012 9097 9130 9132 9134-9138 9264 9303-9304 9313 9332 9401 9424 9466 9472 9474 9544 9597 9665 9677 9700 9722 9734 9758 9834 9841 9848 10050 10175 10183 10267 10277 10311 10337 10446 10470 10508 10529 10566 10691 10772 10828 10961 11108 11132 11145 11239 11241 11273- 11276 11293 11408 11484 11513 11596 11604 11607 11620 11695 11823 11909 11927 11942 12000 12077 12160 12245 12255-12256 12292 12305 12308 12363 12383 12404-12405 12426 12438 12511 12570 12601 12605 12630 12700 12706 12754 12875 12913 12916 12935 12957 12993 13002 13009 13020-13021 13062 13135-13136 13141 13254 13283 13318- 13319 13336 13394 13400 13472 13479 13481 13488-13489 13495-13496 13499 13507 13511-13512 13516 13551 13555 13568 13575 13590 13613 13630 13644 13713 13740-13742 13866-13867 13882 13884 13888
fetal brain	GIBCO	HFB001	51 70 211-213 215-222 224-229 445 586-588 598 608 703-710 712-716 1068 1148 1178 1184 1193 1308 1516 1556 1774 1778 1957 1974 1976-1977 2010 2025-2029 2134-2135 2145 2161 2171 2174 2220 2223 2257 2266 2283 2444 2449 2510 2555 2563 2569 2590 2597 2614 2617 2717 2719-2723 2726 2729- 2734 2809 2997 3002 3081 3083 3086 3109 3226-3237 3239 3257 3272 3278 3282-3283 3286 3356 3419 3460 3479 3492 3495 3544 3548 3557 3590 3604-3605 3625 3627 3634 3673 3689 3697 3709 3722 3797 3810 3839 3885 4006 4011 4019 4022 4025 4040 4054 4059 4095 4194 4201 4253 4277 4282 4355 4364 4383 4399 4405 4410 4412 4434 4473 4480 4498- 4504 4507-4508 4517 4543 4654 4689 4694 4730-4733 4735 4755 4783 4820-4823 4825-4830 4845 4885 4940 4949 4957 4962 4972 4985 5017 5019 5022 5031 5037 5108 5132 5167 5171-5172 5262 5380 5481 5521 5523 5527 5553 5616 5656 5711 5740 5788 5801 5894 5902 5906 5908 5923 5938 5979- 5989 6057 6082 6096 6125 6147 6159 6161-6163 6165 6207 6212-6213 6215-6222 6241 6257 6288 6336 6369 6374 6419 6422 6512 6551 6555 6595 6598 6607 6711 6767 6788 6823- 6825 6860 6871 6879 6892-6894 6900 6909-6910 7058 7118- 7119 7169 7220 7222 7224-7225 7228-7229 7231-7233 7275 7426 7431 7444 7481-7483 7485-7488 7560-7567 7569 7608 7743 7768 7792 7814 7845 7864 7930 7977 7995 8093 8095 8110 8140 8226 8235 8262 8345 8358 8361 8370 8372 8387 8441-8443 8445 8447 8450-8455 8520 8535 8558 8597 8603 8648 8663-8666 8677 8702 8742-8749 8811 8838-8839 8943 8951 9010 9092 9134 9137 9257 9287 9304 9317 9455 9457 9466 9472 9475 9484 9510 9515 9533 9553 9567 9644-9645 9647-9649 9734 9758 9781 9785-9786 9791 9832-9837 9927- 9928 9939 9942 9970 10053 10175 10275 10277 10296 10329 10375-10378 10434 10464 10486 10496 10645 10679 10691 10778 10782 10791 10838-10844 10928 11019-11025 11027 11032 11055 11061 11108 11132 11145 11153 11208 11239 11343 11483 11513 11588 11596 11604 11606 11620-11621 11668 11691-11695 11818 11867 11869 11929-11930 12006 12033 12039 12041 12044 12047 12066 12078 12197 12218

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12327 12375 12405 12411 12424 12438 12521-12522 12564 12570 12576 12582 12590 12599 12601 12604 12611 12626 12630 12637-12640 12670 12674 12688 12694-12695 12703 12734 12748 12754 12785 12835 12840 12913 12916-12917 12929-12930 12935 12940 12946 12959 12989 12993 13020 13051-13052 13054 13073 13083 13090 13108-13110 13117 13131 13136 13148 13158 13160 13169 13184-13186 13254 13263 13277 13295 13389 13394 13438 13456 13477 13479- 13481 13489-13490 13494-13500 13502-13503 13506 13512 13516 13535-13536 13555 13575 13590 13592 13605-13606 13613 13616 13627 13630 13644-13645 13660 13670 13679 13687 13713 13793 13803 13838 13861 13866 13868-13869 13875 13888 13891 13896
macrophage	Invitrogen	HMP001	1002 2253 3548 4011 4058 4201 4246 4282 5526 8093 8262 11137 12039 12426 12511 12521 13888
infant brain	Columbia University	IB2002	6 89 142 211 276 307 518 589-590 598 644 717-718 720-721 773 841 921-924 926-932 937 1023 1091 1147-1150 1289 1493 1522-1525 1557-1564 1724 1778 1928 1947 1976 1978 2097 2111 2138 2172 2218-2223 2257 2283 2401 2418-2419 2444 2449 2516 2555 2563 2569 2575 2597 2627 2809 2818 2880 2932 3087 3166 3226 3241-3245 3272 3435 3474 3476-3477 3481 3483-3486 3488-3489 3492 3494-3495 3497 3538 3544 3548 3572 3595 3597 3669 3671-3672 3709 3720 3722 3737 3797 3817 3885 3985 3997-3999 4006 4011 4022-4031 4040 4095 4201 4246 4253 4277 4297 4355 4405 4410 4434 4676 4689 4767 4775 4831-4834 4837 4885 4962 4983 4998 5017- 5019 5021-5031 5035-5037 5040 5095 5143 5164 5167 5169 5233-5236 5380 5505 5517-5519 5523 5536 5546-5548 5691 5695 5724 5750 5766 5788 5801 5895 6027 6048 6082 6095 6111 6119 6132 6135 6147 6223 6301-6303 6305-6307 6374 6411 6459 6555 6563 6591-6595 6601 6606-6607 6609-6611 6613-6614 6624 6711 6767 6799 6805 6909 6946 7018 7052 7067 7118 7133 7166 7168-7169 7386 7464 7469 7473 7571- 7573 7697-7698 7716 7814 7827-7828 7905 7934 7977 8071- 8073 8084 8098-8104 8235 8320 8331 8351 8354-8356 8364- 8365 8370 8372 8376 8452 8520 8572 8667-8668 8750-8752 8813 8830 8863 8883-8885 8950 8958 8963 9040-9041 9251 9257 9267 9293-9298 9313 9424 9454 9456-9457 9466 9510 9514-9515 9533 9542 9556 9576-9577 9597 9626 9646 9722 9758 9787 9903-9904 9988 10027 10138-10139 10155-10160 10284 10296 10319 10346 10496 10536-10542 10557 10670- 10672 10680 10682 10778 10791 10897 10971 11028-11030 11052 11100-11109 11122 11132 11192 11392 11403-11404 11447 11513 11568 11595 11606 11626 11638 11818 11927 11931-11933 12028 12030-12031 12033-12034 12036-12039 12041 12047 12049 12146 12155-12157 12160 12327 12344 12363 12383-12385 12402 12405-12408 12424 12439 12521- 12522 12570 12590 12601 12611 12615-12616 12626 12639 12684-12685 12688 12696-12697 12707 12725-12727 12729 12748-12749 12754 12763-12764 12830 12904 12913 12916- 12917 12923 12929 12959 12977 12990 12996 13000 13047 13051 13054 13062 13073 13082-13084 13117 13141 13187- 13188 13196 13218-13219 13249 13257 13277 13284-13285 13351 13389 13394-13395 13456 13458 13479-13481 13488 13494-13495 13499 13503 13512 13516 13530 13535 13575 13607-13608 13613 13616 13641 13649 13659 13679 13705- 13706 13708 13713 13793 13798-13801 13803 13861 13869 13872 13875 13883-13884 13888 13891-13893 13896
infant brain	Columbia University	IB2003	6 46 746 1914 1947 1959 1994 2111 2220 2257 2516 2962 3166 3226 3272 3435 3572 3885 4277 4377 4410 4833 4837 5029-5030 5040 5147 5259 5851 6147 6423 6595 6598 6611

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			7145 7169 7716 8262 8354-8355 8364 8452 8863 9264 9457 9515 9556 9577 9626 9646 9715 9781 9928 9970 10027 10329 10376 10557 10791 11083 11289 11406 11459 11513 11663 11933 12039 12405 12546 12570 12601 12616 12685 12754 12913 12916 12954 12977 12990 13000 13056 13062 13195 13257 13392 13456 13458 13480 13481 13488 13497 13499 13506-13507 13511-13512 13514 13516 13549 13616-13617 13649 13793 13861 13884 13888 13891 13896
infant brain	Columbia University	IBM002	1564-1565 1976 2218 2420 3166 4391 5788 6147 6302 10329 11108 11513 12039 12729 12830 13062 13257 13512 13617 13803 13859 13861
infant brain	Columbia University	IBS001	927 931 1564 2915 3166 3737 3885 5029 5044 5095 5143 5701 5894-5895 6135 6307 7018 8452 8963 9424 9556 9626 10296 10542 11083 11100 11108 11167 12383 12611 12785 13257 13280 13479 13495 13506 13617 13679 13713 13896
lung, fibroblast	Stratagene	LFB001	67 235 552 641 746 1346 2090 2186 2543 2770 2812 2871 3203 3537 3548 3634 3812 3839 4073 4253 4434 4654 4783 4786 4821 4940 4957 4963 4985 5163 5172 5492 5523 5788 5911 5938 6027 6048 6057 6223 6272 6322 6599 6873 6886 6997 7204 7759 7815 7933 7977 8226 8235 8262 8354 8452 8648 8742 8791 8830 8863 8898 8944 8948 8951 9000 9076 9097 9128 9290 9304 9414 9455 9466 9472 9476 9503 9544 9563 9671 10000 10050 10342 10376 10434 10447 10679 10760 10857 11055 11094 11289 11402 11607 11818 11837 12000 12006 12178 12363 12405 12462 12582 12617 12636 12670 12754 12913 12916-12917 12925 12940 13126 13377 13394 13446 13456 13494 13497 13499 13502 13575 13613 13670 13679 13691 13795 13797 13867-13868 13882
lung tumor	Invitrogen	LGT002	51 69 88 142 158 211 444 598 608 722-723 733 795-797 799 1004 1023 1135-1145 1308 1338 1346 1493 1526-1533 1535 1566-1569 1626 1654 1816 1841 1848 1860 1976 1983 2090 2150 2161 2173 2223 2257 2266 2296-2297 2342 2402 2449 2483 2555 2569 2576 2591 2611 2623 2724 2809 2868 2880 2926 3088 3166 3272 3347 3571 3658-3666 3673 3722 3737 3797 3839 3885 4000-4002 4006 4011 4025 4032-4034 4060 4133 4201 4246 4253 4277 4282 4340-4341 4384 4388 4391 4399 4402 4405 4434 4543 4622 4671 4686 4767 4783 4791 4833-4834 4836 4885 4903 4940 4957 4987 4998 5001 5017- 5018 5030 5037 5052 5108 5163 5210 5227-5232 5422 5451 5520-5528 5581 5627 5637 5674 5693 5713 5724 5748 5766 5772 5788 5894-5895 5902 5907 5917 5938 5990 6005 6020 6094 6129 6147 6171 6224-6225 6239 6241 6253 6322 6336 6404-6410 6461 6508 6595-6598 6624 6765 6793 6798 6851 6870 6873 6994 7003 7008 7045-7047 7053-7055 7067 7085 7109 7116 7139 7141 7158 7169 7187 7468 7517 7524 7579 7608 7676 7687 7716 7761 7825-7826 8074-8078 8105-8106 8139 8235 8298 8323 8335 8345 8354 8359 8363 8365 8370 8372 8375 8456 8563 8633 8648 8678 8741 8792 8798 8805 8831 8863 8870 8989 9002 9010 9012 9032-9037 9039 9051 9076 9080 9092 9128 9257 9269-9271 9273-9274 9276 9299- 9301 9399 9414 9424 9457 9466 9472 9480 9484-9485 9517 9533 9536 9539 9544 9567 9612 9626 9665 9677 9689 9700 9703 9758 9773 9784 9788 9838-9841 9870 9928-9929 9942 9970 9983-9986 10140-10143 10149 10161 10175 10275 10296 10319 10330 10346 10349 10386 10496 10508 10561 10591- 10593 10673-10674 10742 10774 10778 10782 10788 10802 10836 10971 11031-11033 11064 11108 11132 11182-11191 11393-11395 11406 11459 11462 11560 11565 11588 11596 11604 11606-11607 11615 11618 11629 11821 11823 11845 11869 11932 11934 11961 11978-11980 12000 12006 12017 12022 12033 12078 12080 12127 12150-12154 12178 12236

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12327 12363 12371 12379 12386-12393 12409 12424 12521 12570 12590 12616-12618 12630 12637 12674 12691 12693 12698-12699 12716 12749 12754 12760 12762 12830 12832- 12833 12842 12904 12907 12913 12917 12923 12993 15020 13031-13032 13035 13060 13062 13064 13072 13083 13090 13136 13150 13193 13197 13202 13234 13277 13279 13281- 13282 13295-13296 13381-13383 13385-13386 13394 13400 13456 13477 13479-13480 13484 13488-13489 13492 13494 13496-13497 13499 13503 13506-13507 13511 13554 13575 13597 13616 13630 13646 13649 13659-13660 13670 13701- 13704 13713 13743 13782 13788-13789 13791-13792 13802- 13803 13864 13867-13868 13872 13882-13884 13888 13892
lymphocytes	ATCC	LPC001	142 316 1034 1977 2161 2342 2367 2483 2513 2529 2932 2962 3272 3711 3722 3839 4006 4277 4282 4405 4434 4836 4970 5037 5239 5451 5706 5796 5924 5941 6048 6147 6301 6765 6793 6805 6815 7133 7171 7275 7320 7687 7815 8033 8093 8095 8105 8110 8246 8262 8345 8365 8368 8370 8535 8664 8674 8722 8834 8858 8898 8919 8963 9012 9257 9456-9457 9484 9539 9544 9560 9758 9928 9939 10175 10201 10284 10333 10496 10520 10529 10679 10744 10766 11032 11108 11508 11513 11519 11853 11862 12033 12160 12363 12387 12402 12424 12438 12520 12560 12570 12663 12830 12913 12923 12968 13021 13066 13072 13085 13140 13147-13148 13394 13479 13488 13495 13499 13507 13575 13867 13869 13888
leukocyte	GIBCO	LUC001	21 49 51 67 83 88 94 142 211 316 326 340 368 371 403 438 443-455 464 485 518-523 525 530 532-535 591-592 616 724- 726 744 800 841 889 943 1004 1346 1556 1570-1572 1826 1914 1916 1927 1959 1976-1977 2095 2103-2107 2124-2127 2134 2138 2145 2161 2163 2175 2215 2223 2237 2266 2343 2363 2412 2421 2449 2483 2529 2555 2569 2575 2597 2617- 2618 2695-2696 2827 2876-2877 2899 2903 2961 2965-2975 3002 3035-3038 3040-3046 3109 3132 3166 3199 3203 3207 3246-3251 3265 3272 3286-3287 3312 3344 3356 3361 3378 3400 3434 3451 3468 3479 3484 3494 3503 3552 3590 3610 3627 3634 3704 3709 3720 3722 3725 3757 3797 3804 3810 3839 3885 3985 3996 4006 4009-4011 4019 4022-4023 4025 4035-4037 4058 4060 4194 4253 4269 4277 4297 4341 4362 4388 4390-4391 4396 4399-4400 4402 4403 4410 4412 4431 4434 4534 4543 4594 4615 4630 4641 4651-4663 4670 4688- 4689 4694 4699-4706 4736 4755 4758-4759 4767 4775 4783 4791 4798 4828 4835-4840 4845 4865 4930 4940 4947-4948 4957 4962 4964 4972 4976 4985 4991 4998 5001 5003 5017 5022 5030 5037 5040 5075-5076 5108 5118 5143 5163 5171- 5172 5313 5481 5503 5505 5521 5523 5526 5535 5549 5552 5656 5691 5724 5726 5740 5750 5766 5772 5788 5794 5796 5801 5865 5874 5894-5895 5906 5908 5923-5924 5928 5938 5989 6027 6042 6057 6063-6064 6082 6094-6103 6125 6130- 6137 6142 6147 6166-6167 6171 6181 6214 6226 6239 6253 6301 6307 6371 6374 6418 6512 6662 6716 6730 6788 6792 6799 6815 6836 6860 6873 6876-6877 6886-6887 6945 6975 6979 7018 7037 7056 7058 7067 7116 7118 7137 7155 7158 7171 7275 7315 7384-7385 7387-7389 7391-7393 7395-7398 7452-7463 7468 7494 7608 7671 7676 7687 7714 7733 7792 7815 7845 7864 7870 7905 7930 8093 8107 8110 8120 8139- 8140 8224 8226 8262 8276 8320 8363-8365 8368 8375 8387 8432 8452 8456 8520 8535-8536 8539 8562-8563 8577 8579 8597 8599-8601 8603-8605 8608 8640-8646 8648 8664 8669 8674 8677 8691 8702 8722 8753 8755 8798 8815-8816 8830 8838-8839 8858 8863 8870 8876 8898 8943-8944 8948 8951 9001 9010 9012 9061 9076 9092 9097 9128 9257 9304 9454-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			9456 9466 9472-9475 9484 9497 9511 9515 9517 9529 9536 9542 9556 9567 9612 9626 9702-9703 9723 9731-9738 9745 9752 9758 9762-9770 9780-9781 9789 9791 9808 9832 9842 9927-9928 9939 9942 9970 10000 10175 10275 10319 10329- 10331 10333 10345-10346 10412 10428 10430 10433 10435- 10436 10453-10454 10456 10465 10470 10475 10488 10496 10513 10566 10645 10679 10683 10691 10774 10776 10778 10788 10791 10795 10802 10891 10928 10930 10935-10941 10948 10961-10962 10964-10967 11034 11055 11108 11132 11136 11145 11239 11289 11405-11406 11459 11483 11519 11588 11604 11606 11618 11620 11693 11695 11805 11809- 11816 11818 11830 11833 11848 11850-11856 11868 11927 11932 11934-11935 11937-11939 11954 11988 12000 12006 12009 12028 12033 12037 12039 12047 12053 12092 12097 12118 12127 12143 12159-12160 12178 12186 12327 12336 12363 12375 12387 12402 12404-12405 12410 12424 12438 12442 12490 12511 12521-12522 12556 12560 12564 12570 12590 12599 12601 12605 12615-12617 12636 12643 12653 12660 12670 12672-12680 12693 12700-12701 12706-12707 12715 12735 12754 12823 12895 12904 12910 12913 12916- 12918 12923 12925 12935 12945 12947 12955-12956 12972 12977 12993 13002 13020-13021 13051 13062 13066 13072- 13073 13082 13085 13117 13126 13130-13131 13135 13138- 13140 13147-13151 13161 13169 13189 13254 13295 13391 13394 13425 13436 13442 13456 13477 13479 13488-13490 13494-13496 13498-13503 13505-13507 13512 13530 13546 13550-13551 13554 13557-13564 13575-13581 13590 13592- 13593 13609 13613 13616 13627 13630 13645-13646 13660 13679 13713 13782 13803 13864 13866-13869 13872 13883 13885 13888 13893
leukocyte	Clontech	LUC003	536 539 541-545 593 728 1552 1927 1974 3089 3252-3253 3434 3548 3709 3711 3722 3797 4011 4019 4040 4060 4194 4201 4277 4282 4622 4707 4791 4841-4842 4949 4998 5001 5030 5345 5895 6052 6138 6227 6419 6595 6754 6765 6767 6788 6911-6912 7049 7139 7171 7464 7575-7577 8093 8110 8116 8365 8370 8375 8592 8648 8830 8863 8944 9466 9544 9612 9758 9771 9773 9790 9929 10326 10346 10679 10779 10961 11035-11036 11132 11401 11513 11853 11940 12160 12256 12405 12670 12674 12681 12840 12904 12906 13020 13051 13162 13280 13400 13488 13511 13516 13554 13670 13679 13860 13869 13883 13889
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	83 142 360 447 841 1061 1346 1516 1573 1724 1959 1963 2159 2175 2343 2367 2513 2652 2812 2876 2961 3001 3272 3345 3604 3627 3722 3754 3839-3840 3985 3988 4040 4194 4246 4341 4515 4568 4641 4667 4862 4940 5075 5132 5163 5481 5492 5523 5740 5788 6008 6112 6119 6147 6189 6195 6272 6287 6418 6423 6508 6563 6726 6860 6870 7134 7166 7169 7275 7294 7579 7677 7748 7831 7852 7980 8110 8116 8226 8235 8262 8320 8345 8363 8370 8456 8563-8564 8633 8838 9001-9002 9128 9296 9304 9315 9484 9542 9544 9646 9703 9758 9780-9781 9808 9999 10007 10027 10296 10346 10470 11145 11239 11289 11401 11406 11508 11596 11606 11620 11823 11899 11950 12019 12107 12160 12292 12329 12363 12405 12436 12523 12599 12658 12670 12749 12754 12774 12842 12930 13020 13296 13394 13458 13489 13498 13501 13507 13551 13554 13575 13613 13616 13649 13660 13743 13775 13868
mammary gland	Invitrogen	MMG001	51 67 142 449 594 598 616 708 729-733 1004 1060 1194-1196 1310-1315 1329 1536-1541 1826 1848 1858 1914 1947 1974 1976-1978 2174-2175 2283 2299 2310 2336 2343 2403-2406 2449 2483 2555 2563 2576 2597 2611 2614 2617 2812 2827

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			2926 3191 3207 3490 3503 3673 3714-3715 3722 3737 3777 3796 3807-3819 3885 4003-4004 4060 4330 4346 4355 4391 4399 4434 4543 4671 4767 4791 4836-4837 4843 4940 4964 4975 4985 4998 5001 5017 5019 5022 5052 5108 5155 5163 5168-5169 5269 5345-5347 5466 5526-5527 5529 5581 5615 5724 5772 5778 5788 5794 5894-5895 5902 5907 5911 5917 5923-5924 6048 6057 6064 6094 6109 6125 6147 6156-6157 6215 6228 6321 6430 6458 6496-6499 6545 6579 6598-6599 6607 6711 6765 6780 6793 6797 6799 6805 6880 6931 6979 6987 6996 7012-7013 7048 7054 7057 7104 7141 7158 7169 7517 7578-7581 7583 7872 7937-7940 8110 8139 8156 8224 8262 8292 8298 8336 8359 8363 8365 8372 8452 8619 8628 8646 8648 8722 8758-8759 8782 8813 8815 8863 8882 8939 8963 8983 9012 9097 9111 9139-9141 9143 9157 9164 9264 9313 9327 9347 9466 9484 9511 9517 9544 9553 9563 9577 9646 9700 9703 9734 9746 9780 9791 9844-9846 9927-9928 9942 10006-10007 10051-10055 10144 10146-10147 10162 10285 10330 10346 10439 10490-10491 10496 10542 10557 10600 10628 10645 10691 10729 10772 10796 10983 11038 11108 11132 11216-11217 11277-11279 11396-11397 11406 11459 11513 11596 11606-11607 11626 11628 11823 11830 11833 11902 11941-11943 11979 12000 12009 12037 12047 12078 12093 12146 12160 12181 12258-12263 12281 12327 12371 12383 12387 12395 12424 12426 12438 12442 12484 12511 12564 12570 12590 12594 12601 12605 12609 12615- 12616 12618 12621 12653 12670 12691 12699 12702-12703 12749 12771 12791-12794 12834-12835 12885 12898 12905 12913 12916-12917 12920 12923 12955 12976-12977 13002 13020 13035 13047 13062 13064 13066 13072-13073 13084 13090 13092 13127 13135 13169 13190 13193 13195 13249 13254 13296 13320-13322 13392 13456 13477 13479-13480 13488-13489 13494 13497-13499 13505-13507 13512 13514 13516 13546 13551 13554-13555 13590 13611-13612 13631 13649 13670 13713 13743-13745 13838 13864 13866-13867 13869 13872 13875 13882-13885 13888 13891
induced neuron cells	Stratgene	NTD001	88 1493 1552 1561 2034 2090 2510 2522 2570 2576 2623 3226 3272 3839 4006 4058 4282 4384 4694 4783 4888 5103-5104 5172 5523 5541-5542 5684 5766 5788 5794 5938 6082 6195 6418 6449 6607 6660 6972 7058 7494 7815 7937 8370 8929- 8930 8996 9000 9003 9128 9157 9289-9291 9472 9928 10275 10550 10729 10760 11607 11736 11818 12039 12075 12094 12256 12363 12381 12423 12522 12707 12735 12863 12906 12958-12959 12963 13020 13052 13054 13196 13202 13310 13368 13378 13438 13479 13486 13506-13507 13546 13616 13654 13659 13691 13795 13891
retinoid acid induced neuronal cells	Stratgene	NTR001	1552 3839 3885 4282 4434 5030 9308 9466 11108 11132 12034 12039 12405 12424 12570 12905 13047
neuronal cells	Stratgene	NTU001	88 708 1552 1561 1947 2223 2490 2614 3272 3610 3625 3627 4032 4201 4253 4297 4337 4434 4543 4622 4641 5104 5163 5523 5541 5684 5788 6094 6147 6307 6601 6862 7755 8648 8740 8996 9097 9128 9289 9308 9466 9511 9544 10333 10779 10963 11032 11108 11132 12034 12039 12075 12405 12424 12570 12590 12706 12749 12830 12905 12917 12963 13035 13073 13280 13490 13507 13613 13616
pituitary gland	Clontech	PIT004	1148 5674 6068 6371 7759 8093 10430 12605 12636 12658 12916 13021 13082 13875
placenta	Clontech	PLA003	3885 4025 5030 5536 5711 5923 8349 8367 9921 12033 12076 12403 12511 13655 13885
prostate	Clontech	PRT001	67 83 142 225 235 379 486 572 616 1286 1316-1329 1538

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
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rectum	Invitrogen	REC001	6 67 142 683 731 997 1178 1909 1959 2005 2023 2596 2611 2614 2809 2926 3314 3333 3455 3722 3780 3870 4173 4355 4837 4949 4987 5526 5580 5615 5674 5691 5724 5788 5895 5909 5924 6057 6112 6195 6765 6805 7815 7833 8095 8664 8863 9517 9539 9544 9884 9927 10400 10666 11401 11513 11606 11985 12160 12327 12428 12693 12848 12910 12977 13051 13064 13072 13420 13494 13497 13507 13512 13515- 13516 13866 13869 13884 13888
salivary gland	Clontech	SAL001	67 731 800 997 1054 1914 2267 2395 2529 3136 3595 3627 4011 4192 4246 4330 4434 4641 4957 4987 5040 5052 5163 5451 5481 5706 5723 5788 5895 6219 6621 6801 6900 6975 7045 7733 8110 8372 8535 8563 8635 8830 8951 9000 9010 9051 9313 9472 9475 9671 9724 9758 9927 10027 11145 11695 11725 12017 12284 12363 12424 12427 12570 12609 12670 12674 12693 12977 13035 13307 13554 13617 13867 13872 13889 13891
salivary gland	Clontech	SALS03	1516 1724 1858 5030 6186 13657 13864
skin fibroblast	ATCC	SFB001	2251-2252 5788 6068 12511
skin fibroblast	ATCC	SFB002	6068 8951 12511
skin fibroblast	ATCC	SFB003	4025 5895 7741
small intestine	Clontech	SIN001	142 319 627 654 1034 1063 1197-1198 1330-1338 1340-1359 1575 1646 1774 1814 1978 2161 2347-2354 2409 2876 3046 3419 3460 3605 3716-3718 3737 3797 3837-3839 3841-3843 3845-3857 3885 3986 4060 4201 4301 4351 4385 4568 4689 4694 5076 5163 5270-5273 5304 5326 5365 5367-5372 5374 5503 5550 5701 5772 6064 6094 6171 6288 6427 6430-6432 6438 6510-6522 6598 6615 6793 6815 6997-6998 7016-7018 7054 7058 7072 7309 7450 7604 7769 7811 7873-7876 7955 7957 7959-7962 7964 8120 8298 8350 8452 8830 8863 8950- 8951 8966 9010 9073-9075 9119 9126 9128 9155-9166 9303 9544 9560 9780 9884 9928-9929 10008-10010 10061-10068 10097 10262 10330 10351 10601 10630-10634 10760 10983 11061 11219 11296-11308 11310-11313 11513 11620 11693 12182-12183 12280-12287 12327 12363 12488 12707 12799- 12801 12922 12991 13012-13014 13035 13051 13064 13297 13307 13328-13332 13335 13382 13499 13506 13554 13560 13575 13631 13695 13714 13747-13749 13751 13882 13884
skeletal muscle	Clontech	SKM001	1104 1346 2363 2367 2495 2555 2876 2880 3555 3634 3722 4011 4022 4194 4201 4253 4277 4282 4434 4641 4940 4972 4998 5343 5481 5523 5801 6005 6336 6873 7408 7995 8110 8120 8235 8262 8292 8345 8372 8576 8740 8830 8936 8951

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
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skeletal muscle	Clontech	SKM002	8535
skeletal muscle	Clontech	SKMs03	6336 6962 8936
skeletal muscle	Clontech	SKMs04	770 1724 3797 4277 6336 12405 13658
spinal cord	Clontech	SPC001	83 142 390 415 598 668 708 731 1184 1199-1207 1360-1375 1377-1396 1516 1574-1576 1595-1596 1849 1927 2070 2129 2161 2311-2314 2345 2355-2368 2423-2424 2430 2484 2529 2569 2576 2876 3215 3249 3272 3283 3532 3584 3627 3634 3711 3719-3722 3737 3839 3860-3884 4011 4025 4038-4039 4043 4055-4056 4173 4246 4282 4354 4375 4391 4434 4681 4767 4781 4808 4964 4985 4998 5037 5163 5233 5274-5277 5375-5392 5394-5402 5523 5569-5570 5581 5615 5723 5788 5835 5902 5928 5936 6047 6078 6082 6211 6288 6374 6433- 6435 6512 6523-6531 6534 6595 6616 6625-6626 6788 6894 6979 6999 7018-7026 7126 7166 7359 7473 7642 7653 7807 7814 7877-7879 7965-7968 7970 7972-7980 8105 8108-8110 8139 8246 8298 8345 8363 8368 8482 8603 8646 8884 8898 8981 9010 9012 9076-9078 9098 9167-9179 9184-9189 9264 9302 9304 9319-9320 9455 9466 9520 9530 9544 9556 9567 9781 9895 9901 9928 9942 9947 9969 9999 10007 10069- 10077 10079-10085 10177 10296 10326 10346 10376 10422 10566 10602 10635-10638 10679 10685-10686 10729 10776 11132 11220 11246 11314-11323 11325-11330 11417-11418 11459 11513 11818 12000 12011 12017 12033 12039 12160 12184-12185 12288-12292 12295-12299 12301-12305 12363 12375 12383 12387 12402 12413 12442 12468 12527 12605 12617 12636 12657-12658 12739-12740 12754 12772 12802- 12809 12830 12835 12841-12842 12905 12923 12940 12976 13003 13015 13017-13021 13051-13052 13117 13126 13136 13260 13277 13283 13295 13336-13343 13367 13442 13456 13473 13477 13481 13495 13497 13499-13500 13507 13516 13659 13670 13713 13715-13716 13748 13752-13759 13803 13869 13872 13884-13885 13888 13893 13896
adult spleen	Clontech	SPLc01	800 1927 4032 4834 6064 6135 6195 6446 6788 6873 7166 7455 8966 9929 10744 12402 12564 12590 12691 12904 12933 13082 13500 13506-13507 13516 13575 13864 13869 13883 13889
stomach	Clontech	STO001	21 83 142 1004 1208-1215 1217-1219 1397 1399-1405 1671 2315-2316 2345 2369-2373 2375 2575-2576 2809 2846 2984 3136 3166 3537 3610 3698 3723-3725 3839 3885-3897 4057- 4059 4173 4277 4410 4480 4667 4791 4808 4940 4987 5262 5278-5281 5283-5284 5403-5405 5407-5424 5481 5656 5674 5796 5904 6418 6436-6440 6535-6540 6563 6627-6629 6765 6940 7000-7001 7027-7030 7064 7135 7509 7604 7880-7885 7981-7990 8087 8110 8120 8143 8226 8452 8535 9010 9079- 9081 9191 9193-9196 9304-9306 9313 9317 9321 9715 10007 10011-10013 10086-10093 10178-10179 10603-10605 10640- 10642 11069 11167 11221-11222 11331-11337 11339-11343 11419 11513 11818 12186-12190 12307-12314 12327 12363 12425-12427 12438 12617 12773-12774 12810-12811 12834 13082 13103 13298-13299 13344-13349 13592 13630 13670 13717 13760-13764 13782 13888
thalamus	Clontech	THA002	579 598 616 1065 1148 1220-1221 1223-1226 1407-1432 1597 2266 2317-2319 2340 2342 2376-2378 2380 2431 2444 2555 3093 3230 3286 3537 3722 3726-3732 3737 3898-3902 3904-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			3918 3920-3922 4060-4062 4173 4201 4282 4360 4391 5270 5285-5288 5425-5438 5440-5449 5701 5902 5938 6137 6437 6458 6461 6541-6544 6546-6550 6630 6755 7031 7095 7119 7166 7484 7579 7815 7849 7905 7977 7991-8000 8002-8005 8126-8128 8134 8363 8558 8664 8786 8890 8930 8963 9082- 9085 9128 9197-9199 9201-9216 9251 9264 9308 9503 9515 9556 9646 9703 9928 10014-10017 10027 10094-10100 10102 10267 10496 10606-10608 10643-10650 10696 10891 11145 11223-11225 11344-11355 11406-11407 11420 11513 11604 11695 11791 11950 12022 12107 12191-12199 12315-12331 12363 12375 12405 12428-12430 12688 12706 12735 12748 12754 12812-12813 12815 12835 12914 12959 13020 13023- 13025 13060 13073 13300 13351-13358 13402-13403 13489 13496 13506 13512 13719-13720 13765-13768 13770 13872 13883
thymus	Clontech	THM001	51 142 150 332 346 360 438 546 731 760 895 1004 1104 1227- 1234 1264 1391 1516 1577-1585 1812 1860 1877 2129 2174 2215 2263 2321-2322 2408 2414 2425 2449 2490 2555 2569 2575 2611 2847 2880 3435 3530 3722 3727 3733 3735-3742 3839 3870 4006 4041 4043-4046 4060 4109 4375 4396 4399 4434 4667 4671 4759 4791 4885 4976 4987 5108 5289-5290 5466 5481 5526 5553-5554 5796 5956 5979 6020 6186 6253 6336 6371 6411 6438 6441-6447 6617-6621 6765 6788 6797 6870 6886 6908 6972 6994 7059-7060 7126 7141 7166 7168 7310 7383 7450 7494 7632 7716 7779 7887 7889-7891 8087 8111-8114 8117-8120 8139 8226 8343 8368 8370 8452 8456 8633 8830 8898 8921 8963 9010 9076 9086-9087 9128 9134 9264 9304 9307-9313 9401 9466 9497 9544 9563 9582 9612 9626 9646 9758 9781 9927 9937 9969 10018 10065 10163- 10166 10175 10284 10329 10414 10557 10609-10610 10617 10679 10687-10691 10742 10760 10772 10776 10778 10881 10891 11187 11194 11226-11229 11274 11406 11408-11410 11412 11459 11513 11676 11695 11830 11865 11942 12000 12006 12016 12022 12092 12160 12186 12200-12204 12327 12363 12414-12417 12427 12462 12470 12490 12564 12693 12706 12735 12740 12835 12840 12898 12905 12910 12913- 12914 12916 12977 13020 13036 13051 13062 13111 13126 13141 13295 13301-13305 13326 13351 13391 13396-13397 13456 13484 13498 13505 13507 13512 13516 13546 13713 13803 13805 13808 13866 13869 13885 13888
thymus	Clontech	THMc02	16 27 51 67 142 390 598 1233 1493 1508 1586-1588 1598-1603 1724 1841 1918 1927 1959 1976 1979 1989 2057 2107 2161 2223 2290 2407 2426-2428 2432-2433 2444 2487 2569 2617 3537 3664 3711 3720 3722 3737 3780 3817 4021 4025 4047- 4049 4060 4063-4068 4246 4277 4377 4405 4688 4694 4759 4791 4837 4949 4957 4992 4998 5037 5052 5108 5505 5553 5555-5564 5571-5572 5683 5766 5772 5788 5796 5894 5911 6048 6186 6225 6288 6306 6333 6621 6728 6730 6765 6767 6780 6788 6815 6867 6873 6979 7049 7061-7062 7166 7169 7676 7687 7809 8084 8121 8129-8130 8179 8262 8354 8363 8365 8375 8482 8597 8654 8740 8786 8791 8963 9076 9157 9257 9264 9314 9323-9324 9401 9454 9466 9519 9529 9536 9637 9700 9703 9927-9929 9940 10004 10007 10070 10167 10169-10172 10180 10182 10267 10284 10326 10331 10383 10439 10452 10542 10605 10691 10693-10694 10697 10744 10775 10778 10795 11046 11098 11274 11413-11415 11462 11519 11576 11592 11606 11618 11621 11627-11628 11693 11807 11814 12022 12034 12044 12080-12081 12086 12160 12236 12256 12327 12335 12363 12368 12387 12418-12419 12424 12433 12556 12560 12564 12570 12577 12594 12599 12612 12663 12735 12754 12836-12839 12844 12905 12913

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12955 12977 13020 13035 13037 13051 13062 13072 13087 13193 13280 13295 13398 13404 13456 13488 13499-13500 13503 13507 13516 13533 13535 13546 13611 13613 13630 13646 13649 13659 13670 13678-13679 13713 13769 13775 13803 13806-13808 13810-13811 13869 13872 13882-13883 13885 13888-13889
thyroid gland	Clontech	THR001	49 115 142 360 641 698 800 1004 1134 1193 1233 1235 1237- 1241 1329 1433-1471 1473-1476 1478-1479 1481 1589-1591 1593-1594 1604 1606-1612 1614-1615 1639 1671 1906 1927 1959 1976 1994 2090 2099 2134 2150 2161 2174 2186 2215 2343 2367 2381-2387 2429 2434-2437 2449 2490 2510 2529 2555 2569 2662 2827 2901 2961 2997 3001 3109 3265 3286 3425 3490 3503 3560 3643 3698 3722 3737 3743-3747 3797 3839 3885 3923-3941 3943-3954 3956-3961 4009 4050-4053 4060 4069-4082 4109 4173 4194 4253 4277 4282 4348 4354- 4355 4376 4391 4396 4412 4434 4641 4689 4694 4755 4759 4783 4791 4834 4957 4972 4985 4987 5018 5037 5052 5075- 5076 5108 5147 5163 5171 5270 5292-5294 5317 5380 5450- 5461 5464-5481 5503 5523 5565-5568 5573-5574 5693 5711 5724 5757 5772 5788 5894-5895 5917 5923 5938 5959 5966 6005 6013 6027 6047-6048 6061 6064 6125 6135 6139 6189 6215 6240 6336 6371 6374 6448-6449 6458 6508 6538 6551- 6554 6556-6561 6563-6572 6595 6598 6607 6622-6623 6631- 6636 6793 6803 6815 6873 6899 6955 6958 7032-7038 7040 7043 7063 7066-7067 7079 7116 7155 7233 7275 7455 7669 7743 7792 7839 7845 7857 7892-7893 7910 7930 7989 8006- 8008 8010-8033 8053 8067 8087 8092-8093 8110 8116 8120 8122-8124 8131-8143 8196 8226 8235 8262 8345 8365 8368 8370 8372 8375 8452 8520 8535 8543 8597 8646 8711 8760 8816 8839 8863 8898 8930 8948 8951 8963 8966 9010 9055 9088-9091 9142 9157 9217-9220 9222-9227 9229-9242 9244 9257 9264 9304 9315-9316 9325-9330 9368 9401 9455 9466 9484 9525 9542 9544 9563 9646 9695 9703 9780-9781 9855 9928 9942 9947 10000 10019 10027 10103 10117 10119-10120 10173-10175 10183-10185 10346 10376 10440 10470 10496 10611 10651-10657 10666 10679 10695 10698-10704 10760 10772 10778 10782 10788 10891 11033 11051-11052 11061 11063 11112 11231 11256 11356-11357 11359-11360 11362- 11367 11369-11372 11376 11385 11406 11416 11421-11425 11462 11513 11588 11605-11607 11620 11833 11869 11932 11980 11985 12006 12017 12033 12143 12160 12193 12195 12205 12207-12208 12292 12332-12336 12338-12345 12347 12349-12356 12358-12360 12363 12368 12405 12420 12422 12424 12428 12434-12439 12465 12523 12601 12605 12609- 12611 12617 12636 12645 12670 12691 12707 12740 12749 12754 12768 12775 12777 12817-12824 12830 12840 12845- 12848 12863 12911 12940 12955 12977 13020 13026-13028 13038 13047 13051 13062 13072-13073 13090 13104 13117 13126 13195 13202 13254 13295-13296 13360-13371 13389 13391 13399 13412 13479 13488-13489 13492 13494 13498 13500 13503-13504 13506-13507 13511-13512 13516 13533 13551 13554 13590 13613 13627 13644 13646 13656 13659- 13660 13670 13713 13721 13743 13771-13774 13782 13803 13809 13812-13814 13860 13866-13867 13869 13872 13882 13884-13885 13888 13891 13893
trachea	Clontech	TRC001	83 438 483 858 1006 1034 1242-1245 1359 1483-1494 1616- 1619 1621 1671 2266 2324 2388-2391 2409 2438-2439 2444 2575 3001 3136 3272 3425 3460 3535 3548 3748-3756 3810 3962-3967 4083-4086 4530 4755 4758 4949 4957 4987 5075 5213 5295-5299 5481-5482 5484 5486-5488 5490-5491 5535 5576-5580 5656 5941 6091 6450-6453 6574-6578 6637 6797

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			6955 7041-7042 7049 7068 7204 7347 7733 7864 7894 8034-8043 8045 8120 8139 8144 8563 8635 8646 9012 9092-9099 9245-9251 9317 9331 9333 9484 9503 9517 9734 10020-10022 10027 10097 10121-10123 10125-10127 10284 10344 10478 10612 10658-10659 10705 10812 10948 11145 11233-11239 11373-11376 11428-11429 11942 12022 12209-12211 12292 12361-12363 12365-12366 12438 12440-12441 12611 12617 12734-12735 12825-12826 12900 12904-12905 12916 12923 12965 12972 12976 12989 13029-13030 13306-13308 13372-13373 13492 13670 13713 13722 13775-13781 13803 13884
uterus	Clontech	UTR001	1036 1134 1246-1250 1324 1493 1495-1511 1622 1671 1928 2145 2266 2310 2326 2343 2367 2392-2397 2555 3281 3479 3720 3757-3760 3762 3969-3986 4088-4090 4192 4201 4246 4277 4390-4391 4434 4515 4998 5002 5184 5300-5301 5481 5492-5504 5656 5695 5712 5794 5936 6116 6475 6579-6587 6595 6870 7002 7043-7044 7311 7484 7895-7899 8046-8055 8057-8059 8061 8110 8146-8147 8152 8226 8262 8622 8677 9008 9092 9137 9252-9257 9334 9370 9414 9466 9539 9703 10023-10024 10128-10134 10346 10595 10660-10668 10706-10708 11145 11239 11289 11377 11379-11385 11695 11830 12367-12369 12371-12374 12442-12443 12570 12670 12693 12827-12829 12914 13002 13047 13073 13083-13084 13131 13260 13277 13309-13310 13374-13376 13394 13489 13512 13713 13782 13784-13787 13866 13869

TABLE 2

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1	M36501	Homo sapiens	alpha-2-macroglobulin	118	69
2	AF118090	Homo sapiens	PRO2044	247	59
3	X01683	Homo sapiens	alpha 1-antitrypsin	544	78
4	L27428	Homo sapiens	reverse transcriptase	79	27
5	M22332	Homo sapiens	unknown protein	89	40
6	AF015539	Mytilus edulis	precollagen P	113	33
7	X03325	Homo sapiens	apolipoprotein B fragment	540	83
8	AB019280	Mus musculus	sprouty-4	91	35
9	D88152	Homo sapiens	acetyl-coenzyme A transporter	625	87
10	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	124	58
11	AL049569	Homo sapiens	dJ37C10.5 (KIAA0445)	182	82
12	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	85	37
13	L27428	Homo sapiens	reverse transcriptase	135	61
14	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	266	72
15	U93569	Homo sapiens	putative p150	135	37
16	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	67
17	X53581	Rattus norvegicus	ORF4	124	34
18	AF183961	Homo sapiens	carbon catabolite repression 4 protein homolog	431	75
19	AJ002190	Homo sapiens	dihydroxyacetone phosphate acyltransferase	551	88
20	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	127	45
21	AK001269	Homo sapiens	unnamed protein product	1643	99
22	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	275	58
23	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	123	75
24	AF156550	Mus musculus	putative E1-E2 ATPase	168	58
25	AF119856	Homo sapiens	PRO1851	585	83
26	U49974	Homo sapiens	mariner transposase	187	46
27	G00901	Homo sapiens	Human secreted protein, SEQ ID NO: 4982.	86	30
28	AF295773	Homo sapiens	rat guanine nucleotide dissociation stimulator	126	74
29	AF113685	Homo sapiens	PRO0974	92	73
30	U83303	Homo sapiens	line-1 reverse transcriptase	102	50
31	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	279	75
32	AF003535	Homo sapiens	ORF2-like protein	114	47
33	M15386	Homo sapiens	gamma-globin	370	84
34	M19419	Mus musculus	proline-rich salivary protein	110	35
35	AF211943	Homo sapiens	WW domain-containing protein WWOX	586	83
36	X13885	Nicotiana tabacum	extensin (AA 1-620)	103	35
37	U93563	Homo sapiens	putative p150	127	58
38	U93564	Homo sapiens	putative p150	103	77
39	AF069732	Homo sapiens	ADA2-like protein	524	88
40	X61046	Hydra sp.	mini-collagen	101	34
41	AK000322	Homo sapiens	unnamed protein product	566	80
42	G03646	Homo sapiens	Human secreted protein, SEQ ID NO: 103	103	57

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
43	AF071081	Mycobacterium tuberculosis	7727. proline-rich mucin homolog	104	41
44	AF092135	Homo sapiens	PTD014	228	41
45	Y73353	Homo sapiens	HTRM clone 1870914 protein sequence.	295	56
46	AF118082	Homo sapiens	PRO1902	119	44
47	X78926	Homo sapiens	zinc finger protein	442	52
48	X54326	Homo sapiens	glutamyl-tRNA synthetase	542	81
49	D50645	Homo sapiens	SDF2	321	95
50	M92439	Homo sapiens	leucine-rich protein	344	80
51	U28963	Homo sapiens	Gps2	593	82
52	U41806	Homo sapiens	p60	660	81
53	AF181490	Homo sapiens	prenylcysteine lyase	461	78
54	U93570	Homo sapiens	putative p150	147	36
55	W73499	Homo sapiens	Von Willebrand factor.	529	76
56	AF119851	Homo sapiens	PRO1722	126	57
57	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284	115	61
58	AL021939	Homo sapiens	dJ352A20.2 (aldehyde dehydrogenase family protein)	422	90
59	L24158	Homo sapiens	integrin alpha 9 protein	117	71
60	Y32157	Homo sapiens	Human SH3D1A protein.	530	91
61	X61296	Rattus norvegicus	open reading frame 2	117	31
62	AK002064	Homo sapiens	unnamed protein product	330	80
63	AB012223	Canis familiaris	ORF2	80	56
64	U93570	Homo sapiens	putative p150	113	37
65	U15647	Mus musculus	reverse transcriptase	152	55
66	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	126	54
67	Y48359	Homo sapiens	Human prostate cancer-associated protein 56.	590	99
68	W74879	Homo sapiens	Human secreted protein encoded by gene 151 clone H1LEF62.	368	98
69	AF104921	Homo sapiens	succinyl-CoA synthetase alpha subunit	604	93
70	AF175265	Homo sapiens	vacuolar sorting protein 35	632	88
71	U93571	Homo sapiens	p40	106	33
72	X15324	Homo sapiens	angiotensinogen	330	84
73	Z98204	Hordeum vulgare	extensin	111	38
74	Y30713	Homo sapiens	Amino acid sequence of a human secreted protein.	232	61
75	AF118092	Homo sapiens	PRO2061	453	79
76	M63175	Homo sapiens	autocrine motility factor receptor	190	85
77	M26361	Mus musculus	LINE/tg H-chain fusion protein	153	38
78	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	171	58
79	X78926	Homo sapiens	zinc finger protein	199	37
80	M77381	Homo sapiens	acrosin	98	54
81	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	129	44
82	U93569	Homo sapiens	putative p150	94	38
83	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
84	AF255446	Cryptocodium cohnii	Dipl-associated protein C	129	34
85	R59837	Homo sapiens	Sequence of human microtubule-	82	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			associated protein tau.		
86	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	157	76
87	AF116712	Homo sapiens	PRO2738	91	58
88	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	77	44
89	Y82742	Homo sapiens	DNA replication and repair associated protein (DRASP).	313	79
90	M16961	Homo sapiens	alpha-2-HS-glycoprotein	138	74
91	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	250	56
92	AF220656	Homo sapiens	apoptosis-associated nuclear protein PHLDA1	62	69
93	U65928	Homo sapiens	Jun activation domain binding protein	188	75
94	U93568	Homo sapiens	putative p150	102	48
95	S80119	Rattus sp.	reverse transcriptase homolog	130	53
96	U93563	Homo sapiens	putative p150	242	50
97	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	105	46
98	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	62
99	X74045	Equus caballus	preproalbumin	289	65
100	AF118090	Homo sapiens	PRO2044	269	90
101	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	198	51
102	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	88	53
103	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	225	82
104	AF003535	Homo sapiens	ORF2-like protein	114	47
105	AF130079	Homo sapiens	PRO2852	133	56
106	AF130089	Homo sapiens	PRO2550	107	71
107	M63473	Homo sapiens	alpha-5 type IV collagen	131	45
108	AF116661	Homo sapiens	PRO1438	112	54
109	X92485	Plasmodium vivax	pva1	101	41
110	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	80
111	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	199	69
112	AF194537	Homo sapiens	NAG13	104	44
113	L27428	Homo sapiens	reverse transcriptase	160	34
114	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	137	56
115	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	191	67
116	AF130052	Homo sapiens	PRO0956	163	47
117	L27428	Homo sapiens	reverse transcriptase	117	36
118	U93569	Homo sapiens	putative p150	104	66
119	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	96	66
120	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	81	57
121	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	78	51
122	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	95	80
123	X61296	Rattus norvegicus	open reading frame 2	94	36
124	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	131	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
125	AF119900	Homo sapiens	PRO2822	168	68
126	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	209	58
127	L27428	Homo sapiens	reverse transcriptase	102	35
128	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	99	63
129	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	73
130	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	170	36
131	U93572	Homo sapiens	putative p150	168	38
132	U37263	Homo sapiens	KRAB zinc finger protein; Method: conceptual translation supplied by author	155	57
133	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	137	92
134	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	58	61
135	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	66
136	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	102	38
137	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	230	55
138	AK000496	Homo sapiens	unnamed protein product	127	46
139	X53581	Rattus norvegicus	ORF4	136	38
140	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	158	48
141	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	162	65
142	AF090930	Homo sapiens	PRO0478	127	65
143	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	141	58
144	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	98	65
145	AJ238588	Sciurus vulgaris	cytochrome c oxidase subunit III	417	72
146	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	139	76
147	Y36156	Homo sapiens	Human secreted protein #28.	91	40
148	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	121	70
149	Y76184	Homo sapiens	Human secreted protein encoded by gene 61.	214	85
150	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	95	57
151	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	126	66
152	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	105	51
153	AF119900	Homo sapiens	PRO2822	116	62
154	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	149	66
155	AB009993	Mus musculus	collagen a1(V)	105	36
156	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	155	69
157	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	348	71
158	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	146	54
159	AF247705	Oryctolagus cuniculus	alpha 1 type X collagen	102	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
160	R95913	Homo sapiens	Neural thread protein.	99	56
161	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	52
162	X71442	Rattus norvegicus	ORF 1; putative	96	47
163	U93570	Homo sapiens	putative p150	118	38
164	U23515	Caenorhabditis elegans	weak similarity to adenyl cyclase-associated protein (CAP) and to P. chabaudi adami major merozoite surface antigen protein (PIR:A32555). Final exon overlaps gene predicted on other strand.	93	37
165	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	143	66
166	AF130079	Homo sapiens	PRO2852	143	90
167	L27428	Homo sapiens	reverse transcriptase	200	53
168	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	92	51
169	R95913	Homo sapiens	Neural thread protein.	116	54
170	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	324	85
171	U83303	Homo sapiens	line-1 reverse transcriptase	111	50
172	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	111	69
173	AF130089	Homo sapiens	PRO2550	126	59
174	S80119	Rattus sp.	reverse transcriptase homolog	151	46
175	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	113	53
176	U15647	Mus musculus	reverse transcriptase	104	46
177	M24732	Homo sapiens	lamin-like protein	112	42
178	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	137	38
179	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	143	58
180	AF194537	Homo sapiens	NAG13	92	90
181	U93564	Homo sapiens	putative p150	131	53
182	U93574	Homo sapiens	putative p150	86	46
183	Y14166	Gallus gallus	attachment region binding protein	91	40
184	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	104	64
185	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element.	183	73
186	U93572	Homo sapiens	putative p150	139	64
187	M22332	Homo sapiens	unknown protein	79	41
188	Y87202	Homo sapiens	Human secreted protein sequence SEQ ID NO:241.	75	71
189	U70935	Peromyscus maniculatus	reverse transcriptase	132	37
190	S80119	Rattus sp.	reverse transcriptase homolog	172	43
191	AF194537	Homo sapiens	NAG13	81	75
192	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	112	64
193	X92485	Plasmodium vivax	pva1	96	40
194	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	112	45
195	L27428	Homo sapiens	reverse transcriptase	141	37
196	U93570	Homo sapiens	putative p150	201	41
197	X92485	Plasmodium vivax	pva1	120	48
198	AF130089	Homo sapiens	PRO2550	137	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
199	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	377	84
200	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	119	52
201	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	151	68
202	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	247	78
203	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	126	56
204	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	362	80
205	R59842	Homo sapiens	ApoE4L1 protease.	100	82
206	AF161356	Homo sapiens	HSPC093	78	62
207	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	111	48
208	U83280	Leishmania donovani	39 kDa antigen	121	53
209	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	84	80
210	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	146	72
211	M69197	Homo sapiens	haptoglobin-related protein	344	92
212	AF034611	Homo sapiens	intrinsic factor-B12 receptor precursor; cubilin	123	37
213	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	65
214	V00662	Homo sapiens	cytochrome oxidase I	485	87
215	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	124	80
216	U53512	Mus musculus	nuclear receptor co-repressor	115	47
217	L26953	Homo sapiens	chromosomal protein	143	77
218	U12690	Homo sapiens	cytochrome oxidase subunit II	224	70
219	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	125	75
220	AB018114	Arabidopsis thaliana	RING finger protein-like	111	38
221	D38112	Homo sapiens	ATPase subunit 6	475	84
222	V00662	Homo sapiens	cytochrome B	466	77
223	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	175	85
224	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	125	38
225	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	86	65
226	X77816	Rattus norvegicus	PR-Vbeta1	130	54
227	U09500	Homo sapiens	cytochrome b	274	62
228	AF081104	Mus musculus domesticus	ORF2	111	36
229	AF090942	Homo sapiens	PRO0657	88	57
230	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	76	57
231	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	101	66
232	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPGP94.	116	54
233	AF010400	Homo sapiens	transaldolase-related protein	253	77
234	AF197913	Helicoverpa armigera nuclear polyhedrosis virus	basic DNA-binding protein BDBP	137	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
235	AF090931	Homo sapiens	PRO0483	123	75
236	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	185	86
237	M19503	Homo sapiens	ORF1; putative	99	40
238	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	93	58
239	AF014883	Homo sapiens	NADH dehydrogenase subunit 2	305	65
240	G03102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	60	44
241	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	79	50
242	U15647	Mus musculus	reverse transcriptase	117	47
243	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	56
244	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	94	45
245	AK023542	Homo sapiens	unnamed protein product	82	38
246	X55702	Drosophila melanogaster	polycomb protein	84	31
247	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	65
248	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	154	70
249	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	142	63
250	Y17832	Human endogenous retrovirus K	env protein	297	71
251	U93568	Homo sapiens	p40	103	46
252	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	201	47
253	AF090895	Homo sapiens	PRO0117	139	60
254	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	185	72
255	L27428	Homo sapiens	reverse transcriptase	156	40
256	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	157	59
257	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	118	70
258	AF194537	Homo sapiens	NAG13	141	38
259	B01372	Homo sapiens	Neuron-associated protein.	115	71
260	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	113	53
261	M22332	Homo sapiens	unknown protein	78	45
262	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	70	78
263	X61296	Rattus norvegicus	open reading frame 2	108	36
264	AF016099	Mus musculus	endonuclease/reverse transcriptase	178	45
265	G03303	Homo sapiens	Human secreted protein, SEQ ID NO: 7384.	81	63
266	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WO9901020.	116	84
267	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	118	52
268	AF119855	Homo sapiens	PRO1847	74	70
269	AF109907	Homo sapiens	S164	85	61
270	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	137	63
271	X92485	Plasmodium vivax	pval	107	72
272	AF194537	Homo sapiens	NAG13	167	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
273	U93564	Homo sapiens	p40	104	40
274	L27428	Homo sapiens	reverse transcriptase	142	56
275	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	150	60
276	X61296	Rattus norvegicus	open reading frame 2	96	48
277	AF090931	Homo sapiens	PRO0483	140	65
278	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	231	66
279	AF130089	Homo sapiens	PRO2550	164	60
280	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	98	58
281	L22548	Homo sapiens	collagen type XVII alpha 1	92	38
282	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	68
283	AF116715	Homo sapiens	PRO2829	160	75
284	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	111	53
285	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	94	53
286	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	120	53
287	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	147	66
288	U93572	Homo sapiens	putative p150	125	32
289	AL050399	Arabidopsis thaliana	putative proline-rich protein	142	44
290	X92485	Plasmodium vivax	pval	147	43
291	AB047600	Macaca fascicularis	hypothetical protein	172	66
292	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	108	55
293	D38115	Pongo pygmaeus	NADH dehydrogenase subunit 5	342	71
294	AF090942	Homo sapiens	PRO0657	99	66
295	M61185	Bos taurus	glutamic acid-rich protein	114	44
296	M13100	Rattus norvegicus	unknown protein	107	43
297	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	114	50
298	X92485	Plasmodium vivax	pval	93	78
299	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	127	75
300	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	115	42
301	L24521	Homo sapiens	transformation-related protein	117	60
302	X83413	Human herpesvirus 6	U88	219	49
303	U93567	Homo sapiens	putative p150	130	48
304	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	72	61
305	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	153	68
306	D38112	Homo sapiens	cytochrome c oxidase subunit 3	532	79
307	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	84	53
308	L27428	Homo sapiens	reverse transcriptase	151	72
309	M69297	Homo sapiens	ORF 3	145	43
310	X92485	Plasmodium vivax	pval	81	60
311	L27428	Homo sapiens	reverse transcriptase	103	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
312	AF130079	Homo sapiens	PRO2852	135	49
313	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	110	58
314	AF090928	Homo sapiens	PRO0470	88	48
315	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	175	64
316	U93568	Homo sapiens	putative p150	148	46
317	AF119855	Homo sapiens	PRO1847	108	84
318	P60839	Homo sapiens	Sequence of human serum albumin (HSA) on plasmid pXL53.	175	50
319	W46424	Homo sapiens	Human macrophage stimulating protein (MSP).	237	69
320	AL049547	Homo sapiens	dJ34F7.2 (CREB-RP (G13))	247	64
321	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	110	66
322	AF016099	Mus musculus	endonuclease/reverse transcriptase	102	48
323	AF090930	Homo sapiens	PRO0478	141	72
324	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	126	44
325	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	146	59
326	R59842	Homo sapiens	ApoE4L1 protease.	95	60
327	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	84	61
328	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	123	66
329	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	125	65
330	AF119855	Homo sapiens	PRO1847	121	80
331	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	364	71
332	AK000496	Homo sapiens	unnamed protein product	145	41
333	D00570	Mus musculus	open reading frame (196 AA)	153	53
334	AF119855	Homo sapiens	PRO1847	116	74
335	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	50
336	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	129	56
337	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	107	59
338	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	115	72
339	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	117	50
340	AK022217	Homo sapiens	unnamed protein product	127	70
341	U43360	Peromyscus maniculatus	reverse transcriptase	115	75
342	AF118086	Homo sapiens	PRO1992	141	73
343	X92485	Plasmodium vivax	pval	96	59
344	AF106677	Drosophila melanogaster	dissatisfaction	90	48
345	U12693	Homo sapiens	cytochrome oxidase subunit II	239	91
346	L27428	Homo sapiens	reverse transcriptase	95	56
347	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	69
348	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	81	51
349	X51616	Volvox carteri	SULFATED SURFACE GLYCOPROTEIN 185	110	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
350	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	158	55
351	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	183	60
352	AL390114	Leishmania major	extremely cysteine/valine rich protein	151	51
353	R95913	Homo sapiens	Neural thread protein.	95	56
354	AF061340	Artibeus jamaicensis	cytochrome c oxidase subunit III	346	70
355	AF090895	Homo sapiens	PRO0117	126	60
356	AF016099	Mus musculus	endonuclease/reverse transcriptase	121	48
357	AF118086	Homo sapiens	PRO1992	159	73
358	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	85	89
359	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	98	50
360	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	110	57
361	M13100	Rattus norvegicus	unknown protein	122	34
362	Y36203	Homo sapiens	Human secreted protein #75.	108	63
363	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	83	75
364	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	212	65
365	AF130051	Homo sapiens	PRO0898	136	71
366	AF068294	Homo sapiens	HDCMB45P	188	65
367	M10546	Homo sapiens	cytochrome oxidase I	225	70
368	S80119	Rattus sp.	reverse transcriptase homolog	188	45
369	U70935	Peromyscus maniculatus	reverse transcriptase	75	48
370	AF118082	Homo sapiens	PRO1902	98	79
371	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	40
372	AF014903	Pan troglodytes	NADH dehydrogenase subunit 2	169	41
373	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	93	48
374	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	66
375	G03107	Homo sapiens	Human secreted protein, SEQ ID NO: 7188.	90	80
376	U93568	Homo sapiens	putative p150	140	56
377	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	140	50
378	AF090942	Homo sapiens	PRO0657	154	66
379	U93568	Homo sapiens	putative p150	149	36
380	U93570	Homo sapiens	p40	184	57
381	L27428	Homo sapiens	reverse transcriptase	128	60
382	AF194537	Homo sapiens	NAG13	114	35
383	AF116712	Homo sapiens	PRO2738	109	56
384	D38112	Homo sapiens	cytochrome c oxidase subunit 3	405	81
385	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	63
386	M22334	Homo sapiens	unknown protein	124	39
387	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	97	52
388	D38112	Homo sapiens	NADH dehydrogenase subunit 5	327	94
389	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	157	70
390	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	129	62
391	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	259	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
392	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	137	63
393	U43360	Peromyscus maniculatus	reverse transcriptase	129	54
394	AK023582	Homo sapiens	unnamed protein product	148	46
395	M22332	Homo sapiens	unknown protein	128	41
396	AF118086	Homo sapiens	PRO1992	160	71
397	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	101	52
398	D38112	Homo sapiens	cytochrome c oxidase subunit 3	199	66
399	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	234	78
400	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	107	40
401	AF000996	Homo sapiens	ubiquitous TPR motif, Y isoform	116	61
402	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	145	37
403	AF118082	Homo sapiens	PRO1902	97	55
404	AF202635	Homo sapiens	PPI200	126	55
405	V00662	Homo sapiens	cytochrome oxidase I	352	68
406	AF229067	Homo sapiens	PADI-H protein	129	71
407	AL390114	Leishmania major	extremely cysteine/valine rich protein	197	38
408	L26251	Trypanosoma brucei	CR5	95	46
409	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	310	62
410	X92485	Plasmodium vivax	pva1	96	68
411	M64793	Rattus norvegicus	salivary proline-rich protein	128	40
412	Y19192	Talpa europaea	cytochrome oxidase subunit I	431	83
413	M10546	Homo sapiens	cytochrome oxidase I	299	86
414	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	220	81
415	AF205385	Pan troglodytes	NADH dehydrogenase subunit 5	296	89
416	X58438	Mus musculus	proline rich protein	112	50
417	U70932	Peromyscus leucopus	reverse transcriptase	89	51
418	V00662	Homo sapiens	cytochrome oxidase III	200	84
419	AF017789	Homo sapiens	putative transcription factor CA150	120	41
420	M10546	Homo sapiens	cytochrome oxidase I	183	69
421	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	166	44
422	AF130051	Homo sapiens	PRO0898	158	59
423	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	86	52
424	D38116	Pan paniscus	cytochrome c oxidase subunit 3	342	82
425	U93570	Homo sapiens	putative p150	133	41
426	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	67
427	D13951	Nicotiana tabacum	extensin precursor	140	42
428	L27428	Homo sapiens	reverse transcriptase	104	34
429	R95913	Homo sapiens	Neural thread protein.	118	49
430	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	206	97
431	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	88	55
432	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	98	54
433	J05042	Oryctolagus	alpha-1 (VIII) collagen precursor	91	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		cuniculus			
434	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	105	56
435	U93572	Homo sapiens	putative p150	118	38
436	U93569	Homo sapiens	putative p150	100	30
437	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	126	81
438	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	71
439	U52077	Homo sapiens	mariner transposase	187	52
440	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	80	45
441	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	71
442	AE003727	Drosophila melanogaster	CG16718 gene product	301	48
443	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	221	74
444	U35730	Mus musculus	jerky	159	26
445	X53581	Rattus norvegicus	ORF3	192	46
446	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	142	52
447	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	156	38
448	AF194537	Homo sapiens	NAG13	315	70
449	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	93	66
450	X92099	Brugia pahangi	collagen	126	44
451	AF090930	Homo sapiens	PR00478	88	60
452	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	93	40
453	AF081114	Mus musculus domesticus	ORF2	108	32
454	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	173	65
455	S80119	Rattus sp.	reverse transcriptase homolog	197	54
456	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	89	68
457	R95913	Homo sapiens	Neural thread protein.	114	48
458	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	160	39
459	X92485	Plasmodium vivax	pva1	99	52
460	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	100	52
461	S80119	Rattus sp.	reverse transcriptase homolog	138	48
462	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	211	67
463	X97707	Pongo pygmaeus abelii	stopcodon created by posttranscriptional polyadenylation	229	76
464	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	119	67
465	L27428	Homo sapiens	reverse transcriptase	154	40
466	AK000496	Homo sapiens	unnamed protein product	140	69
467	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	61
468	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	146	69
469	D38112	Homo sapiens	cytochrome c oxidase subunit 3	286	79
470	D38112	Homo sapiens	NADH dehydrogenase subunit 4	448	86
471	M10546	Homo sapiens	cytochrome oxidase I	296	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
472	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	102	48
473	AL080253	Arabidopsis thaliana	putative snRNP protein	103	42
474	X99452	Lycopersicon esculentum	extensin-like protein Dif54	108	25
475	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	68	34
476	AB012223	Canis familiaris	ORF2	78	66
477	AF130089	Homo sapiens	PRO2550	113	71
478	G03652	Homo sapiens	Human secreted protein, SEQ ID NO: 7733.	390	97
479	AF210651	Homo sapiens	NAG18	146	80
480	AB029309	Homo sapiens	Npw38-binding protein NpwBP	103	40
481	AF194537	Homo sapiens	NAG13	118	31
482	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	115	45
483	L27428	Homo sapiens	reverse transcriptase	184	47
484	U93570	Homo sapiens	putative p150	101	50
485	AF194537	Homo sapiens	NAG13	213	52
486	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	82
487	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	204	86
488	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	140	53
489	U93574	Homo sapiens	putative p150	86	54
490	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	83	56
491	AJ271872	Nicotiana glauca	extensin	220	47
492	U11288	Drosophila melanogaster	diaphanous protein	113	33
493	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	184	70
494	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	68
495	AF119900	Homo sapiens	PRO2822	148	65
496	AB026542	Homo sapiens	WASP-family protein	96	38
497	D86853	Catharanthus roseus	extensin	104	34
498	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	109	47
499	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	109	67
500	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	112	62
501	AF119901	Homo sapiens	PRO2831	116	82
502	AF238235	Entamoeba histolytica	diaphanous protein	120	41
503	M22332	Homo sapiens	unknown protein	123	49
504	AF119851	Homo sapiens	PRO1722	204	52
505	X61296	Rattus norvegicus	open reading frame 2	107	45
506	AF118082	Homo sapiens	PRO1902	145	52
507	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	103	68
508	X55685	Lycopersicon esculentum	extensin (class I)	175	39
509	X92485	Plasmodium	pva1	117	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
510	AF090942	Homo sapiens	PRO0657	95	77
511	U93569	Homo sapiens	putative p150	120	54
512	U93574	Homo sapiens	putative p150	140	49
513	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	196	63
514	L27428	Homo sapiens	reverse transcriptase	132	37
515	U93565	Homo sapiens	putative p150	101	45
516	U93574	Homo sapiens	putative p150	178	35
517	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	81	27
518	AF053538	Alvinella pompejana	fibrillar collagen chain FAp1 alpha	112	36
519	X52235	Homo sapiens	ORFII	148	35
520	AF130051	Homo sapiens	PRO0898	98	61
521	L02106	Drosophila melanogaster	ribonucleoprotein	143	40
522	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	202	70
523	U93570	Homo sapiens	putative p150	159	43
524	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	210	100
525	L27428	Homo sapiens	reverse transcriptase	128	38
526	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	96	65
527	X53581	Rattus norvegicus	ORF4	130	42
528	U93570	Homo sapiens	putative p150	195	35
529	AF130089	Homo sapiens	PRO2550	132	43
530	AK024455	Homo sapiens	FLJ00047 protein	126	54
531	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	123	61
532	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	210	44
533	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	109	42
534	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	120	62
535	M64793	Rattus norvegicus	salivary proline-rich protein	124	37
536	R13556	Homo sapiens	Protein encoded downstream of hbc_M oncoprotein.	122	50
537	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	43
538	A23786	Beta vulgaris	chitinase 1	91	33
539	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	39
540	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	102	67
541	S80119	Rattus sp.	reverse transcriptase homolog	191	50
542	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	155	77
543	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: S909.	125	91
544	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	146	62
545	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	74	45
546	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	94	75
547	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	510	86
548	AF000616	Oryza sativa	similar to RING-H2 finger protein	146	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			RHA1a (AF078683)		
549	Y08061	Homo sapiens	Human c-myc protein fragment	128	82
550	B03628	Homo sapiens	Human phospholipase 2 HPPL2	153	77
551	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	121	56
552	X92485	Plasmodium vivax	pva1	103	50
553	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	129	46
554	L27428	Homo sapiens	reverse transcriptase	149	44
555	AF194537	Homo sapiens	NAG13	157	45
556	Y13247	Homo sapiens	FB19 protein	106	42
557	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	100	54
558	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	176	68
559	S80119	Rattus sp.	reverse transcriptase homolog	113	43
560	AY008270	Homo sapiens	cholesteryl ester transfer protein	107	95
561	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	140	63
562	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	347	68
563	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	93	40
564	D38114	Gorilla gorilla	cytochrome c oxidase subunit 3 (COIII)	329	74
565	Y36156	Homo sapiens	Human secreted protein #28.	153	56
566	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	131	48
567	D38112	Homo sapiens	cytochrome c oxidase subunit 3	406	94
568	AF130079	Homo sapiens	PRO2852	101	55
569	AF081114	Mus musculus domesticus	ORF2	123	40
570	L22030	Glycine max	hydroxyproline-rich glycoprotein	65	45
571	D86853	Catharanthus roseus	extensin	168	39
572	AF104415	Mus musculus	gene trap locus-13	179	66
573	AF130089	Homo sapiens	PRO2550	114	56
574	X67863	Mus musculus	T2	115	42
575	S80119	Rattus sp.	reverse transcriptase homolog	101	28
576	S80119	Rattus sp.	reverse transcriptase homolog	150	57
577	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	142	74
578	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	106	57
579	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	46
580	L24521	Homo sapiens	transformation-related protein	110	38
581	D38112	Homo sapiens	cytochrome c oxidase subunit 3	537	84
582	AF090895	Homo sapiens	PRO0117	127	80
583	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	145	70
584	X55681	Lycopersicon esculentum	extensin (class I)	112	38
585	D38112	Homo sapiens	cytochrome c oxidase subunit 3	473	60
586	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	144	68
587	U47855	Araneus diadematus	fibroin-3	124	30
588	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	150	75
589	U93567	Homo sapiens	putative p150	225	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
590	X71602	Nicotiana tabacum	extensin	147	33
591	X57527	Homo sapiens	alpha I(VIII) collagen	103	42
592	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	75	47
593	R28916	Homo sapiens	Type III procollagen (prior art).	116	48
594	R95913	Homo sapiens	Neural thread protein.	116	37
595	U11880	Petromyzon marinus	cytochrome oxidase subunit I	127	52
596	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	84	62
597	L27428	Homo sapiens	reverse transcriptase	158	40
598	M55251	Canis familiaris	glycoprotein 80	559	86
599	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
600	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	143	33
601	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	154	54
602	X73481	Drosophila hydei	mst101(2)	107	42
603	M81321	Macaca fascicularis	proline-rich protein	114	39
604	X05561	Homo sapiens	alpha-1 chain precursor (AA -27 to 917) (2953 is 2nd base in codon)	109	42
605	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	82	62
606	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	83	64
607	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	107	44
608	L27428	Homo sapiens	reverse transcriptase	147	43
609	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	113	61
610	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	151	82
611	U93568	Homo sapiens	putative p150	144	32
612	AB022223	Arabidopsis thaliana	extensin protein-like	186	58
613	Z70684	Caenorhabditis elegans	F28D1.8	108	49
614	M11901	Rattus norvegicus	proline-rich salivary protein	133	36
615	X92485	Plasmodium vivax	pva1	120	42
616	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	175	89
617	U83280	Leishmania donovani	39 kDa antigen	111	51
618	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	137	67
619	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	53
620	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	92	45
621	AF130089	Homo sapiens	PRO2550	123	34
622	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	133	59
623	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	127	45
624	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	205	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
625	X07882	Homo sapiens	Po protein	119	39
626	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	70	100
627	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	141	51
628	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	141	54
629	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	115	46
630	X63368	Homo sapiens	HSJ1b	151	52
631	AF130089	Homo sapiens	PRO2550	155	47
632	X92485	Plasmodium vivax	pva1	102	61
633	K03205	Homo sapiens	salivary proline-rich protein precursor	102	39
634	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	171	74
635	X92485	Plasmodium vivax	pva1	95	73
636	S80119	Rattus sp.	reverse transcriptase homolog	114	58
637	U15647	Mus musculus	reverse transcriptase	170	42
638	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	76
639	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	83	36
640	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	96	34
641	X61296	Rattus norvegicus	open reading frame 2	166	35
642	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	127	35
643	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24, HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	115	35
644	AF081111	Mus musculus domesticus	ORF2	168	33
645	AK027208	Homo sapiens	unnamed protein product	90	51
646	AF016099	Mus musculus	endonuclease/reverse transcriptase	101	59
647	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	149	76
648	AF273441	Pongo pygmaeus	NADH dehydrogenase subunit 3	121	58
649	L27428	Homo sapiens	reverse transcriptase	173	58
650	AF119851	Homo sapiens	PRO1722	176	53
651	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	168	68
652	AF130089	Homo sapiens	PRO2550	130	36
653	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	126	41
654	AK000385	Homo sapiens	unnamed protein product	195	63
655	AB041881	Rattus norvegicus	cytoplasmic dynein heavy chain	158	100
656	X61047	Hydra sp.	mini-collagen	60	38
657	M22332	Homo sapiens	unknown protein	100	50
658	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	143	62
659	AF194537	Homo sapiens	NAG13	95	48
660	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	120	50
661	U83303	Homo sapiens	line-1 reverse transcriptase	86	32
662	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	169	53
663	W48351	Homo sapiens	Human breast cancer related protein	120	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
664	U15647	Mus musculus	reverse transcriptase	148	50
665	R95913	Homo sapiens	Neural thread protein.	161	59
666	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	134	80
667	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	117	44
668	AB018705	Mus musculus	ORF2	115	32
669	D38112	Homo sapiens	NADH dehydrogenase subunit 4	280	75
670	X53581	Rattus norvegicus	ORF4	71	39
671	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	201	66
672	R95913	Homo sapiens	Neural thread protein.	144	78
673	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	164	46
674	AF118082	Homo sapiens	PRO1902	137	49
675	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	43
676	D00570	Mus musculus	open reading frame (251 AA)	112	72
677	AF194537	Homo sapiens	NAG13	238	56
678	M13100	Rattus norvegicus	unknown protein	146	51
679	U15647	Mus musculus	reverse transcriptase	123	54
680	R95913	Homo sapiens	Neural thread protein.	145	55
681	R59842	Homo sapiens	ApoE4L1 protease.	107	63
682	AF130089	Homo sapiens	PRO2550	94	51
683	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	129	69
684	AF093748	Homo sapiens	KH type splicing regulatory protein; KSRP	93	50
685	U93569	Homo sapiens	putative p150	133	58
686	G03095	Homo sapiens	Human secreted protein, SEQ ID NO: 7176.	117	64
687	Y36243	Homo sapiens	Human secreted protein encoded by gene 20.	69	73
688	AF116712	Homo sapiens	PRO2738	133	56
689	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	134	53
690	U93563	Homo sapiens	putative p150	132	49
691	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	349	70
692	AF090895	Homo sapiens	PRO0117	115	63
693	AF130089	Homo sapiens	PRO2550	132	80
694	S80119	Rattus sp.	reverse transcriptase homolog	101	43
695	U15647	Mus musculus	reverse transcriptase	120	64
696	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	132	59
697	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	128	72
698	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	182	47
699	D38112	Homo sapiens	cytochrome c oxidase subunit I	459	83
700	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	148	73
701	AF003535	Homo sapiens	ORF2-like protein	125	49
702	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	89	41
703	L27428	Homo sapiens	reverse transcriptase	255	50
704	AF130089	Homo sapiens	PRO2550	87	55
705	G03052	Homo sapiens	Human secreted protein, SEQ ID NO:	113	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7133.		
706	Y79140	Homo sapiens	Human haemopoietic stem cell regulatory protein SCM3.	211	88
707	U15647	Mus musculus	reverse transcriptase	94	47
708	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	153	66
709	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	107	50
710	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	163	64
711	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	65
712	U93565	Homo sapiens	putative p150	108	33
713	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	108	37
714	M24732	Homo sapiens	lamin-like protein	92	35
715	D38112	Homo sapiens	cytochrome c oxidase subunit 3	306	79
716	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	462	85
717	AF004715	Homo sapiens	jerky gene product homolog	100	42
718	X92485	Plasmodium vivax	pval	84	48
719	AF130089	Homo sapiens	PRO2550	132	74
720	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	125	43
721	AK024455	Homo sapiens	FLJ00047 protein	108	68
722	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	146	46
723	X83413	Human herpesvirus 6	U88	269	41
724	X92485	Plasmodium vivax	pval	117	43
725	X92485	Plasmodium vivax	pval	97	41
726	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	102	73
727	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	43
728	A23786	Beta vulgaris	chitinase I	91	33
729	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	49
730	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	131	59
731	W49717	Homo sapiens	Protein polymer adhesive substrate PFAS1-C.	148	29
732	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	95	45
733	X96731	Ostertagia circumcincta	cuticular collagen	104	37
734	AF130089	Homo sapiens	PRO2550	118	40
735	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	166	100
736	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	494	86
737	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	188	69
738	D38112	Homo sapiens	cytochrome c oxidase subunit 3	593	91
739	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	102	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
740	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	111	54
741	A23786	Beta vulgaris	chitinase I	106	36
742	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	71	72
743	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	184	61
744	AE003629	Drosophila melanogaster	CG17108 gene product	76	36
745	U93563	Homo sapiens	putative p150	145	50
746	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	68	66
747	AF217973	Homo sapiens	unknown	113	79
748	AC006161	Arabidopsis thaliana	putative CENP-B/ARS-binding protein-like protein	112	31
749	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	106	47
750	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	54
751	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	99	72
752	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	85	48
753	X92485	Plasmodium vivax	pval	89	73
754	U93563	Homo sapiens	putative p150	186	68
755	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	50
756	AF194537	Homo sapiens	NAG13	138	40
757	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	112	79
758	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	119	61
759	AF130079	Homo sapiens	PRO2852	138	40
760	X92485	Plasmodium vivax	pval	88	77
761	U93050	Mus musculus	poly(A) binding protein II	95	35
762	V01555	Human herpesvirus 4	BYRF1, encodes EBNA-2 (Dambaugh et al, 1984; Dillner et al, 1984)	80	41
763	V00662	Homo sapiens	ATPase 6	337	83
764	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	117	41
765	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	423	81
766	R95913	Homo sapiens	Neural thread protein.	114	66
767	V00662	Homo sapiens	cytochrome oxidase I	223	83
768	D38112	Homo sapiens	NADH dehydrogenase subunit 4	268	83
769	V00662	Homo sapiens	cytochrome oxidase I	357	81
770	D38112	Homo sapiens	NADH dehydrogenase subunit 4	296	71
771	AF026211	Caenorhabditis elegans	Similar to cuticular collagen	95	39
772	AK024455	Homo sapiens	FLJ00047 protein	108	53
773	X92485	Plasmodium vivax	pval	95	39
774	AF130051	Homo sapiens	PRO0898	123	38
775	AB012223	Canis familiaris	ORF2	174	51
776	AB028664	Paralichthys olivaceus	cytochrome oxidase subunit-3	268	57
777	V00662	Homo sapiens	cytochrome oxidase I	436	85
778	X52235	Homo sapiens	ORFII	125	47
779	U93569	Homo sapiens	putative p150	235	49

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
780	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	262	76
781	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	239	70
782	AF090942	Homo sapiens	PRO0657	146	69
783	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	85	66
784	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	209	62
785	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	184	60
786	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	158	60
787	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	293	86
788	AF130089	Homo sapiens	PRO2550	153	64
789	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	131	57
790	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	100	51
791	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	116	80
792	Y36203	Homo sapiens	Human secreted protein #75.	104	77
793	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	117	58
794	AF090930	Homo sapiens	PRO0478	130	68
795	AK024455	Homo sapiens	FLJ00047 protein	114	61
796	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	141	70
797	AF130089	Homo sapiens	PRO2550	273	85
798	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	134	66
799	AF130051	Homo sapiens	PRO0898	162	80
800	G03560	Homo sapiens	Human secreted protein, SEQ ID NO: 7641.	179	70
801	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	75	51
802	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	103	34
803	D38484	Hylobates syndactylus	Cytochrome C oxidase subunit I (COXI)	263	70
804	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	112	41
805	X92485	Plasmodium vivax	pval	103	38
806	AF194537	Homo sapiens	NAG13	285	51
807	AF121360	Drosophila melanogaster	DNZDHC/NEW1 zinc finger protein 11	179	47
808	X92485	Plasmodium vivax	pval	131	46
809	D13951	Nicotiana tabacum	extensin precursor	88	41
810	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	174	73
811	U93565	Homo sapiens	putative p150	118	38
812	AF118082	Homo sapiens	PRO1902	88	54
813	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	132	42
814	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	114	50
815	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	113	43
816	K02576	Homo sapiens	salivary proline-rich protein 1	148	40

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
817	AF217449	Schistosoma mekongi	NADH dehydrogenase subunit 6	102	37
818	AB012223	Canis familiaris	ORF2	101	54
819	X71602	Nicotiana tabacum	extensin	162	45
820	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	154	36
821	R95913	Homo sapiens	Neural thread protein.	153	61
822	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	125	61
823	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	364	57
824	U43360	Peromyscus maniculatus	reverse transcriptase	121	48
825	AF194537	Homo sapiens	NAG13	224	58
826	U97674	Mesocricetus auratus	cytochrome c oxidase chain 1	437	72
827	AF051782	Homo sapiens	diaphanous 1	108	38
828	AF194537	Homo sapiens	NAG13	92	45
829	D38112	Homo sapiens	cytochrome c oxidase subunit 3	492	75
830	M64791	Rattus norvegicus	salivary proline-rich protein	110	46
831	X55685	Lycopersicon esculentum	extensin (class 1)	108	31
832	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	117	34
833	U93564	Homo sapiens	putative p150	84	40
834	U93563	Homo sapiens	putative p150	262	54
835	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	214	80
836	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhla.	107	48
837	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	158	76
838	AF194537	Homo sapiens	NAG13	153	60
839	U52077	Homo sapiens	mariner transposase	344	67
840	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	104	46
841	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	130	92
842	M64791	Rattus norvegicus	salivary proline-rich protein	114	36
843	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	196	43
844	X92485	Plasmodium vivax	pva1	102	73
845	X61048	Hydra sp.	mini-collagen	106	41
846	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	48
847	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	54
848	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	128	68
849	AF194537	Homo sapiens	NAG13	141	46
850	U43360	Peromyscus maniculatus	reverse transcriptase	121	45
851	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	153	58
852	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	220	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
853	X92485	Plasmodium vivax	pval	127	45
854	AF134305	Homo sapiens	Scar3	99	38
855	D38112	Homo sapiens	NADH dehydrogenase subunit 2	343	68
856	S80119	Rattus sp.	reverse transcriptase homolog	159	56
857	AF130089	Homo sapiens	PRO2550	112	40
858	AK024372	Homo sapiens	unnamed protein product	129	50
859	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	103	76
860	D38112	Homo sapiens	cytochrome c oxidase subunit 3	279	80
861	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	96	44
862	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	83	40
863	AF210651	Homo sapiens	NAG18	122	63
864	AF016099	Mus musculus	endonuclease/reverse transcriptase	109	51
865	X55685	Lycopersicon esculentum	extensin (class I)	115	34
866	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	107	80
867	X92485	Plasmodium vivax	pval	105	41
868	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	127	62
869	X92485	Plasmodium vivax	pval	105	38
870	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	90	56
871	Y27571	Homo sapiens	Human secreted protein encoded by gene No. 5.	128	72
872	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	123	36
873	AF130089	Homo sapiens	PRO2550	160	82
874	AF118082	Homo sapiens	PRO1902	143	65
875	U93564	Homo sapiens	putative p150	180	44
876	M10546	Homo sapiens	cytochrome oxidase I	248	75
877	U83303	Homo sapiens	line-1 reverse transcriptase	127	52
878	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	106	35
879	U11288	Drosophila melanogaster	diaphanous protein	93	46
880	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhia.	71	47
881	B08942	Homo sapiens	Human secreted protein sequence encoded by gene 18 SEQ ID NO:99.	95	40
882	AF130089	Homo sapiens	PRO2550	137	44
883	AF090942	Homo sapiens	PRO0657	142	73
884	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	97	60
885	X61296	Rattus norvegicus	open reading frame 2	106	43
886	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	91	57
887	X14963	Homo sapiens	collagen-like protein (447 AA)	130	51
888	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	117	55
889	L25616	Homo sapiens	CG1 protein	150	62
890	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	171	66
891	Y86472	Homo sapiens	Human gene 52-encoded protein	107	40

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			fragment, SEQ ID NO:387.		
892	X52318	Bos taurus	histone H2A.Z (AA 1-127)	356	79
893	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	102	46
894	D38112	Homo sapiens	cytochrome c oxidase subunit 1	173	75
895	X92485	Plasmodium vivax	pval	109	47
896	L76159	Homo sapiens	FRG1 gene product	100	35
897	D50926	Homo sapiens	The KIAA0136 gene product is novel.	280	89
898	X04011	Homo sapiens	precursor polypeptide	114	95
899	M90656	Homo sapiens	gamma-glutamylcysteine synthetase	101	90
900	R95913	Homo sapiens	Neural thread protein.	95	75
901	L27428	Homo sapiens	reverse transcriptase	81	47
902	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	104	53
903	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	105	76
904	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	126	37
905	AF130089	Homo sapiens	PRO2550	88	82
906	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	230	50
907	L27428	Homo sapiens	reverse transcriptase	114	64
908	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	142	71
909	U93570	Homo sapiens	putative p150	130	41
910	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	91	63
911	L27428	Homo sapiens	reverse transcriptase	168	46
912	X92485	Plasmodium vivax	pval	91	60
913	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	103	64
914	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	96	64
915	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	121	51
916	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	87	77
917	M12099	Mus musculus	proline-rich protein	129	44
918	M15530	Homo sapiens	B-cell growth factor	88	51
919	AF130079	Homo sapiens	PRO2852	158	88
920	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	103	77
921	X53581	Rattus norvegicus	ORF4	124	32
922	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	110	50
923	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	99	36
924	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	80	47
925	AC006127	Homo sapiens	BRG-1-HUMAN; nuclear protein GRB1; homeotic gene regulator; SNF2-BETA; MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR; POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4	442	92
926	L17318	Rattus norvegicus	proline-rich proteoglycan	126	39
927	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	321	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
928	AC006161	Arabidopsis thaliana	putative CENP-B/ARS-binding protein-like protein	97	35
929	X02873	Daucus carota	put. precursor	112	38
930	U93563	Homo sapiens	putative p150	125	70
931	AB012223	Canis familiaris	ORF2	202	50
932	AF053538	Alvinella pompejana	fibrillar collagen chain Fap1 alpha	114	37
933	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	107	57
934	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	283	54
935	U41017	Caenorhabditis elegans	repetitive region; weakly similar to E. gracilis major membrane skeletal protein (PIR:A43417)	107	33
936	U47855	Araneus diadematus	fibroin-3	109	33
937	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	95	43
938	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	108	50
939	M13101	Rattus norvegicus	unknown protein	121	40
940	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	117	46
941	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	88	62
942	L27428	Homo sapiens	reverse transcriptase	86	45
943	U93564	Homo sapiens	putative p150	279	40
944	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	110	48
945	L27428	Homo sapiens	reverse transcriptase	238	66
946	AF194537	Homo sapiens	NAG13	146	47
947	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	81	35
948	AC006161	Arabidopsis thaliana	putative CENP-B/ARS-binding protein-like protein	113	37
949	AF194537	Homo sapiens	NAG13	106	66
950	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	74	75
951	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	78	66
952	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	85	72
953	U44838	Glycine max	extensin	145	39
954	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	131	39
955	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	128	53
956	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	103	74
957	AF130089	Homo sapiens	PRO2550	120	37
958	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	115	71
959	AF090942	Homo sapiens	PRO0657	83	63
960	L27428	Homo sapiens	reverse transcriptase	121	30
961	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	157	68
962	AF090942	Homo sapiens	PRO0657	138	61
963	U83280	Leishmania donovani	39 kDa antigen	101	53
964	U93566	Homo sapiens	p40	102	31

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
965	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	104	63
966	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	136	40
967	AF090930	Homo sapiens	PRO0478	158	80
968	AB012223	Canis familiaris	ORF2	94	36
969	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	127	54
970	X53581	Rattus norvegicus	ORF4	163	43
971	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	109	56
972	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	82	47
973	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	95	80
974	G03095	Homo sapiens	Human secreted protein, SEQ ID NO: 7176.	74	51
975	U93574	Homo sapiens	putative p150	140	43
976	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	79	65
977	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	116	55
978	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	148	63
979	AF130114	Homo sapiens	PRO2459	121	61
980	K03202	Homo sapiens	salivary proline-rich protein precursor	99	40
981	AF116909	Homo sapiens	unknown	115	42
982	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	106	75
983	Y14674	Plasmodium falciparum	glutamate--cysteine ligase	106	66
984	AF229067	Homo sapiens	PADI-H protein	152	60
985	AF119900	Homo sapiens	PRO2822	142	48
986	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	70
987	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	106	60
988	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	81	51
990	U35730	Mus musculus	jerky	133	29
991	AF113685	Homo sapiens	PRO0974	136	63
992	U52077	Homo sapiens	mariner transposase	497	77
993	Z97211	Schizosaccharomyces pombe	kinesin-like protein	197	47
994	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	68
995	U93563	Homo sapiens	putative p150	157	50
996	AB015802	Acetobacter xylinus	similar to cellulose complementing protein of A. xylinum ATCC23869	140	54
997	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	144	60
998	D38116	Pan paniscus	cytochrome c oxidase subunit I	352	75
999	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	524	78
1000	V00662	Homo sapiens	URF I (NADH dehydrogenase subunit)	377	70
1001	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	109	50
1002	AL390114	Leishmania major	extremely cysteine/valine rich protein	249	61
1003	M14702	Murine leukemia	pol polyprotein	206	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		virus			
1004	Z21507	Homo sapiens	human elongation factor-1-delta	511	85
1005	L27428	Homo sapiens	reverse transcriptase	176	63
1006	D58112	Homo sapiens	NADH dehydrogenase subunit 5	332	77
1007	AF090895	Homo sapiens	PRO0117	162	66
1008	G05102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	140	65
1009	U44838	Glycine max	extensin	166	33
1010	AF251290	Plasmodium falciparum	glutamic acid-rich protein	114	52
1011	L27428	Homo sapiens	reverse transcriptase	114	52
1012	AF130089	Homo sapiens	PRO2550	114	77
1013	G04092	Homo sapiens	Human secreted protein, SEQ ID NO: 8173.	81	44
1014	AF090895	Homo sapiens	PRO0117	97	65
1015	AF130089	Homo sapiens	PRO2550	168	83
1016	AF079367	Mesocricetus auratus	cytochrome c oxidase subunit III	276	52
1017	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	94	44
1018	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	114	46
1019	AF090944	Homo sapiens	PRO0663	137	50
1020	Y21166	Homo sapiens	Human bcl2 proto-oncogene mutant protein fragment 14.	84	36
1021	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	140	37
1022	AL049608	Arabidopsis thaliana	extensin-like protein	105	34
1023	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	152	52
1024	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	66
1025	M12140	Homo sapiens	envelope protein	143	62
1026	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	200	58
1027	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	266	67
1028	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	97	31
1029	G02950	Homo sapiens	Human secreted protein, SEQ ID NO: 7031.	102	56
1030	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	76	63
1031	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	74	56
1032	X90568	Homo sapiens	Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from L.ABEIT@EMBL-Heidelberg.DE	389	100
1033	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	96	40
1034	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	316	60
1035	AF194537	Homo sapiens	NAG13	208	52
1036	L27428	Homo sapiens	reverse transcriptase	166	51
1037	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	44
1038	AF116638	Homo sapiens	PRO1546	56	61
1039	U93570	Homo sapiens	putative p150	138	40
1040	AF130089	Homo sapiens	PRO2550	150	91
1041	AK024455	Homo sapiens	FLJ00047 protein	151	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1042	Y36156	Homo sapiens	Human secreted protein #28.	97	41
1043	U93568	Homo sapiens	putative p150	124	34
1044	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	208	71
1045	U93563	Homo sapiens	putative p150	246	54
1046	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	131	64
1047	U93563	Homo sapiens	putative p150	127	30
1048	AF130114	Homo sapiens	PRO2459	117	67
1049	U12919	Mus musculus	adenyl cyclase type VII	170	68
1050	AC008054	Leishmania major	L8453.1	129	30
1051	X99467	Medicago truncatula	ENOD20	110	38
1052	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	150	76
1053	AF116712	Homo sapiens	PRO2738	109	44
1054	M96256	Homo sapiens	rapamycin binding protein	168	56
1055	U15647	Mus musculus	reverse transcriptase	86	37
1056	AL024498	Homo sapiens	dJ417M14.2 (novel serine/threonine-protein kinase (ortholog of mouse and rat MAK (male germ cell-associated kinase)))	190	72
1057	AF090942	Homo sapiens	PRO0657	103	63
1058	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	156	68
1059	AF081114	Mus musculus domesticus	ORF2	134	47
1060	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	180	83
1061	U70935	Peromyscus maniculatus	reverse transcriptase	126	45
1062	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	84	55
1063	U15647	Mus musculus	reverse transcriptase	95	38
1064	U93567	Homo sapiens	putative p150	128	58
1065	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	130	66
1066	X92485	Plasmodium vivax	pval	119	62
1067	U93567	Homo sapiens	p40	161	48
1068	D38112	Homo sapiens	cytochrome c oxidase subunit 3	540	84
1069	U93570	Homo sapiens	putative p150	107	59
1070	AF321051	Chalimolobus tuberculatus	cytochrome c oxidase subunit III	333	71
1071	U93567	Homo sapiens	p40	99	28
1072	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	105	66
1073	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	59
1074	U93572	Homo sapiens	putative p150	140	53
1075	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	66	43
1076	AL049608	Arabidopsis thaliana	extensin-like protein	105	37
1077	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	94	66
1078	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	81	57
1079	G04091	Homo sapiens	Human secreted protein, SEQ ID NO:	83	35

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			8172.		
1080	AF162149	Mycoplasma bovis	variable surface lipoprotein	103	41
1081	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	148	75
1082	U43360	Peromyscus maniculatus	reverse transcriptase	121	42
1083	U93564	Homo sapiens	p40	97	42
1084	AF229067	Homo sapiens	PADI-H protein	145	61
1085	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	221	60
1086	U88573	Homo sapiens	NBR2	165	67
1087	Y36156	Homo sapiens	Human secreted protein #28.	93	72
1088	AF194537	Homo sapiens	NAG13	142	62
1089	B08976	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:133.	93	62
1090	AF194537	Homo sapiens	NAG13	155	40
1091	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	103	35
1092	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	195	40
1093	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	91	46
1094	X53581	Rattus norvegicus	ORF4	106	62
1095	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	129	51
1096	Y86473	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:388.	72	33
1097	U40342	Mus musculus	ninein	152	44
1098	M24732	Homo sapiens	lamin-like protein	92	37
1099	X92485	Plasmodium vivax	pva1	111	67
1100	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	156	86
1101	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	90
1102	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	158	71
1103	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	97	36
1104	U93572	Homo sapiens	putative p150	168	56
1105	U93570	Homo sapiens	putative p150	96	40
1106	L27428	Homo sapiens	reverse transcriptase	188	43
1107	X53581	Rattus norvegicus	ORF4	141	43
1108	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	344	77
1109	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	126	68
1110	U93569	Homo sapiens	putative p150	156	38
1111	AF118086	Homo sapiens	PRO1992	135	54
1112	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	71	63
1113	AF016099	Mus musculus	endonuclease/reverse transcriptase	124	62
1114	L27428	Homo sapiens	reverse transcriptase	200	40
1115	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	101	50
1116	L27428	Homo sapiens	reverse transcriptase	122	70
1117	G00637	Homo sapiens	Human secreted protein, SEQ ID NO:	148	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4718.		
1118	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	116	65
1119	D38484	Hylobates syndactylus	Cytochrome C oxidase subunit 1 (COXI)	315	89
1120	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	115	76
1121	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	136	68
1122	AF013990	Homo sapiens	ubiquitin C-terminal hydrolase	163	50
1123	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	94	55
1124	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	154	65
1125	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	53
1126	AF130089	Homo sapiens	PRO2550	76	72
1127	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	92	59
1128	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	80	59
1129	AF119855	Homo sapiens	PRO1847	146	70
1130	AF194537	Homo sapiens	NAG13	182	66
1131	L27428	Homo sapiens	reverse transcriptase	173	38
1132	U93570	Homo sapiens	putative p150	119	34
1133	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	157	68
1134	AJ004810	Zea mays	cytochrome P450 monooxygenase	79	87
1135	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	70
1136	G01502	Homo sapiens	Human secreted protein, SEQ ID NO: 5583.	81	73
1137	AB018705	Mus musculus	ORF2	138	36
1138	L20321	Homo sapiens	protein serine/threonine kinase	150	63
1139	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	60
1140	AF194537	Homo sapiens	NAG13	115	33
1141	U93564	Homo sapiens	putative p150	135	51
1142	D86853	Catharanthus roseus	extensin	142	37
1143	D00570	Mus musculus	open reading frame (251 AA)	213	50
1144	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	62	38
1145	Z70684	Caenorhabditis elegans	F28D1.8	105	32
1146	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	79	54
1147	Y36156	Homo sapiens	Human secreted protein #28.	151	62
1148	A23786	Beta vulgaris	chitinase 1	98	37
1149	AF129756	Homo sapiens	BAT2	177	52
1150	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	147	73
1151	L27428	Homo sapiens	reverse transcriptase	77	31
1152	U34044	Homo sapiens	selenium donor protein	238	48
1153	AK024455	Homo sapiens	FLJ00047 protein	78	78
1154	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	197	67
1155	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	120	64
1156	U25281	Rattus norvegicus	SH3 domain binding protein	98	34
1157	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1158	AF194537	Homo sapiens	NAG13	106	48
1159	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	357	69
1160	U93572	Homo sapiens	p40	89	47
1161	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	184	68
1162	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	123	57
1163	AF116712	Homo sapiens	PRO2738	129	69
1164	V00662	Homo sapiens	cytochrome oxidase I	465	69
1165	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	118	57
1166	L26163	Mus musculus	histone H1c	104	37
1167	X70343	Nicotiana sylvestris	extensin	95	33
1168	AF130051	Homo sapiens	PRO0898	117	43
1169	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	104	48
1170	L27428	Homo sapiens	reverse transcriptase	149	33
1171	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	108	62
1172	AF030277	Tragelaphus spekkii	cytochrome oxidase subunit III	266	54
1173	L22030	Glycine max	hydroxyproline-rich glycoprotein	87	38
1174	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	168	45
1175	U43627	Arabidopsis thaliana	extensin	111	42
1176	U43627	Arabidopsis thaliana	extensin	98	29
1177	U93565	Homo sapiens	putative p150	89	58
1178	J01047	Caenorhabditis elegans	collagen	108	39
1179	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	68
1180	AF016099	Mus musculus	endonuclease/reverse transcriptase	113	36
1181	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	134	65
1182	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	107	62
1183	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	124	45
1184	D38112	Homo sapiens	NADH dehydrogenase subunit 2	418	86
1185	U87607	Rattus norvegicus	putative RNA binding protein 1	106	41
1186	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	381	75
1187	D38112	Homo sapiens	cytochrome c oxidase subunit 1	434	79
1188	U83303	Homo sapiens	line-1 reverse transcriptase	75	35
1189	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	159	68
1190	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	146	68
1191	AF118086	Homo sapiens	PRO1992	146	81
1192	W12842	Homo sapiens	Truncated pro-alpha1(III) chain.	106	35
1193	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	67	34
1194	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	116	74
1195	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	132	82

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1196	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	75	48
1197	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	254	73
1198	U93570	Homo sapiens	p40	103	30
1199	AL390114	Leishmania major	extremely cysteine/valine rich protein	145	39
1200	AK024455	Homo sapiens	FLJ00047 protein	115	56
1201	AF090942	Homo sapiens	PRO0657	88	64
1202	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	124	70
1203	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	113	46
1204	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	81	41
1205	U35730	Mus musculus	jerky	107	27
1206	U15647	Mus musculus	reverse transcriptase	191	45
1207	U15647	Mus musculus	reverse transcriptase	124	50
1208	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	140	58
1209	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	91	54
1210	AF119900	Homo sapiens	PRO2822	160	81
1211	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	68
1212	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	45
1213	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	125	61
1214	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	102	61
1215	G03560	Homo sapiens	Human secreted protein, SEQ ID NO: 7641.	101	46
1216	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	270	58
1217	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	105	46
1218	AC002483	Homo sapiens	putative product from mRNA sequence CG003 from BRCA2 region; match to U50534 (NID:g1685103)	378	97
1219	AF090895	Homo sapiens	PRO0117	130	58
1220	AF113685	Homo sapiens	PRO0974	117	60
1221	X61295	Rattus norvegicus	L1 retroposon, a portion of its ORF2 sequence	126	50
1222	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	148	70
1223	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	99	56
1224	U93574	Homo sapiens	putative p150	93	44
1225	AF130051	Homo sapiens	PRO0898	133	69
1226	U93563	Homo sapiens	putative p150	125	47
1227	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	220	47
1228	U93564	Homo sapiens	putative p150	116	47
1229	W21733	Homo sapiens	NIP-1 encoded by clone 59.	138	63
1230	U15647	Mus musculus	reverse transcriptase	105	42
1231	U93563	Homo sapiens	putative p150	299	54
1232	R95913	Homo sapiens	Neural thread protein.	138	51
1233	AF130079	Homo sapiens	PRO2852	203	70
1234	X53581	Rattus norvegicus	ORF3	106	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1235	AF118086	Homo sapiens	PRO1992	144	81
1236	X92485	Plasmodium vivax	pva1	125	71
1237	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	75
1238	U93572	Homo sapiens	putative p150	133	40
1239	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	69	56
1240	AF130089	Homo sapiens	PRO2550	136	41
1241	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	109	53
1242	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	75
1243	G02752	Homo sapiens	Human secreted protein, SEQ ID NO: 6833.	87	45
1244	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	128	58
1245	U93570	Homo sapiens	putative p150	161	50
1246	Z70684	Caenorhabditis elegans	F28D1.8	121	45
1247	AF257305	Homo sapiens	ASH1	576	89
1248	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	98	68
1249	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	107	43
1250	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	91
1251	U63542	Homo sapiens	FAP protein	116	61
1252	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	109	53
1253	AF068294	Homo sapiens	HDCMB45P	251	63
1254	AF090895	Homo sapiens	PRO0117	111	60
1255	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	201	75
1256	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	51
1257	AB033032	Homo sapiens	KIAA1206 protein	115	80
1258	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	122	60
1259	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	137	68
1260	AB032906	Hylobates pileatus	dopamine receptor D4	96	35
1261	AF022985	Caenorhabditis elegans	Similar to collagen; coded for by C. elegans cDNA yk553.3; coded for by C. elegans cDNA yk66d5.3; coded for by C. elegans cDNA yk71e4.3; coded for by C. elegans cDNA yk553.5; coded for by C. elegans cDNA yk66d5.5; coded for by C. elegans cDNA yk71e4.5	106	38
1262	U93566	Homo sapiens	p40	182	39
1263	L20096	Manduca sexta	ribosomal protein s7	227	59
1264	AF119901	Homo sapiens	PRO2831	103	71
1265	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	219	97
1266	D90279	Homo sapiens	collagen alpha 1(V) chain precursor	120	42
1267	L27428	Homo sapiens	reverse transcriptase	111	41
1268	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	126	68
1269	AF016099	Mus musculus	endonuclease/reverse transcriptase	102	34

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1270	AF130089	Homo sapiens	PRO2550	96	69
1271	U12707	Homo sapiens	Wiskott-Aldrich syndrome protein	121	45
1272	AF165310	Homo sapiens	ATP cassette binding transporter 1	243	100
1273	R95913	Homo sapiens	Neural thread protein.	110	70
1274	X92485	Plasmodium vivax	pval	106	65
1275	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	104	56
1276	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	53	36
1277	X03725	Mus musculus	ORF 2 (466 aa)	103	41
1278	U93570	Homo sapiens	putative p150	98	43
1279	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	159	83
1280	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	167	71
1281	AJ271871	Nicotiana glauca	putative extensin	105	36
1282	K03205	Homo sapiens	salivary proline-rich protein precursor	119	32
1283	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	66
1284	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	135	50
1285	A31039	Nicotiana glauca	PRP3	112	36
1286	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	116	72
1287	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	289	67
1288	S80119	Rattus sp.	reverse transcriptase homolog	112	33
1289	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	203	76
1290	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	151	53
1291	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	128	82
1292	AF130089	Homo sapiens	PRO2550	127	62
1293	AF003535	Homo sapiens	ORF2-like protein	101	48
1294	Y19610	Homo sapiens	SEQ ID NO 328 from WO9922243.	100	42
1295	L27428	Homo sapiens	reverse transcriptase	126	36
1296	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	140	71
1297	L24433	Oncorhynchus mykiss	complement component C3	359	31
1298	AC004381	Homo sapiens	SA gene	443	55
1299	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	180	64
1300	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	135	66
1301	D84391	Mus musculus	reverse transcriptase	106	48
1302	D13951	Nicotiana glauca	extensin precursor	134	42
1303	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	73
1304	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	93	38
1305	Y13620	Homo sapiens	BCL9	102	39
1306	U93567	Homo sapiens	putative p150	245	63
1307	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	130	70
1308	AL355774	Streptomyces coelicolor A3(2)	putative integral membrane protein	136	40
1309	W54966	Homo sapiens	Synthetic human type III collagen	124	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SYN-C3.		
1310	M20670	Plasmodium vivax	circumsporozoite protein	107	34
1311	AF151366	Arabidopsis thaliana	arginine/serine-rich protein	114	36
1312	G03099	Homo sapiens	Human secreted protein, SEQ ID NO: 7180.	76	43
1313	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	109	85
1314	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	111	37
1315	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	123	62
1316	R95913	Homo sapiens	Neural thread protein.	98	58
1317	AF113685	Homo sapiens	PRO0974	170	47
1318	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	122	61
1319	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	99	68
1320	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	270	56
1321	U93569	Homo sapiens	putative p150	124	37
1322	AF090931	Homo sapiens	PRO0483	111	85
1323	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	85	44
1324	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	131	43
1325	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	144	54
1326	AF194537	Homo sapiens	NAG13	125	49
1327	L27428	Homo sapiens	reverse transcriptase	111	45
1328	U93568	Homo sapiens	putative p150	112	30
1329	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	110	51
1330	L27428	Homo sapiens	reverse transcriptase	142	53
1331	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	98	88
1332	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	55
1333	X71602	Nicotiana tabacum	extensin	113	35
1334	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	129	41
1335	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	112	50
1336	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	102	68
1337	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	95	51
1338	U43360	Peromyscus maniculatus	reverse transcriptase	114	60
1339	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	142	55
1340	X55685	Lycopersicon esculentum	extensin (class I)	123	31
1341	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	118	70
1342	X71629	Mus musculus	mngl	106	57
1343	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	105	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1344	G03435	Homo sapiens	Human secreted protein, SEQ ID NO: 7516.	116	85
1345	AF161356	Homo sapiens	HSPC093	88	88
1346	J01435	Rattus norvegicus	ATPase	348	66
1347	U93563	Homo sapiens	putative p150	142	36
1348	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	87	66
1349	AF090942	Homo sapiens	PRO0657	152	54
1350	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	143	63
1351	U93572	Homo sapiens	putative p150	113	84
1352	X92485	Plasmodium vivax	pval	130	70
1353	X61047	Hydra sp.	mini-collagen	105	36
1354	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	128	46
1355	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	39
1356	AF194537	Homo sapiens	NAG13	148	63
1357	AF130079	Homo sapiens	PRO2852	139	73
1358	X53581	Rattus norvegicus	ORF4	208	43
1359	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	50
1360	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	328	69
1361	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	126	65
1362	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	97	47
1363	X53581	Rattus norvegicus	ORF4	110	35
1364	U93569	Homo sapiens	putative p150	123	41
1365	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	114	63
1366	X61294	Rattus norvegicus	L1 retroposon, a portion of its ORF2 sequence	153	43
1367	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	69	80
1368	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	80	46
1369	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	113	26
1370	X92485	Plasmodium vivax	pval	106	46
1371	U90946	Dictyostelium discoideum	myosin heavy chain kinase B	114	62
1372	L27428	Homo sapiens	reverse transcriptase	98	61
1373	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	124	80
1374	U49974	Homo sapiens	mariner transposase	137	57
1375	AC004891	Homo sapiens	contactin-like; similar to U87224 (PID:g1857710)	234	58
1376	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	132	60
1377	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	317	51
1378	AF118082	Homo sapiens	PRO1902	102	42
1379	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	186	45
1380	U93567	Homo sapiens	putative p150	116	38
1381	U49973	Homo sapiens	ORF1; MER37; putative transposase	218	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			similar to pogo element		
1382	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	87	66
1383	AF090895	Homo sapiens	PRO0117	68	82
1384	U93570	Homo sapiens	putative p150	178	39
1385	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	132	43
1386	AF130089	Homo sapiens	PRO2550	142	35
1387	L27428	Homo sapiens	reverse transcriptase	163	49
1388	X61296	Rattus norvegicus	open reading frame 2	123	44
1389	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	138	67
1390	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	147	57
1391	U93570	Homo sapiens	putative p150	110	28
1392	R95913	Homo sapiens	Neural thread protein.	104	35
1393	L27428	Homo sapiens	reverse transcriptase	101	39
1394	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	147	47
1395	AF216972	Homo sapiens	p8 protein	118	49
1396	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	160	58
1397	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	312	62
1398	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	97	62
1399	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	54
1400	X92485	Plasmodium vivax	pva1	124	39
1401	U93563	Homo sapiens	putative p150	131	36
1402	X67863	Mus musculus	T2	160	48
1403	K02576	Homo sapiens	salivary proline-rich protein 1	94	39
1404	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	84	73
1405	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	71	71
1406	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	138	31
1407	AF134304	Homo sapiens	Scar2	118	40
1408	Y08061	Homo sapiens	Human c-myc protein fragment.	121	82
1409	U93574	Homo sapiens	putative p150	179	43
1410	U93563	Homo sapiens	putative p150	98	43
1411	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	124	46
1412	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	149	56
1413	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	148	48
1414	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	155	82
1415	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	92	52
1416	AF119855	Homo sapiens	PRO1847	82	70
1417	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	130	34
1418	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	99	39
1419	AF130079	Homo sapiens	PRO2852	114	69
1420	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	133	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1421	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	115	44
1422	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	111	77
1423	R95913	Homo sapiens	Neural thread protein.	128	80
1424	L26953	Homo sapiens	chromosomal protein	104	34
1425	U83280	Leishmania donovani	39 kDa antigen	105	51
1426	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	98	75
1427	U83303	Homo sapiens	line-1 reverse transcriptase	149	40
1428	AF090895	Homo sapiens	PRO0117	111	75
1429	AF119855	Homo sapiens	PRO1847	88	56
1430	AF229067	Homo sapiens	PADI-H protein	157	51
1431	D38112	Homo sapiens	cytochrome c oxidase subunit 3	509	79
1432	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	333	62
1433	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	149	57
1434	AF161356	Homo sapiens	HSPC093	180	46
1435	U93570	Homo sapiens	putative p150	116	48
1436	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	171	73
1437	U83280	Leishmania donovani	39 kDa antigen	106	80
1438	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	103	73
1439	U15647	Mus musculus	reverse transcriptase	233	44
1440	L27428	Homo sapiens	reverse transcriptase	78	40
1441	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	115	68
1442	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	77	63
1443	M22332	Homo sapiens	unknown protein	153	62
1444	M11901	Rattus norvegicus	proline-rich salivary protein	102	40
1445	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	101	66
1446	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	125	74
1447	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	90	66
1448	X76208	Drosophila melanogaster	protein 33-specific exons	123	48
1449	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	178	79
1450	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	109	45
1451	S80119	Rattus sp.	reverse transcriptase homolog	115	54
1452	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	70	63
1453	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	105	40
1454	AK024455	Homo sapiens	FLJ00047 protein	109	53
1455	AC007258	Arabidopsis thaliana	Hypothetical protein	105	37
1456	AF194537	Homo sapiens	NAG13	208	52
1457	U63542	Homo sapiens	FAP protein	111	84
1458	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	111	65
1459	AF090931	Homo sapiens	PRO0483	84	43

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1460	R95913	Homo sapiens	Neural thread protein.	106	69
1461	R95913	Homo sapiens	Neural thread protein.	109	40
1462	U93564	Homo sapiens	putative p150	237	42
1463	AB029309	Homo sapiens	Npw38-binding protein NpwBP	97	37
1464	U44838	Glycine max	extensin	97	33
1465	AL050341	Homo sapiens	dJ39G22.1 (rearranged L-myc fusion sequence (ZN-15 related zinc finger protein))	121	45
1466	L27428	Homo sapiens	reverse transcriptase	94	34
1467	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	58
1468	Y17221	Homo sapiens	Human secreted protein (clone Rk317-3).	98	48
1469	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	123	55
1470	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	147	67
1471	AF109907	Homo sapiens	S164	133	35
1472	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	142	36
1473	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	90
1474	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	157	45
1475	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	398	58
1476	U49974	Homo sapiens	mariner transposase	201	59
1477	U49974	Homo sapiens	mariner transposase	206	60
1478	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	117	72
1479	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	146	82
1480	U93567	Homo sapiens	putative p150	202	42
1481	K02576	Homo sapiens	salivary proline-rich protein 1	101	46
1482	U87607	Rattus norvegicus	putative RNA binding protein 1	100	37
1483	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	124	75
1484	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	108	62
1485	U15647	Mus musculus	reverse transcriptase	115	73
1486	AF194537	Homo sapiens	NAG13	132	42
1487	M11902	Mus musculus	proline-rich salivary protein	118	40
1488	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	102	64
1489	AF009668	multiple sclerosis associated retrovirus	polyprotein	110	48
1490	AK023542	Homo sapiens	unnamed protein product	114	37
1491	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	133	50
1492	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	184	47
1493	Y12713	Mus musculus	Pro-Pol-3UTPase polyprotein	222	53
1494	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	94	50
1495	AF109907	Homo sapiens	S164	259	45
1496	R95913	Homo sapiens	Neural thread protein.	110	51
1497	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	299	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1498	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	158	65
1499	L26953	Homo sapiens	chromosomal protein	104	67
1500	AF090895	Homo sapiens	PRO0117	145	68
1501	U93572	Homo sapiens	p40	115	42
1502	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	133	50
1503	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	143	56
1504	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	119	69
1505	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	105	52
1506	AF109907	Homo sapiens	S164	184	43
1507	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	288	67
1508	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	131	69
1509	AK000241	Homo sapiens	unnamed protein product	167	72
1510	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	153	60
1511	S62928	Homo sapiens	PRB1M protein precursor	157	39
1512	AB012223	Canis familiaris	ORF2	116	40
1513	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	109	59
1514	AF220264	Homo sapiens	MOST-1	108	80
1515	X53581	Rattus norvegicus	ORF4	96	44
1516	V00662	Homo sapiens	cytochrome oxidase III	433	74
1517	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	263	70
1518	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	266	70
1519	M24732	Homo sapiens	lamin-like protein	107	44
1520	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	131	51
1521	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	81	68
1522	AF194537	Homo sapiens	NAGI3	116	42
1523	X92485	Plasmodium vivax	pva1	85	42
1524	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	125	50
1525	AB041228	Homo sapiens	G protein-coupled receptor TGR-1	220	100
1526	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	70
1527	U52077	Homo sapiens	mariner transposase	237	56
1528	L27428	Homo sapiens	reverse transcriptase	189	40
1529	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	355	78
1530	L13610	Mus musculus	IFN-response element binding factor 2	90	37
1531	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	90	64
1532	U11288	Drosophila melanogaster	diaphanous protein	138	38
1533	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	429	63
1534	L27428	Homo sapiens	reverse transcriptase	249	55
1535	U93570	Homo sapiens	putative p150	114	31
1536	AF130089	Homo sapiens	PRO2550	111	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1537	X55687	Lycopersicon esculentum	extensin (class II)	63	28
1538	U15647	Mus musculus	reverse transcriptase	110	42
1539	AK024455	Homo sapiens	FLJ00047 protein	139	80
1540	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	128	48
1541	AC024788	Caenorhabditis elegans	Hypothetical protein Y46E12A.d	80	46
1542	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	132	73
1543	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	90	32
1544	G02971	Homo sapiens	Human secreted protein, SEQ ID NO: 7052.	71	63
1545	R95913	Homo sapiens	Neural thread protein.	118	55
1546	D38116	Pan paniscus	cytochrome c oxidase subunit 1	218	78
1547	D38112	Homo sapiens	cytochrome c oxidase subunit 1	370	71
1548	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	119	65
1549	AJ004810	Zea mays	cytochrome P450 monooxygenase	140	70
1550	AF113685	Homo sapiens	PRO0974	115	47
1551	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	172	75
1552	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	366	94
1553	W40113	Homo sapiens	Human alpha-2(IV) collagen protein.	117	59
1554	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	138	76
1555	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	113	40
1556	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	502	89
1557	AF130089	Homo sapiens	PRO2550	98	55
1558	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	109	43
1559	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	183	52
1560	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	180	52
1561	AF202893	Mus musculus	Kif21b	254	85
1562	M63421	Drosophila melanogaster	csp32	104	39
1563	G03652	Homo sapiens	Human secreted protein, SEQ ID NO: 7733.	129	69
1564	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	98	59
1565	AJ132106	Bos taurus	SCO-spondin	114	40
1566	AL390114	Leishmania major	extremely cysteine/valine rich protein	119	66
1567	AF161356	Homo sapiens	HSPC093	100	38
1568	AF119851	Homo sapiens	PRO1722	94	72
1569	L27428	Homo sapiens	reverse transcriptase	107	48
1570	X99451	Lycopersicon esculentum	extensin-like protein Dif10	104	32
1571	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	126	59
1572	X73481	Drosophila hydei	mst101(2)	105	41
1573	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	133	50
1574	G04063	Homo sapiens	Human secreted protein, SEQ ID NO:	154	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			8144.		
1575	D38112	Homo sapiens	NADH dehydrogenase subunit 4	323	83
1576	AF062008	Caenorhabditis elegans	unknown	111	54
1577	X92485	Plasmodium vivax	pva1	81	57
1578	U93570	Homo sapiens	p40	102	33
1579	AF090944	Homo sapiens	PRO0663	132	59
1580	AL137798	Homo sapiens	dJ1182A14.5.1 (novel gene (isoform 1))	182	53
1581	X92485	Plasmodium vivax	pva1	120	44
1582	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	160	47
1583	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	135	54
1584	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	119	52
1585	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	82	55
1586	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	152	60
1587	D28482	Homo sapiens	SCR2	390	83
1588	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	122	59
1589	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	50
1590	AF118078	Homo sapiens	PRO1848	118	59
1591	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	56	78
1592	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	118	80
1593	U93571	Homo sapiens	p40	170	77
1594	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	230	51
1595	L27428	Homo sapiens	reverse transcriptase	138	45
1596	X97707	Pongo pygmaeus abelii	stopcodon created by posttranscriptional polyadenylation	139	61
1597	X98710	Homo sapiens	COL1A1 and PDGFB fusion transcript	107	31
1598	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	97	58
1599	AF210651	Homo sapiens	NAG18	86	89
1600	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	148	48
1601	J03770	Mus musculus	homeobox protein	99	35
1602	AF119901	Homo sapiens	PRO2831	119	56
1603	AL031673	Homo sapiens	dJ694B14.1 (PUTATIVE novel KRAB box protein with 18 C2H2 type Zinc finger domains)	233	44
1604	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	66
1605	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	89	44
1606	D88461	Rattus rattus	N-WASP	123	43
1607	AF090942	Homo sapiens	PRO0657	107	61
1608	U35730	Mus musculus	jerky	105	34
1609	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	108	45
1610	B06334	Homo sapiens	Human subtilisin-kexin isoenzyme 1.	474	84
1611	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	101	90
1612	AK024455	Homo sapiens	FLJ00047 protein	83	55
1613	D86853	Catharanthus	extensin	123	39

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		roseus			
1614	AF119851	Homo sapiens	PRO1722	135	59
1615	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	142	57
1616	AF194537	Homo sapiens	NAG13	154	63
1617	AF119851	Homo sapiens	PRO1722	91	62
1618	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	48
1619	AK024455	Homo sapiens	FLJ00047 protein	147	60
1620	AF217973	Homo sapiens	unknown	116	67
1621	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	102	41
1622	K02576	Homo sapiens	salivary proline-rich protein 1	108	40
1623	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	135	44
1624	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	322	62
1625	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	356	72
1626	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	113	65
1627	X92485	Plasmodium vivax	pval	90	45
1628	AF090895	Homo sapiens	PRO0117	156	61
1629	AF116661	Homo sapiens	PRO1438	87	54
1630	M13100	Rattus norvegicus	unknown protein	109	76
1631	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	147	60
1632	AF119851	Homo sapiens	PRO1722	107	70
1633	M64792	Rattus norvegicus	salivary proline-rich protein	109	46
1634	L27428	Homo sapiens	reverse transcriptase	109	38
1635	AF118082	Homo sapiens	PRO1902	80	40
1636	R95913	Homo sapiens	Neural thread protein.	118	88
1637	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	79	60
1638	U93570	Homo sapiens	putative p150	128	54
1639	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	127	69
1640	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	171	68
1641	AF194537	Homo sapiens	NAG13	140	66
1642	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	101	50
1643	M64793	Rattus norvegicus	salivary proline-rich protein	117	33
1644	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	50
1645	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	70
1646	L27428	Homo sapiens	reverse transcriptase	86	84
1647	X92485	Plasmodium vivax	pval	137	40
1648	U15647	Mus musculus	reverse transcriptase	93	68
1649	K02576	Homo sapiens	salivary proline-rich protein 1	131	41
1650	AF116712	Homo sapiens	PRO2738	107	57
1651	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	139	72
1652	X05472	Rattus	ORF 3	84	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		<i>norvegicus</i>			
1653	G00588	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4669.	122	71
1654	U93566	<i>Homo sapiens</i>	p40	117	52
1655	AF217536	<i>Homo sapiens</i>	truncated mevalonate kinase	141	70
1656	AF090895	<i>Homo sapiens</i>	PRO0117	125	60
1657	X92485	<i>Plasmodium vivax</i>	pval	114	45
1658	AF010144	<i>Homo sapiens</i>	neuronal thread protein AD7c-NTP	192	61
1659	Y86473	<i>Homo sapiens</i>	Human gene 52-encoded protein fragment, SEQ ID NO:388.	73	30
1660	Y91577	<i>Homo sapiens</i>	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	331	74
1661	G03438	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7519.	127	69
1662	U49973	<i>Homo sapiens</i>	ORF1; MER37; putative transposase similar to pogo element	312	67
1663	S80119	<i>Rattus sp.</i>	reverse transcriptase homolog	99	59
1664	U43360	<i>Peromyscus maniculatus</i>	reverse transcriptase	106	45
1665	M76729	<i>Homo sapiens</i>	pro-alpha-1 type V collagen	172	47
1666	W48351	<i>Homo sapiens</i>	Human breast cancer related protein BCRB2.	97	54
1667	AF169388	<i>Mus musculus</i>	alpha 4 collagen IV	84	38
1668	W48351	<i>Homo sapiens</i>	Human breast cancer related protein BCRB2.	84	66
1669	U49973	<i>Homo sapiens</i>	ORF1; MER37; putative transposase similar to pogo element	428	80
1670	M29622	<i>Mus musculus</i>	open reading frame 2	74	46
1671	W90838	<i>Homo sapiens</i>	Human lymphocyte targeted peptide #6.	98	100
1672	G00328	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4409.	55	58
1673	AF090931	<i>Homo sapiens</i>	PRO0483	72	39
1674	AF051782	<i>Homo sapiens</i>	diaphanous 1	116	49
1675	U57361	<i>Rattus norvegicus</i>	collagen XII alpha 1	108	48
1676	AF182844	<i>Homo sapiens</i>	VPS28 protein	395	95
1677	L27428	<i>Homo sapiens</i>	reverse transcriptase	189	47
1678	G02532	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 6613.	142	53
1679	U93565	<i>Homo sapiens</i>	putative p150	214	40
1680	AK002129	<i>Homo sapiens</i>	unnamed protein product	128	57
1681	X03145	<i>Homo sapiens</i>	pot. ORF V	93	48
1682	X63005	<i>Mus musculus</i>	proline-rich protein	108	38
1683	AF118082	<i>Homo sapiens</i>	PRO1902	117	42
1684	R13556	<i>Homo sapiens</i>	Protein encoded downstream of hhc_M oncoprotein.	157	58
1685	R95913	<i>Homo sapiens</i>	Neural thread protein.	92	66
1686	G02485	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 6566.	111	61
1687	X61296	<i>Rattus norvegicus</i>	open reading frame 2	104	38
1688	AB012223	<i>Canis familiaris</i>	ORF2	98	39
1689	U49973	<i>Homo sapiens</i>	ORF1; MER37; putative transposase similar to pogo element	278	72
1690	U52077	<i>Homo sapiens</i>	mariner transposase	175	56
1691	G03203	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7284.	83	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1692	AF061128	Plasmodium falciparum	merozoite surface protein 1	85	44
1693	X77722	Homo sapiens	interferon alpha/beta receptor	89	60
1694	M13100	Rattus norvegicus	unknown protein	94	40
1695	AF202635	Homo sapiens	PP1200	114	60
1696	AK001116	Homo sapiens	unnamed protein product	127	53
1697	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	162	53
1698	AF118078	Homo sapiens	PRO1848	93	42
1699	X92485	Plasmodium vivax	pval	147	49
1700	M63819	Plasmodium falciparum	malaria antigen	101	64
1701	AF090930	Homo sapiens	PRO0478	146	76
1702	AB009993	Mus musculus	collagen a1(V)	94	40
1703	AL390114	Leishmania major	extremely cysteine/valine rich protein	169	66
1704	AF130089	Homo sapiens	PRO2550	145	38
1705	X83413	Human	U88	113	58
1706	S60088	Homo sapiens	putative adhesion molecule=ADMLX	151	86
1707	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	176	52
1708	AF130079	Homo sapiens	PRO2852	174	41
1709	Y28682	Homo sapiens	Human pp392_3 secreted protein.	557	99
1710	M14423	Mus musculus	pro-alpha-1 type I collagen	112	34
1711	D13623	Rattus sp.	p34 protein	128	45
1712	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	84	41
1713	X97675	Homo sapiens	plakophilin 2b	121	60
1714	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	102	51
1715	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	171	48
1716	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	99	63
1717	S80119	Rattus sp.	reverse transcriptase homolog	140	57
1718	L27428	Homo sapiens	reverse transcriptase	103	46
1719	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	154	78
1720	AF130089	Homo sapiens	PRO2550	106	35
1721	G03652	Homo sapiens	Human secreted protein, SEQ ID NO: 7733.	147	49
1722	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	111	72
1723	AF016099	Mus musculus	endonuclease/reverse transcriptase	132	60
1724	X92485	Plasmodium vivax	pval	96	62
1725	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	249	52
1726	M81321	Macaca fascicularis	proline-rich protein	132	45
1727	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	119	69
1728	U93564	Homo sapiens	p40	129	58
1729	U93574	Homo sapiens	putative p150	113	76
1730	AF130089	Homo sapiens	PRO2550	136	61
1731	L05608	Cercopithecine	glycoprotein gl	100	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		herpesvirus 2			
1732	U15647	Mus musculus	reverse transcriptase	138	36
1733	U93574	Homo sapiens	putative p150	187	43
1734	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	64
1735	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	102	64
1736	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	118	64
1737	G00490	Homo sapiens	Human secreted protein, SEQ ID NO: 4571.	110	58
1738	AF090942	Homo sapiens	PRO0657	163	55
1739	U11288	Drosophila melanogaster	diaphanous protein	149	46
1740	L27428	Homo sapiens	reverse transcriptase	108	33
1741	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	76	54
1742	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	165	59
1743	AC003682	Homo sapiens	R28830_1	179	63
1744	X65165	Volvox carteri	extensin	173	49
1745	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	114	62
1746	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	89	41
1747	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	115	42
1748	U93565	Homo sapiens	putative p150	125	37
1749	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	121	45
1750	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	139	53
1751	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	87	80
1752	L27428	Homo sapiens	reverse transcriptase	133	42
1753	U93570	Homo sapiens	putative p150	126	57
1754	U22376	Homo sapiens	alternatively spliced product using exon 13A	134	50
1755	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	175	76
1756	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	60
1757	U54788	Mus musculus	Wiskott-Aldrich Syndrome Protein	158	44
1758	Y86579	Homo sapiens	Human gene 92-encoded protein fragment, SEQ ID NO:496.	109	88
1759	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	123	73
1760	Y86579	Homo sapiens	Human gene 92-encoded protein fragment, SEQ ID NO:496.	113	92
1761	Y86579	Homo sapiens	Human gene 92-encoded protein fragment, SEQ ID NO:496.	110	81
1762	U08020	Mus musculus	collagen pro-alpha-1 type I chain	105	34
1763	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	90	45
1764	U93569	Homo sapiens	putative p150	148	36
1765	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	45
1766	X02873	Daucus carota	put. precursor	112	47
1767	X92485	Plasmodium vivax	pval	100	45
1768	R95913	Homo sapiens	Neural thread protein.	96	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1769	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	51
1770	X97675	Homo sapiens	plakophilin 2b	115	70
1771	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	151	58
1772	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	131	85
1773	AF130089	Homo sapiens	PRO2550	158	69
1774	U23552	Ailuropoda melanoleuca	cytochrome b	206	78
1775	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	98	53
1776	AF116715	Homo sapiens	PRO2829	134	67
1777	AC008054	Leishmania major	L8453.1	114	28
1778	AF037364	Homo sapiens	paraneoplastic neuronal antigen MA1	397	73
1779	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	132	60
1780	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	168	64
1781	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	80	36
1782	AF174482	Homo sapiens	polycomb 3	133	46
1783	U93563	Homo sapiens	putative p150	196	70
1784	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	59
1785	AF194537	Homo sapiens	NAG13	114	38
1786	U21123	Drosophila melanogaster	ena polypeptide	120	44
1787	AF200187	cercopithicine herpesvirus 15	EBNA2-like protein	108	30
1788	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	97	56
1789	M64792	Rattus norvegicus	salivary proline-rich protein	128	40
1790	X92485	Plasmodium vivax	pva1	98	51
1791	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	114	34
1792	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	197	81
1793	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	145	71
1794	AF104923	Homo sapiens	putative transcription factor	142	59
1795	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	133	60
1796	AC003113	Arabidopsis thaliana	F24O1.6	57	62
1797	M22332	Homo sapiens	unknown protein	118	29
1798	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	100	71
1799	AL390114	Leishmania major	extremely cysteine/valine rich protein	154	37
1800	U93570	Homo sapiens	p40	103	56
1801	X99452	Lycopersicon esculentum	extensin-like protein Dif54	101	28
1802	L27428	Homo sapiens	reverse transcriptase	102	34
1803	L27428	Homo sapiens	reverse transcriptase	141	43
1804	M18933	Mus musculus	alpha-1 type-III collagen precursor	118	30
1805	X92485	Plasmodium vivax	pva1	106	67
1806	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	118	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1807	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	105	33
1808	X97675	Homo sapiens	plakophilin 2b	154	61
1809	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	53
1810	X92485	Plasmodium vivax	pval	133	54
1811	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	121	66
1812	Y17833	Human endogenous retrovirus K	env protein	119	81
1813	AF119851	Homo sapiens	PRO1722	130	58
1814	X53581	Rattus norvegicus	ORF4	158	50
1815	G03473	Homo sapiens	Human secreted protein, SEQ ID NO: 7554.	111	74
1816	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	153	68
1817	M19155	Plasmodium falciparum	S-antigen precursor	164	50
1818	AF118082	Homo sapiens	PRO1902	90	75
1819	W40353	Homo sapiens	Human unspecified protein from US5702907.	110	52
1820	U93563	Homo sapiens	putative p150	114	35
1821	U41538	Caenorhabditis elegans	proline rich	95	52
1822	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	154	45
1823	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	53
1824	AF130089	Homo sapiens	PRO2550	128	40
1825	AF090944	Homo sapiens	PRO0663	103	45
1826	AC003113	Arabidopsis thaliana	F24O1.18	107	40
1827	AF194537	Homo sapiens	NAG13	85	28
1828	AF009668	multiple sclerosis associated retrovirus	polyprotein	185	41
1829	AF016099	Mus musculus	endonuclease/reverse transcriptase	155	42
1830	X69465	Sus scrofa	ryanodine receptor 1	516	86
1831	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	108	40
1832	U88966	Homo sapiens	rapamycin associated protein FRAP2	434	89
1833	M19155	Plasmodium falciparum	S-antigen precursor	105	32
1834	AF085809	Mus musculus	synapsin 1b	98	33
1835	AK023003	Homo sapiens	unnamed protein product	393	81
1836	Y41740	Homo sapiens	Human PRO701 protein sequence.	429	78
1837	M36913	Zea mays	cell wall protein (put.); putative	72	35
1838	X63005	Mus musculus	proline-rich protein	98	40
1839	X83413	Human herpesvirus 6	U88	149	45
1840	AF134304	Homo sapiens	Scar2	87	37
1841	AC024772	Caenorhabditis elegans	contains similarity to Mus musculus alpha-NAC, muscle-specific form (GB:U48363)	131	25
1842	AB002366	Homo sapiens	KIAA0368	153	75
1843	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	140	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1844	AL035526	Arabidopsis thaliana	extensin-like protein	93	33
1845	D26156	Homo sapiens	hSNF2b	91	34
1846	M14228	Gallus gallus	c-beta-3 beta-tubulin	598	83
1847	AK022217	Homo sapiens	unnamed protein product	97	56
1848	AJ250042	Homo sapiens	Rab5 GDP/GTP exchange factor homologue	174	83
1849	W23949	Homo sapiens	Human phosphoinositide 3OH-kinase p101 subunit	143	28
1850	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	101	63
1851	AB017114	Homo sapiens	AD 3	113	100
1852	D00570	Mus musculus	open reading frame (251 AA)	174	55
1853	A67510	Mus musculus	MUS MUSCULUS GENOMIC DNA CONTAINING N ALLELE OF FV1 GENE.	133	42
1854	U49974	Homo sapiens	mariner transposase	214	82
1855	U93569	Homo sapiens	p40	95	31
1856	D89729	Homo sapiens	CRM1 protein	475	90
1857	AF090895	Homo sapiens	PRO0117	89	36
1858	AF015926	Homo sapiens	ezzrin-radixin-moesin binding phosphoprotein-50	117	73
1859	D13721	Gallus gallus	NF-kB p65 subunit	223	56
1860	K03204	Homo sapiens	salivary proline-rich protein precursor	111	32
1861	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	195	52
1862	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	331	69
1863	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	80	35
1864	L27428	Homo sapiens	reverse transcriptase	84	51
1865	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	106	46
1866	U53585	Mycobacterium avium	fibronectin attachment protein	86	36
1867	AF255446	Cryptocodium cohnii	Dip1-associated protein C	134	45
1868	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	81	63
1869	AP000001	Pyrococcus horikoshii	235aa long hypothetical protein	108	40
1870	M13100	Rattus norvegicus	unknown protein	121	53
1871	X67863	Mus musculus	T2	101	35
1872	S80119	Rattus sp.	reverse transcriptase homolog	151	43
1873	W73633	Homo sapiens	Human secreted protein clone.	140	44
1874	U57053	Homo sapiens	myosin-ID	203	82
1875	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	54
1876	M21097	Homo sapiens	CD19 differentiation antigen	432	79
1877	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	150	52
1878	U25281	Rattus norvegicus	SH3 domain binding protein	108	36
1879	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	117	48
1880	X73113	Homo sapiens	fast MyBP-C	599	77
1881	AX028128	Homo sapiens	unnamed protein product	162	43
1882	G03789	Homo sapiens	Human secreted protein, SEQ ID NO:	138	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7870.		
1883	Y00664	Homo sapiens	open reading frame 1 (AA 1 - 86)	74	34
1884	U86587	Mus musculus	phosphatidylinositol 3-kinase catalytic subunit p110 delta	204	77
1885	X67337	Homo sapiens	Human pre-mRNA cleavage factor 1 68 kDa subunit	148	37
1886	Y13829	Homo sapiens	MBNL protein	117	63
1887	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	119	80
1888	R95913	Homo sapiens	Neural thread protein.	91	64
1889	L39059	Homo sapiens	transcription factor SL1	92	34
1890	M69297	Homo sapiens	ORF 3	169	48
1891	R95913	Homo sapiens	Neural thread protein.	91	62
1892	Z28201	Saccharomyces cerevisiae	ORF YKL202w	95	51
1893	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	90	51
1894	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	183	73
1895	Y10055	Homo sapiens	phosphoinositide 3-kinase	564	84
1896	AF093775	Mus musculus	alpha-actinin 3	375	85
1897	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	82	66
1898	M21904	Homo sapiens	4F2 heavy chain antigen	386	80
1899	AB028997	Homo sapiens	K1A1074 protein	145	38
1900	U97553	murid herpesvirus 4	unknown	98	41
1901	AB011142	Homo sapiens	K1A0570 protein	209	95
1902	AF194537	Homo sapiens	NAG13	161	55
1903	U93564	Homo sapiens	putative p150	142	33
1904	M29399	Homo sapiens	erythrocyte membrane protein band 4.2	413	90
1905	Y27400	Homo sapiens	Human P450 reductase functional fragment sequence.	294	67
1906	Y28503	Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	167	100
1907	AF128625	Homo sapiens	CDC42-binding protein kinase beta	509	89
1908	AB029147	Cucumis sativus	expressed in cucumber hypocotyls	98	41
1909	X13783	Homo sapiens	alpha-1 type 2 collagen (714 AA)	87	43
1910	AF240630	Mus musculus	IQ motif containing GTPase activating protein 1	330	48
1911	AF129075	Homo sapiens	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)	511	90
1912	AF011450	Mus musculus	type XV collagen	87	28
1913	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	124	75
1914	AF171230	Vigna unguiculata	phosphatidic acid phosphatase beta	112	53
1915	AF016099	Mus musculus	endonuclease/reverse transcriptase	100	47
1916	M94131	Homo sapiens	mucin	97	37
1917	X13885	Nicotiana tabacum	extensin (AA 1-620)	120	34
1918	AF186605	Homo sapiens	MLL2 protein	115	29
1919	M12130	Mus musculus	RNA polymerase II	498	83
1920	AL049794	Homo sapiens	dJ777L9.1 (novel protein similar to mouse kinesin-like proteins KIF1A and KIF1B)	514	90
1921	D83703	Homo sapiens	peroxisome assembly factor-2	233	64
1922	Y11922	Homo sapiens	Human 5' EST secreted protein SEQ ID No: 522.	162	77

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1923	AC002481	Homo sapiens	similar to nitrogen permease regulator; similar to P39923 (PID:g730170), match to AA233630 (NID:g1856833) and AA399402 (NID:g2053147)	223	79
1924	D82060	Homo sapiens	membrane protein with histidine rich charge clusters	115	40
1925	U49974	Homo sapiens	mariner transposase	195	61
1926	S80119	Rattus sp.	reverse transcriptase homolog	104	40
1927	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	79	68
1928	S79639	Homo sapiens	EXT1=putative tumour suppressor/hereditary multiple exostoses candidate gene	430	88
1929	X58063	Brugia pahangi	major protein component of the microfilarial sheath	104	43
1930	AF119855	Homo sapiens	PRO1847	132	64
1931	AJ005577	Homo sapiens	6-phosphofructo-2-kinase	326	90
1932	AF020261	Santalum album	proline rich protein	93	33
1933	AJ272204	Homo sapiens	hypothetical protein	321	52
1934	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	116	39
1935	A61971	unidentified	MCSP	328	79
1936	U93564	Homo sapiens	putative p150	217	54
1937	U97553	murid herpesvirus 4	unknown	113	38
1938	AF194537	Homo sapiens	NAG13	90	37
1939	AF226044	Homo sapiens	HSNFRK	403	85
1940	X83413	Human	U88	303	50
1941	AJ007628	Rattus norvegicus	ELK channel 1	112	38
1942	AF104328	Arabidopsis thaliana	cell wall-plasma membrane linker protein homolog	135	35
1943	AF130089	Homo sapiens	PRO2550	93	63
1944	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	102	34
1945	M19419	Mus musculus	proline-rich salivary protein	121	40
1946	U57316	Homo sapiens	histone acetyltransferase	132	73
1947	AL163302	Homo sapiens	human type XVIII collagen	79	34
1948	AB020746	Arabidopsis thaliana	protein kinase-like protein	117	36
1949	AJ011738	Homo sapiens	In11b	209	85
1950	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	155	48
1951	AF119569	Homo sapiens	patched 2	166	89
1952	AB002107	Homo sapiens	hPer	118	39
1953	X98834	Homo sapiens	zinc finger protein Hsa12	430	70
1954	Y19641	Homo sapiens	SEQ ID NO 359 from WO9922243.	96	64
1955	U93569	Homo sapiens	putative p150	157	44
1956	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	85	53
1957	AB013729	Mus musculus	semaphorin Y	106	38
1958	AC005360	Homo sapiens	FAA	338	68
1959	AJ223075	Homo sapiens	TRIP protein	598	95
1960	AC004022	Homo sapiens	serum paraoxonase/arylesterase 3	147	62
1961	AF076776	Drosophila melanogaster	helicase DOMINO A	157	45
1962	AF265355	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	587	77
1963	AF229642	Mus musculus	DXlmx46e protein	127	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1964	U72520	Mus musculus	mena protein	89	31
1965	W40309	Homo sapiens	Human ITAK protein.	179	32
1966	AJ388557	Canis familiaris	zinc finger protein	826	56
1967	Y92515	Homo sapiens	Human OXRE-12.	224	53
1968	Y17832	Human endogenous retrovirus K	pol protein	187	49
1969	Y41245	Homo sapiens	Human Y218 protein.	220	78
1970	AB052738	Sus scrofa	Smad3	366	85
1971	AB007644	Arabidopsis thaliana	contains similarity to phytoeyanin/early nodulin-like protein-gene id:K19P17.3	106	32
1972	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	122	57
1973	AL357472	Homo sapiens	VPS33B	112	31
1974	AF151902	Homo sapiens	CGI-144 protein	112	95
1975	AL137260	Homo sapiens	hypothetical protein	148	92
1976	U89505	Homo sapiens	Hlark	408	89
1977	U67328	Mus musculus	NIPI-like protein	168	73
1978	AK026435	Homo sapiens	unnamed protein product	601	94
1979	Y14318	Homo sapiens	peroxisomal ABC-transporter	507	96
1980	U63630	Homo sapiens	MCM4	570	90
1981	AF118090	Homo sapiens	PRO2044	154	84
1982	AF016370	Homo sapiens	U4/U6 small nuclear ribonucleoprotein hPrp3	422	63
1983	AB011154	Homo sapiens	KIAA0582 protein	420	80
1984	AB011422	Homo sapiens	Trad	201	67
1985	AL390156	Homo sapiens	hypothetical protein	230	97
1986	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	163	44
1987	M12523	Homo sapiens	albumin Venezia	411	91
1988	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	145	63
1989	Y36156	Homo sapiens	Human secreted protein #28.	107	80
1990	AF161356	Homo sapiens	HSPC093	156	57
1991	G03443	Homo sapiens	Human secreted protein, SEQ ID NO: 7524.	132	72
1992	AF119851	Homo sapiens	PRO1722	126	52
1993	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	228	60
1994	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	40
1995	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	118	58
1996	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	57
1997	X75068	Bos taurus	plasmalemmal porin	85	85
1998	Y64869	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1030.	92	80
1999	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	275	79
2000	AF118078	Homo sapiens	PRO1848	111	57
2001	S80119	Rattus sp.	reverse transcriptase homolog	120	61
2002	AB011110	Homo sapiens	KIAA0538 protein	146	73
2003	M15530	Homo sapiens	B-cell growth factor	94	64
2004	AF225918	Mus musculus	intestinal cell kinase	216	77
2005	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	125	85
2006	D84391	Mus musculus	reverse transcriptase	135	38
2007	AF090930	Homo sapiens	PRO0478	101	86

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2008	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	156	66
2009	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	165	49
2010	AF113685	Homo sapiens	PRO0974	124	63
2011	AF130079	Homo sapiens	PRO2852	141	78
2012	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	94	51
2013	AF090944	Homo sapiens	PRO0663	67	53
2014	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	151	58
2015	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	223	75
2016	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	137	78
2017	L26953	Homo sapiens	chromosomal protein	120	74
2018	G03646	Homo sapiens	Human secreted protein, SEQ ID NO: 7727.	68	57
2019	G03646	Homo sapiens	Human secreted protein, SEQ ID NO: 7727.	64	42
2020	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	334	63
2021	L26953	Homo sapiens	chromosomal protein	112	64
2022	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	139	69
2023	U93569	Homo sapiens	putative p150	187	89
2024	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	80	72
2025	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	142	71
2026	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	77	66
2027	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	372	73
2028	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	80
2029	AF194537	Homo sapiens	NAG13	158	57
2030	L26251	Trypanosoma brucei	CR5	110	41
2031	AF197913	Helicoverpa armigera nuclear polyhedrosis virus	basic DNA-binding protein BDBP	149	55
2032	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	115	80
2033	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	157	82
2034	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	133	75
2035	G03646	Homo sapiens	Human secreted protein, SEQ ID NO: 7727.	104	67
2036	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	71
2037	AF130089	Homo sapiens	PRO2550	146	55
2038	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	81	73
2039	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	66
2040	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2041	B01372	Homo sapiens	Neuron-associated protein.	95	79
2042	V01555	Human herpesvirus 4	BYRF1, encodes EBNA-2 (Dambaugh et al, 1984; Dillner et al, 1984)	108	77
2043	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	125	65
2044	AF118086	Homo sapiens	PRO1992	103	64
2045	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	64
2046	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	108	51
2047	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	133	68
2048	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	155	64
2049	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	125	53
2050	AL390114	Leishmania major	extremely cysteine/valine rich protein	112	56
2051	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	70	62
2052	X61045	Hydra sp.	mini-collagen	99	46
2053	X83413	Human herpesvirus 6	U88	148	73
2054	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	75	63
2055	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	104	75
2056	X16524	Dictyostelium discoideum	coding region (AA 1 - 437)	104	51
2057	R95913	Homo sapiens	Neural thread protein.	83	77
2058	AF118080	Homo sapiens	PRO1880	126	61
2059	AJ276003	Homo sapiens	GAR1 protein	136	59
2060	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	120	70
2061	X01918	Drosophila melanogaster	salivary gland glue protein	179	40
2062	U00029	Saccharomyces cerevisiae	Yhr217cp	110	46
2063	AF130051	Homo sapiens	PRO0898	143	80
2064	AF006061	Homo sapiens	placental growth hormone isoform hGH-V3	121	85
2065	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	129	66
2066	U82303	Homo sapiens	unknown	92	68
2067	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	368	79
2068	L27428	Homo sapiens	reverse transcriptase	186	58
2069	AF130051	Homo sapiens	PRO0898	164	73
2070	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	271	73
2071	AF130051	Homo sapiens	PRO0898	110	56
2072	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	67
2073	AF157706	Human herpesvirus 6B	B4	104	49
2074	AL049608	Arabidopsis thaliana	extensin-like protein	120	41
2075	AP002460	Arabidopsis thaliana	gene_id:F1D9.26-unknown protein	150	27
2076	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	130	85

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2077	M11897	Mus musculus	proline-rich salivary protein	125	42
2078	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	66	75
2079	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	185	47
2080	AJ06470	Homo sapiens	cartilage-associated protein (CASP)	139	84
2081	AK024509	Homo sapiens	unnamed protein product	132	83
2082	U93564	Homo sapiens	putative p150	137	67
2083	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	71
2084	B01372	Homo sapiens	Neuron-associated protein.	148	81
2085	AL160371	Leishmania major	probable (bhv-6) u1102, variant a DNA, complete virion genome	114	76
2086	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	255	63
2087	AF194537	Homo sapiens	NAG13	122	78
2088	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	108	74
2089	AF130079	Homo sapiens	PRO2852	149	77
2090	U93574	Homo sapiens	p40	260	96
2091	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	99	76
2092	AF194537	Homo sapiens	NAG13	125	51
2093	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	319	72
2094	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	56
2095	U93572	Homo sapiens	putative p150	195	57
2096	X83413	Human herpesvirus 6	U88	132	57
2097	AF010400	Homo sapiens	transaldolase-related protein	463	89
2098	U93563	Homo sapiens	putative p150	128	35
2099	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	160	43
2100	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	133	43
2101	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	97	71
2102	K02401	Homo sapiens	chorionic somatomammotropin	628	90
2103	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	80
2104	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	309	63
2105	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	192	37
2106	Y59772	Homo sapiens	Human normal ovarian tissue derived protein 49.	261	89
2107	AF202051	Homo sapiens	NM23-H8	680	100
2108	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	127	54
2109	L22029	Glycine max	hydroxyproline-rich glycoprotein	121	36
2110	D26135	Homo sapiens	diacylglycerol kinase gamma	172	100
2111	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	56
2112	X65488	Homo sapiens	hnRNP U protein	117	70
2113	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1.	116	35
2114	AF130051	Homo sapiens	PRO0898	93	62
2115	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	260	53
2116	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	70

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2117	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	304	71
2118	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	70	66
2119	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	118	84
2120	S79410	Mus musculus	nuclear localization signal binding protein	94	94
2121	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	304	73
2122	M11901	Rattus norvegicus	proline-rich salivary protein	83	32
2123	AK025047	Homo sapiens	unnamed protein product	116	48
2124	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	95	72
2125	AF138883	Bos taurus	type II collagen cyanogen bromide fragment CB10	103	40
2126	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	186	100
2127	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	117	52
2128	AF194537	Homo sapiens	NAG13	126	66
2129	AB015802	Acetobacter xylinus	similar to cellulose complementing protein of A. xylinum ATCC23869	109	80
2130	AF187147	Mus musculus	drebrin A	110	38
2131	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	148	42
2132	L36341	Aspergillus nidulans	regulatory protein	130	49
2133	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	119	58
2134	AF116689	Homo sapiens	PRO2168	113	81
2135	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	191	38
2136	M81321	Macaca fascicularis	proline-rich protein	125	43
2137	A18812	Brassica napus	extensin	106	34
2138	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	104	41
2139	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	191	92
2140	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	196	90
2141	Y57285	Homo sapiens	Human GPCR protein (HGPRP) sequence (clone ID Z214673).	507	78
2142	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	201	47
2143	AF090944	Homo sapiens	PRO0663	164	53
2144	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	390	76
2145	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	198	70
2146	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	119	82
2147	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	194	45
2148	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	91	60
2149	AF090942	Homo sapiens	PRO0657	129	66
2150	AF130089	Homo sapiens	PRO2550	372	82
2151	AC009991	Arabidopsis	unknown protein	81	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		thaliana			
2152	AF090942	Homo sapiens	PRO0657	93	53
2153	R13319	Homo sapiens	Partial Human Natural Killer receptor.	215	89
2154	AC008075	Arabidopsis thaliana	F24J5.4	139	36
2155	AL390114	Leishmania major	extremely cysteine/valine rich protein	148	50
2156	S79410	Mus musculus	nuclear localization signal binding protein	112	58
2157	AK024455	Homo sapiens	FLJ00047 protein	152	66
2158	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	85	80
2159	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	165	75
2160	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	145	45
2161	AF119900	Homo sapiens	PRO2822	138	71
2162	AJ223953	Homo sapiens	hPTTG	106	62
2163	AK023542	Homo sapiens	unnamed protein product	76	52
2164	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	118	84
2165	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	137	65
2166	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	348	88
2167	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	108	84
2168	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	114	48
2169	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	125	67
2170	AF130089	Homo sapiens	PRO2550	142	65
2171	Y19609	Homo sapiens	SEQ ID NO 327 from WO9922243.	103	65
2172	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	39
2173	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	91	50
2174	D38435	Homo sapiens	homologue of yeast PMS1	314	96
2175	AF119851	Homo sapiens	PRO1722	230	69
2176	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	100	63
2177	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	44
2178	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	139	42
2179	AL049608	Arabidopsis thaliana	extensin-like protein	286	57
2180	L17318	Rattus norvegicus	proline-rich proteoglycan	148	40
2181	AK024455	Homo sapiens	FLJ00047 protein	97	63
2182	R95913	Homo sapiens	Neural thread protein.	100	69
2183	AF266479	Homo sapiens	rectachrome 1	148	81
2184	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	64	70
2185	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	107	40
2186	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	110	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2187	AF137273	Gallus gallus	alpha 1 (V) collagen	103	43
2188	K03205	Homo sapiens	salivary proline-rich protein precursor	115	36
2189	D90064	Homo sapiens	NCA-W272	271	100
2190	AF130089	Homo sapiens	PRO2550	137	68
2191	X65165	Volvox carteri	extensin	113	62
2192	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	154	59
2193	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	148	59
2194	U52077	Homo sapiens	mariner transposase	257	53
2195	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPGP94.	98	79
2196	D38112	Homo sapiens	NADH dehydrogenase subunit 5	180	77
2197	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	121	65
2198	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	126	64
2199	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	101	67
2200	AJ007042	Homo sapiens	TRX5 protein	264	75
2201	AF130051	Homo sapiens	PRO0898	71	61
2202	AK024455	Homo sapiens	FLJ00047 protein	153	62
2203	U83303	Homo sapiens	line-1 reverse transcriptase	95	52
2204	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	128	82
2205	AF090895	Homo sapiens	PRO0117	163	69
2206	G03806	Homo sapiens	Human secreted protein, SEQ ID NO: 7887.	154	69
2207	R95913	Homo sapiens	Neural thread protein.	103	86
2208	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	144	78
2209	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	100	65
2210	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	111	45
2211	AF090931	Homo sapiens	PRO0483	63	90
2212	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	100	74
2213	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	98	41
2214	M76671	Lycopersicon esculentum	extensin (class II)	137	35
2215	X03717	Homo sapiens	pot. unidentified reading frame	98	54
2216	R95913	Homo sapiens	Neural thread protein.	109	48
2217	AF118086	Homo sapiens	PRO1992	138	79
2218	AF081484	Homo sapiens	alpha-tubulin isoform 1	343	95
2219	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	157	84
2220	AF141347	Homo sapiens	alpha-tubulin	571	94
2221	AF071172	Homo sapiens	HERC2	187	84
2222	M17783	Homo sapiens	glia-derived nexin precursor	529	83
2223	AF081484	Homo sapiens	alpha-tubulin isoform 1	588	85
2224	AK026072	Homo sapiens	unnamed protein product	199	57
2225	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	161	61
2226	Z70684	Caenorhabditis elegans	F28D1.8	126	41
2227	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	124	63

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2228	AF119855	Homo sapiens	PRO1847	108	74
2229	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	122	55
2230	AF090944	Homo sapiens	PRO0663	146	61
2231	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	152	74
2232	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	80	59
2233	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	129	58
2234	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	143	60
2235	AK024455	Homo sapiens	FLJ00047 protein	133	71
2236	Y87103	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	99	59
2237	U87607	Rattus norvegicus	putative RNA binding protein 1	111	38
2238	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	119	63
2239	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	75	65
2240	L27428	Homo sapiens	reverse transcriptase	136	40
2241	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	122	82
2242	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	105	95
2243	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	79	48
2244	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	145	75
2245	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	346	87
2246	U82303	Homo sapiens	unknown	155	79
2247	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	105	45
2248	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	105	47
2249	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	63
2250	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	62
2251	X81206	Drosophila hydei	histone H5.3	101	71
2252	AF155581	Danio rerio	proteasome subunit beta 7	92	52
2253	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	172	60
2254	AF084225	Homo sapiens	cytochrome P450 2E1	114	46
2255	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	156	64
2256	AL132841	Caenorhabditis elegans	Y15E3A.3	147	90
2257	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	297	59
2258	U93563	Homo sapiens	putative p150	218	66
2259	L22650	Homo sapiens	early lymphoid activation protein	82	55
2260	AF194537	Homo sapiens	NAG13	117	56
2261	U43360	Peromyscus maniculatus	reverse transcriptase	130	82
2262	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	86	66
2263	AL021918	Homo sapiens	b34I8.1 (Kruppel related Zinc Finger protein 184)	372	61
2264	AL390114	Leishmania major	extremely cysteine/valine rich protein	122	71

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2265	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	123	79
2266	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	204	95
2267	L29029	Chlamydomonas reinhardtii	amino acid feature: Rod protein domain, aa 266 .. 468; amino acid feature: globular protein domain, aa 32 .. 265	141	58
2268	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	499	84
2269	A11693	Homo sapiens	start codon not included	594	87
2270	AB014534	Homo sapiens	KIAA0654 protein	141	63
2271	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	112	60
2272	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	118	54
2273	Y20852	Homo sapiens	Human neurofilament-H mutant protein fragment 11.	125	35
2274	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	92	66
2275	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	198	64
2276	U15647	Mus musculus	reverse transcriptase	100	72
2277	AJ004810	Zea mays	cytochrome P450 monooxygenase	129	43
2278	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	111	67
2279	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	112	68
2280	L27428	Homo sapiens	reverse transcriptase	150	60
2281	K03202	Homo sapiens	salivary proline-rich protein precursor	142	40
2282	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	321	54
2283	D00570	Mus musculus	open reading frame (251 AA)	169	56
2284	Y02887	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	86	54
2285	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	144	50
2286	AF119901	Homo sapiens	PRO2831	116	82
2287	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	126	73
2288	AF130089	Homo sapiens	PRO2550	102	75
2289	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	70
2290	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	64
2291	L26953	Homo sapiens	chromosomal protein	137	53
2292	AF161356	Homo sapiens	HSPC093	100	57
2293	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	138	68
2294	X03145	Homo sapiens	pot. ORF I	120	43
2295	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	83	52
2296	AK024455	Homo sapiens	FLJ00047 protein	98	66
2297	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	123	73
2298	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	349	73
2299	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	109	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2300	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	100	81
2301	AF251290	Plasmodium falciparum	glutamic acid-rich protein	112	40
2302	AF155232	Pisum sativum	extensin	89	36
2303	AF130089	Homo sapiens	PRO2550	83	50
2304	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	84	51
2305	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	86	30
2306	AP002031	Arabidopsis thaliana	gene_id:K3D20.3~	168	44
2307	AF157321	Homo sapiens	30 kDa protein	309	64
2308	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	57
2309	M76546	Helianthus annuus	hydroxyproline-rich protein	198	42
2310	Y27607	Homo sapiens	Human secreted protein encoded by gene No. 41.	207	100
2311	AF130089	Homo sapiens	PRO2550	106	66
2312	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	117	60
2313	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	114	80
2314	AB032910	Hylobates muelleri	dopamine receptor D4	108	40
2315	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	59
2316	AK024455	Homo sapiens	FLJ00047 protein	134	58
2317	AF238235	Entamoeba histolytica	diaphanous protein	103	51
2318	U15647	Mus musculus	reverse transcriptase	101	37
2319	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	117	51
2320	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	78
2321	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	97	48
2322	D00570	Mus musculus	open reading frame (196 AA)	122	39
2323	AP000616	Oryza sativa	similar to RJNG-H2 finger protein RHA1a (AF078683)	122	75
2324	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	118	79
2325	U44838	Glycine max	extensin	126	36
2326	Y87103	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	99	59
2327	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	408	79
2328	AF194537	Homo sapiens	NAG13	181	66
2329	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	405	75
2330	X53581	Rattus norvegicus	ORF4	116	45
2331	L26953	Homo sapiens	chromosomal protein	108	67
2332	L27428	Homo sapiens	reverse transcriptase	117	76
2333	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	84	50
2334	AF191687	Homo sapiens	alanine-glyoxylate aminotransferase homolog	100	37
2335	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	84	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2336	AL390114	Leishmania major	extremely cysteine/valine rich protein	106	53
2337	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	65
2338	R95913	Homo sapiens	Neural thread protein.	164	67
2339	AF090942	Homo sapiens	PRO0657	122	81
2340	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	107	90
2341	AF090942	Homo sapiens	PRO0657	124	60
2342	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	126	83
2343	AB013454	Rattus norvegicus	NaPi-2 beta	143	77
2344	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	127	73
2345	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	146	45
2346	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	120	40
2347	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	55
2348	Y36203	Homo sapiens	Human secreted protein #75.	138	78
2349	L26953	Homo sapiens	chromosomal protein	131	57
2350	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	65
2351	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	144	58
2352	AF130051	Homo sapiens	PRO0898	155	70
2353	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	134	76
2354	L27428	Homo sapiens	reverse transcriptase	141	71
2355	L26953	Homo sapiens	chromosomal protein	128	66
2356	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	75
2357	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	115	62
2358	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPGP94.	115	50
2359	M76546	Helianthus annuus	hydroxyproline-rich protein	103	43
2360	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	82	80
2361	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	95	72
2362	M64793	Rattus norvegicus	salivary proline-rich protein	117	41
2363	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	98	80
2364	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	152	45
2365	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	85	55
2366	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	101	77
2367	AF093097	Homo sapiens	putative RNA-binding protein Q99	248	97
2368	U52077	Homo sapiens	mariner transposase	227	74
2369	X07882	Homo sapiens	Po protein	102	38
2370	U44838	Glycine max	extensin	102	32
2371	AB012223	Canis familiaris	ORF2	158	60
2372	AF025467	Caenorhabditis	contains similarity to drosophila DNA-	104	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		clcgans	binding protein K10 (NID.g8148)		
2373	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	107	40
2374	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	106	67
2375	AF118086	Homo sapiens	PRO1992	169	65
2376	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	95	55
2377	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	121	59
2378	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	141	70
2379	R95913	Homo sapiens	Neural thread protein.	120	50
2380	U93572	Homo sapiens	putative p150	124	53
2381	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	195	66
2382	U52077	Homo sapiens	mariner transposase	282	67
2383	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	113	43
2384	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	112	37
2385	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	88	75
2386	AF130089	Homo sapiens	PRO2550	160	62
2387	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	166	61
2388	AF130089	Homo sapiens	PRO2550	103	71
2389	AB027890	Schizosaccharomyces pombe	Hypothetical protein	116	100
2390	U93570	Homo sapiens	putative p150	151	54
2391	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	110	71
2392	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	109	67
2393	AE001381	Plasmodium falciparum	hypothetical protein	94	34
2394	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	62
2395	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	57	56
2396	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	107	43
2397	AF210651	Homo sapiens	NAG18	162	54
2398	M11901	Rattus norvegicus	proline-rich salivary protein	116	34
2399	S80864	Homo sapiens	cytochrome c-like polypeptide	115	68
2400	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	141	54
2401	M13100	Rattus norvegicus	unknown protein	148	46
2402	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	133	70
2403	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	366	94
2404	AF113685	Homo sapiens	PRO0974	112	56
2405	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	98	67
2406	R41001	Homo sapiens	Human myotonic dystrophy gene protein.	207	68
2407	AL390114	Leishmania	probable (hmv-6) u1102, variant a	127	63

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		major	DNA, complete virion genome		
2408	G03101	Homo sapiens	Human secreted protein, SEQ ID NO: 7182.	378	95
2409	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO: 125.	250	86
2410	U72520	Mus musculus	mena protein	115	40
2411	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	44
2412	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	109	85
2413	AF119901	Homo sapiens	PRO2831	113	66
2414	R95913	Homo sapiens	Neural thread protein.	93	57
2415	B01372	Homo sapiens	Neuron-associated protein.	104	83
2416	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	130	50
2417	J02459	bacteriophage lambda	K (tail component;199)	720	92
2418	J04694	Mus musculus	alpha-1 type IV collagen	103	43
2419	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	145	61
2420	W26496	Homo sapiens	CD2 associated intracellular protein CAIP LS02-21.	115	80
2421	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	145	38
2422	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	158	73
2423	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	70
2424	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	122	61
2425	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	95	59
2426	U93565	Homo sapiens	putative p150	147	75
2427	AL390114	Leishmania major	extremely cysteine/valine rich protein	246	53
2428	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	138	61
2429	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	112	75
2430	D13892	Homo sapiens	carboxyl methyltransferase	181	68
2431	X97675	Homo sapiens	plakophilin 2b	131	65
2432	G02896	Homo sapiens	Human secreted protein, SEQ ID NO: 6977.	108	70
2433	X03145	Homo sapiens	pot. ORF III	180	82
2434	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	77	86
2435	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	421	67
2436	M64793	Rattus norvegicus	salivary proline-rich protein	111	38
2437	AF210651	Homo sapiens	NAG18	128	72
2438	AF016099	Mus musculus	endonuclease/reverse transcriptase	232	46
2439	AL160493	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	122	53
2440	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	136	80
2441	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	139	54
2442	AF090895	Homo sapiens	PRO0117	115	61
2443	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	125	70

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2444	G00594	Homo sapiens	Human secreted protein, SEQ ID NO: 4675.	71	80
2445	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	81	37
2446	AF090895	Homo sapiens	PRO0117	86	64
2447	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	103	86
2448	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	61
2449	L21936	Homo sapiens	succinate dehydrogenase flavoprotein subunit	168	91
2450	AF090942	Homo sapiens	PRO0657	134	71
2451	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	126	87
2452	K03179	Homo sapiens	pro-alpha-1 type-I collagen	120	44
2453	AF118082	Homo sapiens	PRO1902	143	46
2454	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	114	68
2455	AF130089	Homo sapiens	PRO2550	125	89
2456	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	134	71
2457	Y36243	Homo sapiens	Human secreted protein encoded by gene 20.	93	75
2458	Y09945	Rattus norvegicus	putative integral membrane transport protein	166	46
2459	AF130052	Homo sapiens	PRO0956	75	48
2460	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	162	76
2461	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	123	69
2462	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	157	48
2463	X83413	Human herpesvirus 6	U88	236	50
2464	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	181	53
2465	X83413	Human herpesvirus 6	U88	218	50
2466	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	147	57
2467	X83413	Human herpesvirus 6	U88	196	53
2468	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	61
2469	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	101	46
2470	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	221	56
2471	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	136	63
2472	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	122	94
2473	AF161361	Homo sapiens	HSPC098	120	60
2474	M76546	Helianthus annuus	hydroxyproline-rich protein	142	40
2475	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	130	58
2476	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	78	48
2477	AL160371	Leishmania	probable (hhv-6) u1102, variant a	86	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		major	DNA, complete virion genome		
2478	G01478	Homo sapiens	Human secreted protein, SEQ ID NO: 5559.	96	66
2479	AL033545	Arabidopsis thaliana	extensin-like protein	114	40
2480	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	142	59
2481	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	146	62
2482	AL132902	Caenorhabditis elegans	Y71A12B.4	160	37
2483	AF154502	Homo sapiens	quiescent cell proline dipeptidase	439	88
2484	AF010326	Drosophila melanogaster	short form of CHIP	56	42
2485	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	119	50
2486	W31186	Homo sapiens	Human p160 polypeptide 160.2.	115	60
2487	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	103	74
2488	L26953	Homo sapiens	chromosomal protein	129	68
2489	Y21418	Homo sapiens	Human high mobility group protein HMGI-C mutant fragment 2.	96	46
2490	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	366	94
2491	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	158	76
2492	U12707	Homo sapiens	Wiskott-Aldrich syndrome protein	144	47
2493	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	117	81
2494	X92485	Plasmodium vivax	pva1	116	64
2495	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	92	64
2497	AF161483	Homo sapiens	HSPC134	211	78
2498	X05006	Homo sapiens	S-protein	298	92
2499	AB032911	Hylobates agilis	dopamine receptor D4	89	42
2500	M98502	Mus musculus	pMLZ-4	325	90
2501	Y94920	Homo sapiens	Human secreted protein clone pm412_12 protein sequence SEQ ID NO:46.	569	85
2502	AB049054	Homo sapiens	brain link protein-1	224	90
2503	AF064604	Homo sapiens	KE03 protein	224	37
2504	Z69727	Schizosaccharomyces pombe	putative dna-directed rna polymerase iii 130 kd polypeptide (ec 2.7.7.6)	384	61
2505	M11901	Rattus norvegicus	proline-rich salivary protein	147	43
2506	AJ010604	Mus musculus	L-Sox3 protein	366	87
2507	X83413	Human herpesvirus 6	U88	203	46
2508	AJ277425	Globodera pallida	putative cuticular collagen	125	40
2509	AB017919	Homo sapiens	peptidylarginine deiminase type V	148	81
2510	AF001947	Homo sapiens	U4/U6-associated RNA splicing factor	583	97
2511	AJ238520	Homo sapiens	putative transcription factor-like nuclear regulator	722	100
2512	AL390736	Homo sapiens	bA209J19.1.1 (GW112 protein)	557	84
2513	D84223	Homo sapiens	leucyl tRNA synthetase	1113	100
2514	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	174	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2515	U60803	Homo sapiens	clathrin heavy chain 2	111	92
2516	AJ388557	Canis familiaris	zinc finger protein	826	56
2517	AB027251	Homo sapiens	zinc finger protein (ZFD25)	631	85
2518	AK023160	Homo sapiens	unnamed protein product	168	54
2519	D87326	Mus musculus	GSG2	575	73
2520	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	100	42
2521	X67688	Homo sapiens	transketolase	120	66
2522	AF074086	Homo sapiens	protease	390	86
2523	AF220509	Homo sapiens	transcription associated factor TAFII31L	801	99
2524	AL078463	Homo sapiens	dJ365I19.1 (K1AA0456)	374	92
2525	AF038995	Mus musculus	putative RNA helicase RCK	160	93
2526	M60618	Homo sapiens	nuclear autoantigen	116	75
2527	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	101	57
2528	X68790	Homo sapiens	Bactericidal/Permeability Increasing Protein	136	90
2529	A01592	Homo sapiens	haemoglobin A beta chain	508	94
2530	U89277	Homo sapiens	polyhomeotic 1 homolog	404	79
2531	X90845	Rattus norvegicus	alphaII spectrin	507	87
2532	AL137081	Arabidopsis thaliana	phenylalanine-tRNA synthetase-like protein	178	33
2533	Y18046	Homo sapiens	FGFR1 oncogene partner (FOP)	363	100
2534	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	113	42
2535	X61047	Hydra sp.	mini-collagen	102	38
2536	AB006330	Mus musculus	SOX5	559	94
2537	AC006283	Arabidopsis thaliana	En/Spm-like transposon protein	149	33
2538	AF196779	Homo sapiens	JM11 protein	139	57
2539	AK000741	Homo sapiens	unnamed protein product	233	47
2540	Y18046	Homo sapiens	FGFR1 oncogene partner (FOP)	315	84
2541	U54996	Homo sapiens	HZW10	371	81
2542	G02631	Homo sapiens	Human secreted protein, SEQ ID NO: 6712.	99	45
2543	M95610	Homo sapiens	alpha-2 IX collagen	93	34
2544	AF071173	Mus musculus	Herc2	349	82
2545	AB000516	Homo sapiens	DSIF p160	600	93
2546	AL355178	Homo sapiens	dJ947L8.1.6 (novel CUB and Sushi (SCR repeat) domain protein)	395	90
2547	U93574	Homo sapiens	putative p150	235	76
2548	X80035	Oryctolagus cuniculus	cysteine rich hair keratin associated protein	99	31
2549	U58088	Homo sapiens	Hs-CUL-2	592	86
2550	L26953	Homo sapiens	chromosomal protein	131	63
2551	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	99	61
2552	U59412	Homo sapiens	alpha SNAP	159	54
2553	AF248651	Homo sapiens	RNA-binding protein BRUNOL4	569	93
2554	AJ006519	Rattus norvegicus	ASIC-beta	164	73
2555	U93570	Homo sapiens	putative p150	169	52
2556	AF104328	Arabidopsis thaliana	cell wall-plasma membrane linker protein homolog	105	29
2557	AB028973	Homo sapiens	K1AA1052 protein	610	83
2558	AJ245621	Homo sapiens	CTL2 protein	286	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2559	AF090944	Homo sapiens	PRO0663	174	78
2560	Y17832	Human endogenous retrovirus K	pol protein	411	63
2561	AF109907	Homo sapiens	S164	279	44
2562	A09561	synthetic construct	human serum albumin	680	91
2563	U48359	Gallus gallus	kinesin light chain	575	81
2564	R63235	Homo sapiens	CNS neural thread protein HB4	435	88
2565	D38112	Homo sapiens	NADH dehydrogenase subunit 4	623	89
2566	AF154916	Chlamydomonas reinhardtii	variable flagellar number protein	117	36
2567	AF181637	Drosophila melanogaster	BcDNA.LD34475	261	42
2568	M12530	Homo sapiens	transferrin precursor	693	87
2569	U96915	Homo sapiens	sin3 associated polypeptide p18	651	93
2570	R74205	Homo sapiens	Human death associated protein DAP-2	285	27
2571	AL078593	Homo sapiens	dJ210B1.1 (KJAA0680)	107	37
2572	AF293405	Phaeococcus coccineus	secD-microcylar-endothelium-specific protein	88	39
2573	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195	110	49
2574	AB024601	Pseudomonas aeruginosa	uridylyl transferase	120	37
2575	AB050893	Anadara nodifera	cytochrome c oxidase subunit 1	111	79
2576	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253	130	72
2577	M17697	Homo sapiens	glutamate dehydrogenase	369	61
2578	AF045640	Caenorhabditis elegans	C11D2.4 gene product	264	43
2579	U71382	Homo sapiens	OB binding protein-1	273	86
2580	AF116661	Homo sapiens	PRO1438	114	61
2581	AK000496	Homo sapiens	unnamed protein product	153	55
2582	A67510	Mus musculus	MUS MUSCULUS GENOMIC DNA CONTAINING N ALLELE OF FV1 GENE	190	38
2583	Y44851	Homo sapiens	Human CD39-L66 protein	205	97
2584	AB029151	Homo sapiens	D29	253	73
2585	AF039023	Homo sapiens	Ran-GTP binding protein; RanBP6	765	94
2586	AF054180	Homo sapiens	hematopoietic cell derived zinc finger protein	116	34
2587	AF283645	Homo sapiens	folate transporter/carrier	580	82
2588	AF090930	Homo sapiens	PRO0478	132	67
2589	AC002339	Arabidopsis thaliana	putative ABC transporter	238	34
2590	M34668	Homo sapiens	protein tyrosine phosphatase (EC 3.1.3.48)	627	86
2591	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613	141	63
2592	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3	142	63
2593	R13556	Homo sapiens	Protein encoded downstream of hbc_M oncoprotein	146	54
2594	AF047437	Homo sapiens	sperm acrosomal protein	526	74
2595	U28789	Mus musculus	PACT	528	71
2596	AB002366	Homo sapiens	KIAA0368	615	83
2597	AL049610	Homo sapiens	dJ1055C14.2 (KIAA0026 (transcription factor-like protein	704	93

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2598	G01279	Homo sapiens	MRGX)) Human secreted protein, SEQ ID NO: 5360.	385	79
2599	AF090895	Homo sapiens	PRO0117	142	61
2600	D29763	Mus musculus	seizure-related gene product 6 precursor	119	76
2601	U20158	Homo sapiens	SLP-76	108	53
2602	D38112	Homo sapiens	NADH dehydrogenase subunit 2	242	78
2603	D38112	Homo sapiens	NADH dehydrogenase subunit 2	233	73
2604	L24804	Homo sapiens	p23	259	62
2605	Y12102	Homo sapiens	Human 5' EST secreted protein SEQ ID NO: 415.	132	92
2606	U79284	Homo sapiens	SEC14L	614	81
2607	AF202635	Homo sapiens	PP1200	105	47
2608	AF277374	Homo sapiens	enhancer of polycomb	254	85
2609	X03484	Homo sapiens	raf protein (aa 1-648)	600	82
2610	U15637	Homo sapiens	CD40 binding protein	465	82
2611	U40265	Trypanosoma cruzi	ATPase subunit 6	98	31
2612	AF090942	Homo sapiens	PRO0657	125	48
2613	V00662	Homo sapiens	cytochrome oxidase I	605	82
2614	U46920	Homo sapiens	metaxin	748	94
2615	Y19757	Homo sapiens	SEQ ID NO 475 from WO9922243.	113	87
2616	AK025047	Homo sapiens	unnamed protein product	173	58
2617	D13866	Homo sapiens	alpha-catenin	569	96
2618	U20536	Homo sapiens	cysteine protease Mch2 isoform alpha	588	87
2619	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	608	86
2620	AF190168	Homo sapiens	serum albumin precursor	522	78
2621	A06977	Homo sapiens	albumin	607	93
2622	R14584	Homo sapiens	TGF beta 1 binding protein encoded by clone BPA 13.	339	81
2623	X56698	Xenopus laevis	42Sp48	117	47
2624	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	57
2625	X07881	Homo sapiens	proline-rich protein G1	116	32
2626	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	89	58
2627	A00279	synthetic construct	Human serum albumin	564	95
2628	AK021613	Homo sapiens	unnamed protein product	214	70
2629	M23613	Homo sapiens	nucleophosmin	486	82
2630	AF243424	Homo sapiens	SG2NA beta isoform	256	98
2631	G00506	Homo sapiens	Human secreted protein, SEQ ID NO: 4587.	81	60
2632	A06977	Homo sapiens	albumin	457	74
2633	A06977	Homo sapiens	albumin	563	93
2634	M81088	Rattus norvegicus	EF-1-alpha	165	68
2635	AL359587	Homo sapiens	hypothetical protein	496	82
2636	A03758	Homo sapiens	serum albumin	576	91
2637	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	127	39
2638	U93563	Homo sapiens	putative p150	186	38
2639	U68729	Meloidogyne incognita	cuticle preprocollagen	113	34
2640	AB033056	Homo sapiens	KIAA1230 protein	269	94
2641	AF116712	Homo sapiens	PRO2738	115	61
2642	W48353	Homo sapiens	Human breast cancer related protein	124	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCFLT2.		
2643	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	98	54
2644	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	127	64
2645	AK025116	Homo sapiens	unnamed protein product	104	64
2646	X92485	Plasmodium vivax	pva1	100	47
2647	AF130089	Homo sapiens	PRO2550	122	51
2648	AF194537	Homo sapiens	NAG13	279	83
2649	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	90	66
2650	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	148	63
2651	AF116661	Homo sapiens	PRO1438	112	46
2652	U63542	Homo sapiens	FAP protein	128	79
2653	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	133	46
2654	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	139	72
2655	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	72
2656	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	145	51
2657	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	166	64
2658	B25722	Homo sapiens	Human secreted protein sequence encoded by gene 9 SEQ ID NO:111.	91	88
2659	X92485	Plasmodium vivax	pva1	141	60
2660	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	68	68
2661	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	96	59
2662	AF090931	Homo sapiens	PRO0483	114	74
2663	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	129	57
2664	AF090930	Homo sapiens	PRO0478	170	78
2665	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	460	77
2666	D38112	Homo sapiens	cytochrome c oxidase subunit I	368	67
2667	AF090931	Homo sapiens	PRO0483	90	88
2668	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	121	66
2669	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	169	73
2670	AF194537	Homo sapiens	NAG13	170	42
2671	X86003	Rattus norvegicus	neuron-derived orphan receptor	104	50
2672	U63542	Homo sapiens	FAP protein	139	75
2673	AF090930	Homo sapiens	PRO0478	130	69
2674	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	161	75
2675	AK024455	Homo sapiens	FLJ00047 protein	105	53
2676	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	142	67
2677	AK000496	Homo sapiens	unnamed protein product	110	67
2678	AF116715	Homo sapiens	PRO2829	151	78
2679	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	160	72
2680	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	110	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2681	Y76198	Homo sapiens	6613. Human secreted protein encoded by gene 75.	131	75
2682	U76604	Homo sapiens	180 kDa bullous pemphigoid antigen 2/type XVII collagen	96	37
2683	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	85	55
2684	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	127	80
2685	AF090895	Homo sapiens	PRO0117	81	51
2686	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	119	52
2687	M64793	Rattus norvegicus	salivary proline-rich protein	122	41
2688	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	145	71
2689	AF130089	Homo sapiens	PRO2550	149	78
2690	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	102	47
2691	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	116	74
2692	G03064	Homo sapiens	Human secreted protein, SEQ ID NO: 7145.	130	60
2693	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	106	26
2694	AE001158	Borrelia burgdorferi	conserved hypothetical integral membrane protein	81	37
2695	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	162	76
2696	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	100
2697	AF194537	Homo sapiens	NAG13	126	90
2698	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	69
2699	U93563	Homo sapiens	putative p150	138	37
2700	AF090928	Homo sapiens	PRO0470	177	57
2701	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	75
2702	X92485	Plasmodium vivax	pval	116	50
2703	AK024455	Homo sapiens	FLJ00047 protein	103	57
2704	D38114	Gorilla gorilla	NADH dehydrogenase subunit 2 (ND2)	137	81
2705	AF090895	Homo sapiens	PRO0117	105	51
2706	AF090944	Homo sapiens	PRO0663	121	45
2707	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	104	57
2708	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	157	85
2709	D38112	Homo sapiens	NADH dehydrogenase subunit 1	283	84
2710	AF130079	Homo sapiens	PRO2852	125	48
2711	M22334	Homo sapiens	unknown protein	131	50
2712	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	123	58
2713	S80119	Rattus sp.	reverse transcriptase homolog	230	57
2714	AF090931	Homo sapiens	PRO0483	98	85
2715	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	104	79
2716	L00016	Homo sapiens	urf5	295	93
2717	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	135	82
2718	M81321	Macaca fascicularis	proline-rich protein	117	38

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2719	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	124	57
2720	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1.	147	56
2721	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	132	67
2722	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	129	56
2723	D38112	Homo sapiens	cytochrome c oxidase subunit 1	392	68
2724	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	182	79
2725	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	92
2726	W97293	Homo sapiens	An annexin binding protein (NABP-1).	193	40
2727	U12690	Homo sapiens	cytochrome oxidase subunit II	547	85
2728	V00662	Homo sapiens	cytochrome oxidase I	500	92
2729	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	110	56
2730	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	124	75
2731	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1.	113	57
2732	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	149	51
2733	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1.	101	44
2734	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	288	81
2735	Z74036	Caenorhabditis elegans	contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=58.9, E-value=3.5e-14, N=3	117	37
2736	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	154	62
2737	AK024455	Homo sapiens	FLJ00047 protein	136	60
2738	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	110	63
2739	AP002460	Arabidopsis thaliana	gene_id:F1D9.26-unknown protein	363	90
2740	D38113	Pan troglodytes	cytochrome c oxidase subunit I	358	69
2741	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	143	64
2742	L27428	Homo sapiens	reverse transcriptase	119	45
2743	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	76	63
2744	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	155	79
2745	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	114	51
2746	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	75
2747	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	162	79
2748	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	49
2749	AK024455	Homo sapiens	FLJ00047 protein	165	69
2750	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	167	72
2751	M22332	Homo sapiens	unknown protein	208	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2752	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	125	56
2753	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	150	65
2754	AF220264	Homo sapiens	MOST-1	130	52
2755	AK024455	Homo sapiens	FLJ00047 protein	128	58
2756	AF130051	Homo sapiens	PRO0898	162	73
2757	D38112	Homo sapiens	NADH dehydrogenase subunit 3	259	86
2758	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	124	58
2759	AJ243666	Homo sapiens	NICE-5 protein	118	84
2760	D38112	Homo sapiens	NADH dehydrogenase subunit 4	533	90
2761	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	110	39
2762	U12690	Homo sapiens	cytochrome oxidase subunit II	257	88
2763	Y73345	Homo sapiens	HTRM clone 438283 protein sequence.	624	67
2764	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	156	45
2765	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	58
2766	X92485	Plasmodium vivax	pva1	149	53
2767	AF113685	Homo sapiens	PRO0974	131	63
2768	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	109	56
2769	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	154	71
2770	X97707	Pongo pygmaeus abelii	stopcodon created by posttranscriptional polyadenylation	185	87
2771	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	110	59
2772	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	145	60
2773	AF090944	Homo sapiens	PRO0663	118	62
2774	L26953	Homo sapiens	chromosomal protein	112	58
2775	AF090930	Homo sapiens	PRO0478	127	59
2776	AK024455	Homo sapiens	FLJ00047 protein	154	56
2777	R59843	Homo sapiens	ApoE4Lx2 protease.	103	42
2778	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	101	55
2779	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	64
2780	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	89	56
2782	D38113	Pan troglodytes	NADH dehydrogenase subunit 4	194	97
2783	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	124	68
2784	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	49
2785	U43360	Peromyscus maniculatus	reverse transcriptase	175	50
2786	W58700	Homo sapiens	Human ST-1 partial sequence.	219	100
2787	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	137	90
2788	D38112	Homo sapiens	cytochrome c oxidase subunit 3	519	76
2789	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	104	44
2790	AF130089	Homo sapiens	PRO2550	121	39
2791	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	135	63
2792	G03052	Homo sapiens	Human secreted protein, SEQ ID NO:	124	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7133.		
2793	M10546	Homo sapiens	cytochrome oxidase I	153	80
2794	D38112	Homo sapiens	cytochrome c oxidase subunit 1	461	84
2795	AF090931	Homo sapiens	PRO0483	114	76
2796	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	53
2797	D38112	Homo sapiens	NADH dehydrogenase subunit 2	114	78
2798	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	115	71
2799	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	113	79
2800	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	117	48
2801	X92485	Plasmodium vivax	pval	97	80
2802	D38112	Homo sapiens	cytochrome c oxidase subunit 3	471	80
2803	AF130051	Homo sapiens	PRO0898	118	78
2804	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	78	73
2805	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	143	69
2806	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	102	62
2807	K02401	Homo sapiens	chorionic somatomammotropin	543	88
2808	Y18522	Corvus frugilegus	cytochrome oxidase subunit I	382	60
2809	G01194	Homo sapiens	Human secreted protein, SEQ ID NO: 5275.	555	93
2810	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	399	77
2811	AF007826	Homo sapiens	bax epsilon	94	39
2812	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	220	67
2813	U12690	Homo sapiens	cytochrome oxidase subunit II	495	81
2814	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	112	48
2815	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	102	75
2816	D38112	Homo sapiens	cytochrome c oxidase subunit 3	437	83
2817	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	143	66
2818	X55733	Homo sapiens	initiation factor 4B	458	80
2819	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	132	65
2820	D38112	Homo sapiens	cytochrome c oxidase subunit 3	347	68
2821	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	94	62
2822	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	118	54
2823	AF130079	Homo sapiens	PRO2852	143	54
2824	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	140	52
2825	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	161	67
2826	AF119851	Homo sapiens	PRO1722	104	70
2827	D49489	Homo sapiens	human P5	523	91
2828	M10546	Homo sapiens	cytochrome oxidase I	206	81
2829	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	138	42
2830	AF090931	Homo sapiens	PRO0483	97	80
2831	G03790	Homo sapiens	Human secreted protein, SEQ ID NO:	144	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2832	AF041330	Bodo saltans	7871.		
2833	X92485	Plasmodium vivax	NADH dehydrogenase subunit 5 pval	112 103	35 43
2834	R32010	Homo sapiens	Rp15-TIA-1.	152	54
2835	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	153	59
2836	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	59
2837	AF090931	Homo sapiens	PRO0483	149	81
2838	AF130089	Homo sapiens	PRO2550	123	49
2839	AF090942	Homo sapiens	PRO0657	135	54
2840	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	124	54
2841	AF090895	Homo sapiens	PRO0117	146	55
2842	AF132200	Homo sapiens	PRO1751	98	74
2843	U12690	Homo sapiens	cytochrome oxidase subunit II	194	75
2844	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	61	59
2845	AL390114	Leishmania major	extremely cysteine/valine rich protein	171	37
2846	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	155	69
2847	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	141	58
2848	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	108	65
2849	U12690	Homo sapiens	cytochrome oxidase subunit II	441	77
2850	D38112	Homo sapiens	cytochrome c oxidase subunit 1	490	88
2851	K02401	Homo sapiens	chorionic somatomammotropin	488	90
2852	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	110	49
2853	U83280	Leishmania donovani	39 kDa antigen	131	47
2854	AF090944	Homo sapiens	PRO0663	173	72
2855	V00662	Homo sapiens	ATPase 6	392	71
2856	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	147	50
2857	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICE1) protein sequence.	113	76
2858	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	178	84
2859	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	192	92
2860	Z81068	Caenorhabditis elegans	contains similarity to Pfam domain: PF00102 (Protein-tyrosine phosphatase), Score=232.1, E-value=2.6e-66, N=1-cDNA EST yk299h6.3 comes from this gene-cDNA EST yk420b4.3 comes from this gene-cDNA EST yk439g6.3 comes from this gene-cDNA EST yk299h6.5 comes from this gene-cDNA EST yk420b4.5 comes from this gene-cDNA EST yk439g6.5 comes from this gene	104	36
2861	D38112	Homo sapiens	NADH dehydrogenase subunit 2	444	85
2862	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	168	61
2863	U93564	Homo sapiens	putative p150	132	34

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2864	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	152	50
2865	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	124	76
2866	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	145	46
2867	AF090930	Homo sapiens	PRO0478	161	61
2868	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	117	48
2869	U15647	Mus musculus	reverse transcriptase	197	40
2870	U09500	Homo sapiens	cytochrome b	394	68
2871	U09500	Homo sapiens	cytochrome b	614	92
2872	D38112	Homo sapiens	NADH dehydrogenase subunit 4	516	87
2873	D38112	Homo sapiens	NADH dehydrogenase subunit 4	458	84
2874	D38112	Homo sapiens	NADH dehydrogenase subunit 4	516	92
2875	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	87	55
2876	D38112	Homo sapiens	NADH dehydrogenase subunit 5	624	96
2877	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	160	58
2878	U32174	Dictyostelium discoideum	non-receptor tyrosine kinase	120	33
2879	D38112	Homo sapiens	ATPase subunit 6	141	54
2880	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	140	84
2881	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	93	79
2882	V00662	Homo sapiens	ATPase 6	130	87
2883	AL390114	Leishmania major	probable proteophosphoglycan	117	50
2884	AF119851	Homo sapiens	PRO1722	79	55
2885	X92485	Plasmodium vivax	pva1	106	48
2886	V00662	Homo sapiens	ATPase 6	127	87
2887	D38112	Homo sapiens	NADH dehydrogenase subunit 4	191	83
2888	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	58
2889	X92485	Plasmodium vivax	pva1	107	63
2890	M10546	Homo sapiens	cytochrome oxidase I	163	89
2891	AF090942	Homo sapiens	PRO0657	72	37
2892	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	136	56
2893	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	139	66
2894	AK024455	Homo sapiens	FLJ00047 protein	139	57
2895	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	111	44
2896	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	182	62
2897	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	73
2898	D38112	Homo sapiens	cytochrome c oxidase subunit 3	248	53
2899	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	366	68
2900	X07882	Homo sapiens	Po protein	146	41
2901	V00662	Homo sapiens	cytochrome B	517	91
2902	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	378	67
2903	AF090931	Homo sapiens	PRO0483	117	67
2904	AF003540	Homo sapiens	Krueppel family zinc finger protein	99	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2905	AF130079	Homo sapiens	PRO2852	111	55
2906	D38112	Homo sapiens	cytochrome c oxidase subunit 1	427	79
2907	AF020635	Homo sapiens	PP1200	140	66
2908	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	116	41
2909	U63542	Homo sapiens	FAP protein	155	75
2910	D38114	Gorilla gorilla	cytochrome c oxidase subunit 1 (COI)	446	72
2911	AP002031	Arabidopsis thaliana	gene_id:K3D20.3~	118	35
2912	D38112	Homo sapiens	cytochrome c oxidase subunit 1	435	80
2913	D38116	Pan paniscus	cytochrome c oxidase subunit 1	469	83
2914	D38112	Homo sapiens	cytochrome c oxidase subunit 3	480	80
2915	D38112	Homo sapiens	cytochrome c oxidase subunit 1	488	86
2916	D38112	Homo sapiens	cytochrome c oxidase subunit 3	519	80
2917	D38112	Homo sapiens	cytochrome c oxidase subunit 3	172	80
2918	D38112	Homo sapiens	cytochrome c oxidase subunit 1	512	75
2919	D38112	Homo sapiens	cytochrome c oxidase subunit 1	458	79
2920	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	152	65
2921	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	324	87
2922	D38112	Homo sapiens	cytochrome c oxidase subunit 3	530	84
2923	AF157321	Homo sapiens	30 kDa protein	370	68
2924	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	174	71
2925	D38112	Homo sapiens	NADH dehydrogenase subunit 4	503	88
2926	U47624	Xenopus laevis	alpha(E)-catenin	243	94
2927	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	135	47
2928	D38112	Homo sapiens	cytochrome c oxidase subunit 3	476	78
2929	D38112	Homo sapiens	cytochrome c oxidase subunit 1	465	81
2930	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	151	58
2931	D16480	Homo sapiens	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of trifunctional protein	345	67
2932	D38112	Homo sapiens	NADH dehydrogenase subunit 4	212	95
2933	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	69
2934	X83427	Ornithorhynchus anatinus	cytochrome c oxidase subunit 1	460	82
2935	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	527	83
2936	D38112	Homo sapiens	NADH dehydrogenase subunit 4	448	92
2937	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	183	77
2938	X15081	Crithidia fasciculata	MURF2 protein (AA 1-348)	105	42
2939	AF194537	Homo sapiens	NAG13	151	52
2940	AJ271872	Nicotiana glauca	extensin	165	37
2941	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	91
2942	D38112	Homo sapiens	cytochrome c oxidase subunit 3	387	69
2943	D38112	Homo sapiens	cytochrome c oxidase subunit 3	509	79
2944	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	95
2945	J01415	Homo sapiens	MTND4	429	76
2946	AC010793	Arabidopsis thaliana	F20B17.16	99	41
2947	AF116712	Homo sapiens	PRO2738	132	60
2948	X89658	Homo sapiens	CAP-18 protein	136	49

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2949	V00662	Homo sapiens	cytochrome oxidase I	449	86
2950	D38112	Homo sapiens	NADH dehydrogenase subunit 4	438	82
2951	D38112	Homo sapiens	NADH dehydrogenase subunit 4	363	76
2952	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	92
2953	X56015	Crithidia oncopelti	NADH dehydrogenase subunit 5	102	32
2954	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	110	68
2955	Y76287	Homo sapiens	Fragment of human secreted protein encoded by gene 20.	345	78
2956	D38112	Homo sapiens	cytochrome c oxidase subunit 3	340	71
2957	D38112	Homo sapiens	cytochrome c oxidase subunit 1	456	83
2958	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	102	76
2959	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	96	84
2960	D38112	Homo sapiens	cytochrome c oxidase subunit 1	400	70
2961	X69978	Homo sapiens	XP-G factor	539	88
2962	AF203687	Homo sapiens	prolactin regulatory element-binding protein	453	77
2963	D38112	Homo sapiens	cytochrome c oxidase subunit 1	561	83
2964	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	92
2965	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	119	63
2966	U52077	Homo sapiens	mariner transposase	469	83
2967	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	130	53
2968	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	103	42
2969	X92485	Plasmodium vivax	pval	144	42
2970	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	127	63
2971	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	129	63
2972	Y17221	Homo sapiens	Human secreted protein (clone flk317-3).	91	56
2973	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	101	72
2974	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	130	68
2975	AF130089	Homo sapiens	PRO2550	167	46
2976	V00662	Homo sapiens	cytochrome oxidase I	539	79
2977	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	121	44
2978	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	72
2979	U93568	Homo sapiens	putative p150	122	30
2980	M12099	Mus musculus	proline-rich protein	119	39
2981	Z38128	Mus musculus	histone H1	117	36
2982	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	172	51
2983	AC002291	Arabidopsis thaliana	extensin	110	35
2984	M10546	Homo sapiens	cytochrome oxidase I	295	92
2985	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	171	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2986	U18985	Homo sapiens	triadin	416	83
2987	AF155232	Pisum sativum	extensin	159	41
2988	X03145	Homo sapiens	pot. ORF V	133	44
2989	U12690	Homo sapiens	cytochrome oxidase subunit II	565	84
2990	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	127	53
2991	D38112	Homo sapiens	cytochrome c oxidase subunit I	538	83
2992	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	471	75
2993	D38113	Pan troglodytes	cytochrome c oxidase subunit I	511	72
2994	D38112	Homo sapiens	cytochrome c oxidase subunit I	301	79
2995	D38112	Homo sapiens	cytochrome c oxidase subunit I	526	78
2996	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	634	82
2997	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	158	76
2998	X77816	Rattus norvegicus	PR-Vbeta1	103	50
2999	V00662	Homo sapiens	cytochrome oxidase I	535	78
3000	L38908	Nicotiana tabacum	extensin	146	38
3001	D38112	Homo sapiens	NADH dehydrogenase subunit 2	494	87
3002	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	66
3003	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	117	46
3004	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	93	47
3005	U43627	Arabidopsis thaliana	extensin	118	37
3006	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	150	44
3007	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	114	73
3008	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	111	39
3009	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	84
3010	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	212	77
3011	X65718	Prunus dulcis	extensin	129	42
3012	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	71	76
3013	Z38128	Mus musculus	histone H1	104	32
3014	X56010	Sorghum bicolor	hydroxyproline-rich glycoprotein	102	34
3015	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	80
3016	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	99	34
3017	X55685	Lycopersicon esculentum	extensin (class I)	142	32
3018	AJ133050	Panulirus argus	cytochrome c oxidase subunit I	125	71
3019	G03597	Homo sapiens	Human secreted protein, SEQ ID NO: 7678.	175	68
3020	U93564	Homo sapiens	putative p150	97	57
3021	D38116	Pan paniscus	cytochrome c oxidase subunit I	555	82
3022	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	147	76
3023	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	632	82
3024	AF155232	Pisum sativum	extensin	181	42
3025	V00662	Homo sapiens	cytochrome oxidase I	567	85

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3026	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	130	58
3027	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	141	67
3028	AF130089	Homo sapiens	PRO2550	149	55
3029	AF090944	Homo sapiens	PRO0663	168	76
3030	D38112	Homo sapiens	NADH dehydrogenase subunit 2	122	92
3031	D38112	Homo sapiens	NADH dehydrogenase subunit 4	507	91
3032	D38112	Homo sapiens	NADH dehydrogenase subunit 2	351	87
3033	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	99	75
3034	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	113	85
3035	U93567	Homo sapiens	putative p150	173	41
3036	X92485	Plasmodium vivax	pva1	122	41
3037	AF202635	Homo sapiens	PP1200	128	67
3038	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	151	83
3039	D38112	Homo sapiens	cytochrome c oxidase subunit 1	415	74
3040	D86853	Catharanthus roseus	extensin	198	40
3041	M76546	Helianthus annuus	hydroxyproline-rich protein	110	47
3042	D38112	Homo sapiens	cytochrome c oxidase subunit 3	377	95
3043	S80119	Rattus sp.	reverse transcriptase homolog	106	50
3044	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	137	55
3045	Y36156	Homo sapiens	Human secreted protein #28.	91	58
3046	U93574	Homo sapiens	putative p150	177	49
3047	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	98	37
3048	D38112	Homo sapiens	cytochrome c oxidase subunit 3	568	87
3049	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	144	63
3050	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	80
3051	AK027208	Homo sapiens	unnamed protein product	145	72
3052	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	166	75
3053	AF118082	Homo sapiens	PRO1902	84	50
3054	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	118	41
3055	X92485	Plasmodium vivax	pva1	132	52
3056	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	117	74
3057	AL390114	Leishmania major	extremely cysteine/valine rich protein	99	72
3058	D38112	Homo sapiens	cytochrome c oxidase subunit 3	627	89
3059	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	98	57
3060	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	100	38
3061	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	80
3062	D38112	Homo sapiens	cytochrome c oxidase subunit 3	529	80
3063	AF130051	Homo sapiens	PRO0898	159	71
3064	AF195418	Mus musculus	ODZ3	386	94
3065	Y01158	Homo sapiens	Secreted protein encoded by gene 18	109	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3066	D38112	Homo sapiens	clone HCACJ81.		
3067	AL359782	Trypanosoma brucei	NADH dehydrogenase subunit 2 probable similar to ring-h2 finger protein thal1a.	338 120	80 50
3068	U15647	Mus musculus	reverse transcriptase	134	41
3069	D38112	Homo sapiens	cytochrome c oxidase subunit 3	397	92
3070	AF130089	Homo sapiens	PRO2550	149	55
3071	U93565	Homo sapiens	putative p150	143	37
3072	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	112	45
3073	AF090930	Homo sapiens	PRO0478	135	78
3074	AF130089	Homo sapiens	PRO2550	156	58
3075	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	267	65
3076	U83280	Leishmania donovani	39 kDa antigen	98	51
3077	D38112	Homo sapiens	cytochrome c oxidase subunit 3	626	86
3078	AF116712	Homo sapiens	PRO2738	114	59
3079	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	112	46
3080	D38112	Homo sapiens	cytochrome c oxidase subunit 1	492	80
3081	D38112	Homo sapiens	NADH dehydrogenase subunit 4	523	86
3082	D38112	Homo sapiens	cytochrome c oxidase subunit 3	515	79
3083	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	150	41
3084	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	191	97
3085	U12690	Homo sapiens	cytochrome oxidase subunit II	537	78
3086	D38112	Homo sapiens	ATPase subunit 6	300	58
3087	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	104	37
3088	K02247	Rattus norvegicus	proline-rich protein	108	41
3089	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	130	48
3090	V00662	Homo sapiens	cytochrome oxidase I	597	84
3091	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	221	43
3092	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	392	59
3093	D38116	Pan paniscus	cytochrome c oxidase subunit 1	593	84
3094	D38112	Homo sapiens	cytochrome c oxidase subunit 1	471	76
3095	R63235	Homo sapiens	CNS neural thread protein HB4.	369	98
3096	L26953	Homo sapiens	chromosomal protein	115	57
3097	G00591	Homo sapiens	Human secreted protein, SEQ ID NO: 4672.	124	57
3098	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	91
3099	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	153	96
3100	AC006233	Arabidopsis thaliana	hypothetical protein	65	44
3101	AF289098	Cladrastis kentukea	ENOD2	107	35
3102	AF155232	Pisum sativum	extensin	142	43
3103	AF130089	Homo sapiens	PRO2550	122	81
3104	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	80
3105	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	104	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3106	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	76
3107	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	72
3108	D38112	Homo sapiens	NADH dehydrogenase subunit 4	334	85
3109	U43627	Arabidopsis thaliana	extensin	112	30
3110	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	100
3111	AF130089	Homo sapiens	PRO2550	137	37
3112	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	220	93
3113	A18812	Brassica napus	extensin	128	32
3114	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	63
3115	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	92	69
3116	X92485	Plasmodium vivax	pva1	148	45
3117	D38112	Homo sapiens	cytochrome c oxidase subunit 1	574	80
3118	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	125	41
3119	U43627	Arabidopsis thaliana	extensin	129	32
3120	AF205385	Pan troglodytes	NADH dehydrogenase subunit 5	171	82
3121	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	90	59
3122	AF130051	Homo sapiens	PRO0898	134	82
3123	M81321	Macaca fascicularis	proline-rich protein	158	48
3124	U93563	Homo sapiens	putative p150	126	32
3125	D38114	Gorilla gorilla	NADH dehydrogenase subunit 1 (ND1)	337	92
3126	AF130089	Homo sapiens	PRO2550	155	77
3127	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	76
3128	AF090901	Homo sapiens	PRO0195	109	53
3129	AF003736	Murine leukemia virus	reverse transcriptase	164	40
3130	U25281	Rattus norvegicus	SH3 domain binding protein	88	39
3131	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	71
3132	D86853	Catharanthus roseus	extensin	110	33
3133	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	506	76
3134	V00662	Homo sapiens	cytochrome oxidase 1	583	88
3135	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	68
3136	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	282	60
3137	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	119	54
3138	AF118082	Homo sapiens	PRO1902	118	51
3139	D38112	Homo sapiens	NADH dehydrogenase subunit 4	270	87
3140	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	103	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3141	D38112	Homo sapiens	NADH dehydrogenase subunit 5	353	74
3142	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	126	77
3143	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	72
3144	AF090930	Homo sapiens	PRO0478	138	73
3145	AF155232	Pisum sativum	extensin	110	34
3146	M69008	Homo sapiens	alpha-1 type XIII collagen	107	37
3147	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1.	103	63
3148	D38112	Homo sapiens	cytochrome c oxidase subunit 1	505	84
3149	M77194	Rat leukemia virus	polymerase	167	35
3150	AP002543	Arabidopsis thaliana	gb AAD23015.1-gene_id:F15M7.16-similar to unknown protein	105	31
3151	AK024455	Homo sapiens	FLJ00047 protein	109	59
3152	K02576	Homo sapiens	salivary proline-rich protein 1	89	39
3153	J04794	Homo sapiens	aldehyde reductase (EC 1.1.1.2)	137	58
3154	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	115	70
3155	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	160	53
3156	X92485	Plasmodium vivax	pva1	104	50
3157	AF194537	Homo sapiens	NAG13	207	60
3158	AF063693	Mus musculus	type XIII collagen	104	37
3159	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	91
3160	AF020191	Mus musculus	proline-rich protein 13	107	51
3161	AF194537	Homo sapiens	NAG13	170	76
3162	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	103	41
3163	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	161	58
3164	K03205	Homo sapiens	salivary proline-rich protein precursor	139	46
3165	U93570	Homo sapiens	putative p150	151	68
3166	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	144	71
3167	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	147	66
3168	L27428	Homo sapiens	reverse transcriptase	94	51
3169	X97675	Homo sapiens	plakophilin 2b	103	76
3170	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	54
3171	AK024455	Homo sapiens	FLJ00047 protein	98	61
3172	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	146	38
3173	D38116	Pan paniscus	NADH dehydrogenase subunit 4	467	81
3174	X92485	Plasmodium vivax	pva1	88	69
3175	L26953	Homo sapiens	chromosomal protein	124	78
3176	AF042169	Homo sapiens	putative ATP-dependent mitochondrial RNA helicase	223	95
3177	AF130079	Homo sapiens	PRO2852	96	44
3178	AF273217	Mus musculus	cell proliferation related protein CAP	97	36
3179	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	90	69
3180	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	146	78
3181	AF118082	Homo sapiens	PRO1902	150	58
3182	U60315	Molluscum contagiosum	MC107L	101	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		virus subtype 1			
3183	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	148	61
3184	U93565	Homo sapiens	putative p150	265	58
3185	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	79
3186	U87607	Rattus norvegicus	putative RNA binding protein 1	167	39
3187	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	160	63
3188	S80119	Rattus sp.	reverse transcriptase homolog	152	49
3189	X05300	Rattus norvegicus	ribophorin I	122	46
3190	B01372	Homo sapiens	Neuron-associated protein.	106	80
3191	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	83
3192	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	135	80
3193	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	98	34
3194	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	140	87
3195	AF022985	Caenorhabditis elegans	Similar to collagen	97	40
3196	D38112	Homo sapiens	cytochrome c oxidase subunit 1	452	81
3197	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	110	58
3198	X99452	Lycopersicon esculentum	extensin-like protein Dif54	100	36
3199	D86853	Catharanthus roseus	extensin	119	36
3200	AF025424	Rattus norvegicus	RNA polymerase I 127 kDa subunit	215	74
3201	U93563	Homo sapiens	putative p150	359	77
3202	K03202	Homo sapiens	salivary proline-rich protein precursor	112	37
3203	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	153	84
3204	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	128	39
3205	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	154	76
3206	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	127	64
3207	X97675	Homo sapiens	plakophilin 2b	142	51
3208	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	91	58
3209	AB026512	Ecnomiosa sp. Ecn1	cytochrome c oxidase subunit I	254	62
3210	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	163	59
3211	D38112	Homo sapiens	ATPase subunit 6	447	78
3212	V00662	Homo sapiens	ATPase 6	482	83
3213	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	151	66
3214	D38112	Homo sapiens	ATPase subunit 6	400	72
3215	D38112	Homo sapiens	cytochrome c oxidase subunit 3	569	88
3216	D38112	Homo sapiens	NADH dehydrogenase subunit 5	472	82
3217	AF090930	Homo sapiens	PRO0478	96	64
3218	G03172	Homo sapiens	Human secreted protein, SEQ ID NO:	137	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3219	AF006061	Homo sapiens	7253. placental growth hormone isoform hGH-V3	290	68
3220	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	115	63
3221	D38112	Homo sapiens	cytochrome c oxidase subunit 1	441	71
3222	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	111	59
3223	D38112	Homo sapiens	cytochrome c oxidase subunit 3	497	81
3224	L26953	Homo sapiens	chromosomal protein	95	59
3225	U83280	Leishmania donovani	39 kDa antigen	117	90
3226	AF239615	Manihot esculenta	CRANTZ hydroxyproline-rich glycoprotein	124	43
3227	D38112	Homo sapiens	NADH dehydrogenase subunit 4	442	74
3228	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	172	67
3229	X92591	Mus musculus	transcription factor	109	43
3230	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	81	54
3231	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 1	476	72
3232	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	100	54
3233	U96416	Dennys distinctus timjonesi	cytochrome b	95	40
3234	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	86
3235	M76546	Helianthus annuus	hydroxyproline-rich protein	101	40
3236	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	149	75
3237	D38112	Homo sapiens	NADH dehydrogenase subunit 5	532	76
3238	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	576	89
3239	U93567	Homo sapiens	p40	155	32
3240	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	79
3241	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	145	65
3242	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	76	62
3243	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	138	69
3244	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	115	39
3245	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	138	54
3246	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	153	69
3247	U58736	Caenorhabditis elegans	Similar to cuticular collagen	107	37
3248	U87607	Rattus norvegicus	putative RNA binding protein 1	148	45
3249	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	113	85
3250	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	166	61
3251	U15183	Mycobacterium leprae	proline-rich antigen	109	40
3252	AF130089	Homo sapiens	PRO2550	151	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3253	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	58
3254	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	80
3255	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1.	108	57
3256	J01415	Homo sapiens	cytochrome oxidase subunit 3	156	88
3257	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	206	93
3258	Y36203	Homo sapiens	Human secreted protein #75.	111	77
3259	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	98	57
3260	D38112	Homo sapiens	cytochrome c oxidase subunit 1	345	67
3261	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	97	56
3262	L38908	Nicotiana tabacum	extensin	155	40
3263	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	95	70
3264	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	198	87
3265	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	69
3266	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	158	59
3267	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	105	56
3268	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	72
3269	D38112	Homo sapiens	NADH dehydrogenase subunit 1	200	95
3270	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	138	73
3271	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	151	90
3272	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	193	95
3273	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	111	52
3274	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	87
3275	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	86
3276	S62928	Homo sapiens	PRB1M protein precursor	104	34
3277	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	154	55
3278	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	166	100
3279	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	212	91
3280	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	118	50
3281	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	130	46
3282	M10546	Homo sapiens	cytochrome oxidase 1	303	95
3283	D38112	Homo sapiens	cytochrome c oxidase subunit 1	455	81
3284	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	502	83
3285	AF118086	Homo sapiens	PRO1992	99	88
3286	D38112	Homo sapiens	cytochrome c oxidase subunit 1	489	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3287	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	485	88
3288	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	124	73
3289	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	158	60
3290	X92485	Plasmodium vivax	pva1	99	58
3291	AF116712	Homo sapiens	PRO2738	102	51
3292	AF119851	Homo sapiens	PRO1722	99	86
3293	AF090930	Homo sapiens	PRO0478	141	72
3294	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	151	66
3295	M64793	Rattus norvegicus	salivary proline-rich protein	107	41
3296	AK024455	Homo sapiens	FLJ00047 protein	97	53
3297	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	156	60
3298	AC007654	Arabidopsis thaliana	T19E23.7	97	49
3299	Y17221	Homo sapiens	Human secreted protein (clone fk317-3).	96	44
3300	AJ243905	Caenorhabditis elegans	SF1 protein	104	42
3301	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	96	41
3302	X89453	Rattus norvegicus	DRPLA	83	65
3303	U10099	Homo sapiens	POM-ZP3	227	52
3304	D38112	Homo sapiens	cytochrome c oxidase subunit 3	553	89
3305	L27428	Homo sapiens	reverse transcriptase	144	43
3306	D38112	Homo sapiens	cytochrome c oxidase subunit 3	388	71
3307	AF217374	Acanthaster planci	cytochrome oxidase subunit I	439	78
3308	D38112	Homo sapiens	cytochrome c oxidase subunit 1	439	82
3309	D38112	Homo sapiens	cytochrome c oxidase subunit 1	492	88
3310	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	81	65
3311	X53581	Rattus norvegicus	ORF4	140	48
3312	V00662	Homo sapiens	cytochrome B	487	88
3313	D38112	Homo sapiens	NADH dehydrogenase subunit 1	451	80
3314	V00662	Homo sapiens	cytochrome oxidase I	524	88
3315	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	518	87
3316	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	115	50
3317	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	356	69
3318	U12693	Homo sapiens	cytochrome oxidase subunit II	477	78
3319	Z67990	Caenorhabditis elegans	contains similarity to Pfam domain: PF01484 (Nematode cuticle collagen N-terminal domain), Score=27.5, E-value=0.0001, N=1	75	40
3320	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	126	75
3321	AF090930	Homo sapiens	PRO0478	166	65
3322	X92485	Plasmodium vivax	pva1	104	44
3323	D38112	Homo sapiens	cytochrome c oxidase subunit 3	513	80
3324	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	483	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3325	AF130089	Homo sapiens	PRO2550	121	88
3326	AC026234	Unknown	Contains weak similarity to an unknown protein T23E18.5	191	66
3327	V00662	Homo sapiens	cytochrome B	439	72
3328	U12690	Homo sapiens	cytochrome oxidase subunit II	316	75
3329	AF091711	Homo sapiens	splice variant AKAP350	106	52
3330	U93565	Homo sapiens	putative p150	125	45
3331	AF119851	Homo sapiens	PRO1722	88	72
3332	D38112	Homo sapiens	cytochrome c oxidase subunit 3	489	81
3333	V00662	Homo sapiens	cytochrome oxidase I	544	90
3334	D38112	Homo sapiens	cytochrome c oxidase subunit 1	475	80
3335	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	168	66
3336	AF146688	Takifugu rubripes	serine-threonine kinase 9	101	43
3337	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	101	50
3338	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	110	50
3339	V00662	Homo sapiens	cytochrome oxidase I	458	80
3340	K02401	Homo sapiens	chorionic somatomammotropin	209	97
3341	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	112	52
3342	X65165	Volvox carteri	extensin	146	41
3343	AL390114	Leishmania major	extremely cysteine/valine rich protein	119	51
3344	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	559	84
3345	U12690	Homo sapiens	cytochrome oxidase subunit II	508	89
3346	M11897	Mus musculus	proline-rich salivary protein	96	41
3347	U92455	Mus musculus	WW domain binding protein 7; WBP7	113	38
3348	U83280	Leishmania donovani	39 kDa antigen	105	40
3349	K03205	Homo sapiens	salivary proline-rich protein precursor	113	38
3350	D38112	Homo sapiens	cytochrome c oxidase subunit I	542	79
3351	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	664	88
3352	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	117	85
3353	A18812	Brassica napus	extensin	103	31
3354	M10546	Homo sapiens	cytochrome oxidase I	125	78
3355	M81321	Macaca fascicularis	proline-rich protein	107	44
3356	M10546	Homo sapiens	cytochrome oxidase I	284	90
3357	D38112	Homo sapiens	cytochrome c oxidase subunit 1	513	80
3358	D38112	Homo sapiens	cytochrome c oxidase subunit 1	541	79
3359	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	543	87
3360	D38112	Homo sapiens	cytochrome c oxidase subunit 1	563	86
3361	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	179	57
3362	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	125	62
3363	AF016099	Mus musculus	endonuclease/reverse transcriptase	151	46
3364	D38112	Homo sapiens	cytochrome c oxidase subunit 3	569	82
3365	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	102	40
3366	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	76
3367	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	145	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3368	D38112	Homo sapiens	cytochrome c oxidase subunit 1	587	87
3369	D38112	Homo sapiens	cytochrome c oxidase subunit 1	549	82
3370	AL035526	Arabidopsis thaliana	extensin-like protein	130	39
3371	J04543	Homo sapiens	synexin	101	40
3372	Z29573	Didelphis virginiana	cytochrome c oxidase subunit 3	154	71
3373	U93568	Homo sapiens	putative p150	176	59
3374	L28748	Bos taurus	putative	146	67
3375	D38112	Homo sapiens	cytochrome c oxidase subunit 1	512	75
3376	D38112	Homo sapiens	cytochrome c oxidase subunit 1	509	78
3377	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	135	51
3378	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	557	82
3379	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	120	35
3380	X92485	Plasmodium vivax	pval	124	38
3381	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	110	78
3382	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	108	67
3383	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	86
3384	X98296	Homo sapiens	ubiquitin hydrolase	238	83
3385	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	494	75
3386	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	155	66
3387	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	116	65
3388	W73624	Homo sapiens	Human secreted protein clone aw92.1.	327	62
3389	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	141	76
3390	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	73	61
3391	U35730	Mus musculus	jerky	152	30
3392	U34788	Mus musculus	Wiskott-Aldrich Syndrome Protein	100	41
3393	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	483	77
3394	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	539	81
3395	D38112	Homo sapiens	cytochrome c oxidase subunit 1	608	87
3396	X71602	Nicotiana tabacum	extensin	104	35
3397	L26953	Homo sapiens	chromosomal protein	100	60
3398	AF197832	Cyanocitta cristata	cytochrome oxidase I	488	76
3399	X53581	Rattus norvegicus	ORF4	140	42
3400	D38112	Homo sapiens	cytochrome c oxidase subunit 1	597	85
3401	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	656	89
3402	L26953	Homo sapiens	chromosomal protein	117	63
3403	AF052298	Drosophila silvestris	Y box protein	114	30
3404	U43360	Peromyscus maniculatus	reverse transcriptase	133	53
3405	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	151	65
3406	D38112	Homo sapiens	cytochrome c oxidase subunit 1	277	82
3407	U01849	Trypanosoma	ORF2	94	30

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		brucei			
3408	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	115	65
3409	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	189	86
3410	U93570	Homo sapiens	putative p150	233	52
3411	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	104	44
3412	AF090944	Homo sapiens	PRO0663	97	56
3413	X61048	Hydra sp.	mini-collagen	128	44
3414	AF118086	Homo sapiens	PRO1992	128	81
3415	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	145	61
3416	AF116695	Homo sapiens	PRO2221	169	69
3417	U31778	Human papillomavirus type 20	putative	107	50
3418	X92485	Plasmodium vivax	pva1	97	54
3419	U12690	Homo sapiens	cytochrome oxidase subunit II	195	94
3420	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	144	69
3421	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	139	71
3422	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	111	63
3423	X15917	Paramecium aurelia	ORF4 protein (AA 1-156)	93	41
3424	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	99	69
3425	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	115	60
3426	Y14486	Homo sapiens	cytosolic serine hydroxymethyltransferase	196	61
3427	U93569	Homo sapiens	putative p150	110	44
3428	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	120	67
3429	AB012223	Canis familiaris	ORF2	169	44
3430	X97675	Homo sapiens	plakophilin 2b	118	60
3431	AF220264	Homo sapiens	MOST-1	153	72
3432	X64173	Zea diploperennis	hydroxyproline-rich glycoprotein	104	41
3433	AF113685	Homo sapiens	PRO0974	104	72
3434	AB002306	Homo sapiens	KIAA0308	282	83
3435	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	83
3436	AB012223	Canis familiaris	ORF2	108	43
3437	AK024455	Homo sapiens	FLJ00047 protein	100	65
3438	U52077	Homo sapiens	mariner transposase	381	64
3439	D38112	Homo sapiens	cytochrome c oxidase subunit I	425	84
3440	AK024455	Homo sapiens	FLJ00047 protein	123	63
3441	G02624	Homo sapiens	Human secreted protein, SEQ ID NO: 6705.	90	78
3442	Y36156	Homo sapiens	Human secreted protein #28.	126	71
3443	AF191032	Myxine glutinosa	RING3	84	63
3444	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	141	57
3445	Y08061	Homo sapiens	Human c-myc protein fragment.	88	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3446	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	157	67
3447	U12690	Homo sapiens	cytochrome oxidase subunit II	281	86
3448	AF112481	Homo sapiens	RAD54B protein	392	87
3449	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	98	55
3450	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	133	90
3451	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	418	82
3452	AF130079	Homo sapiens	PRO2852	110	80
3453	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	143	73
3454	AB032254	Homo sapiens	bromodomain adjacent to zinc finger domain 2A	447	85
3455	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	134	62
3456	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	79	68
3457	D38112	Homo sapiens	cytochrome c oxidase subunit 3	545	84
3458	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	134	83
3459	D38112	Homo sapiens	NADH dehydrogenase subunit 2	277	80
3460	AK000867	Homo sapiens	unnamed protein product	474	98
3461	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	123	52
3462	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	89	30
3463	U93568	Homo sapiens	putative p150	100	46
3464	AL390114	Leishmania major	extremely cysteine/valine rich protein	156	43
3465	D38112	Homo sapiens	NADH dehydrogenase subunit 3	340	88
3466	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	119	100
3467	B01372	Homo sapiens	Neuron-associated protein.	142	75
3468	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	103	40
3469	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	139	80
3470	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	207	89
3471	AF116661	Homo sapiens	PRO1438	119	47
3472	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	129	59
3473	AF130089	Homo sapiens	PRO2550	108	86
3474	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	80
3475	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	590	79
3476	AF118086	Homo sapiens	PRO1992	126	69
3477	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	147	47
3478	J01415	Homo sapiens	MTND4	482	78
3479	X03404	Bos taurus	alpha subunit (aa 1-394)	583	89
3480	D38112	Homo sapiens	cytochrome c oxidase subunit I	514	84
3481	G03628	Homo sapiens	Human secreted protein, SEQ ID NO: 7709.	242	80
3482	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	121	61
3483	X83427	Ornithorhynchus anatinus	cytochrome c oxidase subunit I	508	78
3484	Y07754	Homo sapiens	Human secreted protein fragment	549	93

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded from gene 11.		
3485	X97567	Homo sapiens	porl	388	69
3486	X97567	Homo sapiens	porl	608	84
3487	K02401	Homo sapiens	chorionic somatomammotropin	641	93
3488	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	135	71
3489	S62941	Homo sapiens	Ps 2=basic proline-rich protein(PRB1L precursor protein=basic proline-rich proteins (Ps, PmF, PmS, and Pe) precursor) (C-terminal)	116	36
3490	S74728	Homo sapiens	antiquitin=26g turgor protein homolog	549	84
3491	L13329	Homo sapiens	iduronate-2-sulfatase	564	85
3492	X79535	Homo sapiens	beta tubulin	620	88
3493	AF081484	Homo sapiens	alpha-tubulin isoform 1	578	87
3494	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	631	89
3495	AF081484	Homo sapiens	alpha-tubulin isoform 1	616	90
3496	M12140	Homo sapiens	envelope protein	430	53
3497	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	123	70
3498	W48352	Homo sapiens	Human breast cancer related protein BCFLT1.	104	51
3499	R13556	Homo sapiens	Protein encoded downstream of hbc_M oncoprotein.	134	54
3500	Y36156	Homo sapiens	Human secreted protein #28.	143	75
3501	AF113685	Homo sapiens	PRO0974	77	81
3502	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	157	62
3503	AF090944	Homo sapiens	PRO0663	164	81
3504	AF090931	Homo sapiens	PRO0483	103	70
3505	U93570	Homo sapiens	p40	258	47
3506	AB016601	Drosophila alpina	cytochrome c oxidase subunit I	108	82
3507	AB016601	Drosophila alpina	cytochrome c oxidase subunit I	108	82
3508	AF194537	Homo sapiens	NAG13	449	78
3509	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	153	60
3510	Z70684	Caenorhabditis elegans	F28D1.8	102	37
3511	AC008113	Arabidopsis thaliana	F12A21.10	90	48
3512	M64791	Rattus norvegicus	salivary proline-rich protein	104	33
3513	AF090944	Homo sapiens	PRO0663	115	52
3514	AF240630	Mus musculus	IQ motif containing GTPase activating protein 1	152	67
3515	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	123	48
3516	AF090942	Homo sapiens	PRO0657	128	47
3517	M10546	Homo sapiens	cytochrome oxidase I	286	56
3518	AF255661	Cryptosporidium parvum	Dinap1-interacting protein 5; Dip5	108	36
3519	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	209	93
3520	M11901	Rattus norvegicus	proline-rich salivary protein	102	38
3521	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	131	64
3522	AL359782	Trypanosoma	possible (hhv-6) u1102, variant a dna,	105	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		brucei	complete virion genome.		
3523	R95913	Homo sapiens	Neural thread protein.	118	72
3524	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	59
3525	L27428	Homo sapiens	reverse transcriptase	162	50
3526	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	118	58
3527	AF090930	Homo sapiens	PRO0478	146	66
3528	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	169	50
3529	AF194537	Homo sapiens	NAG13	119	88
3530	U93564	Homo sapiens	putative p150	234	84
3531	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	208	63
3532	U12690	Homo sapiens	cytochrome oxidase subunit II	275	92
3533	AF090931	Homo sapiens	PRO0483	126	66
3534	W05278	Homo sapiens	Tumour necrosis factor-related gene product CL6.5.40.	117	85
3535	G03076	Homo sapiens	Human secreted protein, SEQ ID NO: 7157.	173	77
3536	U21123	Drosophila melanogaster	ena polypeptide	117	45
3537	AF209061	Eubranchipus sp.	cytochrome c oxidase I	127	80
3538	D38112	Homo sapiens	NADH dehydrogenase subunit 3	174	85
3539	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	118	45
3540	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	88	50
3541	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	128	71
3542	U74612	Homo sapiens	hepatocyte nuclear factor-3/fork head homolog 11A	111	77
3543	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	149	69
3544	D38112	Homo sapiens	cytochrome c oxidase subunit 1	470	80
3545	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	120	54
3546	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	106	42
3547	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	584	83
3548	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	635	95
3549	D38112	Homo sapiens	cytochrome c oxidase subunit 3	661	91
3550	D38112	Homo sapiens	cytochrome c oxidase subunit 1	607	86
3551	AK024455	Homo sapiens	FLJ00047 protein	88	51
3552	W88957	Homo sapiens	Polypeptide fragment encoded by gene 128.	500	86
3553	D38113	Pan troglodytes	NADH dehydrogenase subunit 4	228	95
3554	AF130092	Homo sapiens	PRO2620	165	93
3555	AL121845	Homo sapiens	dJ583P15.5.1 (novel protein (isoform 1))	659	91
3556	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	170	72
3557	D38112	Homo sapiens	cytochrome c oxidase subunit 3	599	88
3558	D38112	Homo sapiens	cytochrome c oxidase subunit 3	578	84
3559	AK000385	Homo sapiens	unnamed protein product	138	47
3560	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	112	61
3561	X97675	Homo sapiens	plakophilin 2b	123	65
3562	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	94	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6595.		
3563	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	198	90
3564	X86029	Vigna unguiculata	extensin-like protein	141	36
3565	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	77	60
3566	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	94
3567	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	203	93
3568	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	72
3569	S62928	Homo sapiens	PRB1M protein precursor	102	44
3570	D86853	Catharanthus roseus	extensin	123	40
3571	U93574	Homo sapiens	putative p150	279	56
3572	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	94	82
3573	U45964	Herpesvirus papio	LMP1	127	35
3574	Y08319	Homo sapiens	kinesin-2	254	55
3575	X97675	Homo sapiens	plakophilin 2b	134	54
3576	AF003151	Caenorhabditis elegans	contains similarity to an RNA recognition motif	137	43
3577	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	126	66
3578	U80447	Caenorhabditis elegans	coded for by C. elegans cDNA yk187f6.5; coded for by C. elegans cDNA yk187f6.3; coded for by C. elegans cDNA yk146f11.5	117	50
3579	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	126	31
3580	AJ249395	Globodera pallida	NADH-ubiquinone oxidoreductase subunit 4	85	33
3581	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	139	55
3582	X97675	Homo sapiens	plakophilin 2b	125	73
3583	L26953	Homo sapiens	chromosomal protein	101	55
3584	S80343	Homo sapiens	arginyl-tRNA synthetase, ArgRS	110	67
3585	X97675	Homo sapiens	plakophilin 2b	116	84
3586	X92485	Plasmodium vivax	pval	124	50
3587	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	56
3588	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	136	56
3589	U63542	Homo sapiens	FAP protein	128	75
3590	D38112	Homo sapiens	cytochrome c oxidase subunit 3	642	88
3591	D38112	Homo sapiens	NADH dehydrogenase subunit 1	612	87
3592	K02401	Homo sapiens	chorionic somatomammotropin	576	86
3593	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	108	40
3594	V00662	Homo sapiens	cytochrome oxidase I	459	76
3595	AC008262	Arabidopsis thaliana	F4N2.10	136	31
3596	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	126	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3597	AF116645	Homo sapiens	PRO1708	623	91
3598	M23028	Human herpesvirus 4	nuclear antigen precursor	121	35
3599	W88816	Homo sapiens	Polypeptide fragment encoded by gene 58.	100	33
3600	X92485	Plasmodium vivax	pval	156	36
3601	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	78
3602	AK000496	Homo sapiens	unnamed protein product	150	68
3603	AF083929	Mus musculus	ES18	98	40
3604	D38112	Homo sapiens	cytochrome c oxidase subunit 1	537	83
3605	U12690	Homo sapiens	cytochrome oxidase subunit II	548	85
3606	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	158	57
3607	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO: 250.	429	75
3608	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	122	65
3609	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	184	88
3610	D38112	Homo sapiens	NADH dehydrogenase subunit 5	224	80
3611	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	481	70
3612	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	166	92
3613	D38112	Homo sapiens	cytochrome c oxidase subunit 1	582	83
3614	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	167	91
3615	U12690	Homo sapiens	cytochrome oxidase subunit II	582	77
3616	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	101	40
3617	D38112	Homo sapiens	cytochrome c oxidase subunit I	591	85
3618	AB037275	Cynomolgus Epstein-Barr Virus TsB-B6	EBNA-1	119	42
3619	AF061944	Homo sapiens	kinase deficient protein KDP	581	91
3620	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	100	33
3621	AL049608	Arabidopsis thaliana	extensin-like protein	105	27
3622	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	69
3623	S71569	Neocallimastix patriciarum, Peptide, 860 aa	Xylanase B, XYL B [EC 3.2.1.8]	108	43
3624	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	101	37
3625	D38112	Homo sapiens	NADH dehydrogenase subunit 5	390	83
3626	D38112	Homo sapiens	cytochrome c oxidase subunit 1	582	84
3627	D38112	Homo sapiens	cytochrome c oxidase subunit 3	637	90
3628	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	169	39
3629	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	142	77
3630	U93564	Homo sapiens	putative p150	330	90
3631	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	148	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3632	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	100	80
3633	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	139	65
3634	U74071	Phascolosoma sp. 'California'	cytochrome c oxidase subunit 1	248	72
3635	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	121	87
3636	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	128	65
3637	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	63
3638	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	159	51
3639	X65582	Mus musculus	alpha-2 collagen	102	53
3640	AF090942	Homo sapiens	PRO0657	97	76
3641	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	146	69
3642	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	118	55
3643	X14576	Murine leukemia virus	gag p15 protein	134	44
3644	AF130051	Homo sapiens	PRO0898	177	48
3646	G03064	Homo sapiens	Human secreted protein, SEQ ID NO: 7145.	120	59
3647	AK000385	Homo sapiens	unnamed protein product	105	40
3648	V00662	Homo sapiens	cytochrome oxidase I	533	83
3649	AF090944	Homo sapiens	PRO0663	129	73
3650	AF090944	Homo sapiens	PRO0663	129	73
3651	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	88	60
3652	AF090930	Homo sapiens	PRO0478	92	57
3653	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	148	73
3654	AB018440	Echinococcus multilocularis	NADH dehydrogenase subunit 2	100	32
3655	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	165	68
3656	AF161356	Homo sapiens	HSPC093	106	48
3657	AF090930	Homo sapiens	PRO0478	158	85
3658	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	128	82
3659	U93574	Homo sapiens	putative p150	117	44
3660	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	149	51
3661	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	67	70
3662	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	99	62
3663	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	154	45
3664	Y27571	Homo sapiens	Human secreted protein encoded by gene No. 5.	136	77
3665	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	128	59
3666	U47855	Araneus diadematus	fibroin-3	109	39
3667	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	604	88
3668	K02401	Homo sapiens	chorionic somatomammotropin	636	93

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3669	AF083929	Mus musculus	ES18	133	46
3670	J01415	Homo sapiens	MTND4	620	87
3671	AK025047	Homo sapiens	unnamed protein product	160	60
3672	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	106	31
3673	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	766	94
3674	U74612	Homo sapiens	hepatocyte nuclear factor-3/fork head homolog 11A	113	69
3675	U80447	Caenorhabditis elegans	coded for by C. elegans cDNA yk187f6.5; coded for by C. elegans cDNA yk187f6.3; coded for by C. elegans cDNA yk146f11.5	113	39
3676	R63235	Homo sapiens	CNS neural thread protein HB4.	197	68
3677	U52077	Homo sapiens	mariner transposase	500	74
3678	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	97
3679	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	191	86
3680	AC003113	Arabidopsis thaliana	F24O1.6	102	83
3681	AF005370	Alcelaphine herpesvirus 1	putative immediate early protein	153	42
3682	G01502	Homo sapiens	Human secreted protein, SEQ ID NO: 5583.	111	62
3683	AP002543	Arabidopsis thaliana	gb AAD23015.1~gene_id:F15M7.16~similar to unknown protein	131	40
3684	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	146	64
3685	U93572	Homo sapiens	putative p150	158	43
3686	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	98	43
3687	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	106	54
3688	L26953	Homo sapiens	chromosomal protein	128	76
3689	D38112	Homo sapiens	cytochrome c oxidase subunit 1	563	87
3690	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	109	67
3691	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	122	75
3692	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	165	85
3693	M20789	Homo sapiens	alpha-1 type I collagen	141	43
3694	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	50
3695	AF210651	Homo sapiens	NAG18	124	67
3696	AF130079	Homo sapiens	PRO2852	94	53
3697	Y19192	Talpa europaea	cytochrome oxidase subunit I	618	85
3698	D38112	Homo sapiens	NADH dehydrogenase subunit 2	414	86
3699	D38112	Homo sapiens	cytochrome c oxidase subunit 1	487	76
3700	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	109	42
3701	AF217374	Acanthaster planci	cytochrome oxidase subunit 1	563	85
3702	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	106	48
3703	D38112	Homo sapiens	cytochrome c oxidase subunit 1	522	79
3704	D67066	Bos taurus	N-WASP	219	42
3705	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	100	51
3706	G03798	Homo sapiens	Human secreted protein, SEQ ID NO:	115	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7879.		
3707	Z70684	Caenorhabditis elegans	F28D1.8	105	37
3708	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	74
3709	D38112	Homo sapiens	cytochrome c oxidase subunit 1	558	88
3710	AF217374	Acanthaster planci	cytochrome oxidase subunit 1	512	85
3711	D38112	Homo sapiens	NADH dehydrogenase subunit 2	186	80
3712	AF197854	Melithreptus lunatus	cytochrome oxidase I	189	83
3713	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	95
3714	AB029027	Homo sapiens	KIAA1104 protein	141	81
3715	L26251	Trypanosoma brucei	CR5	73	31
3716	R95913	Homo sapiens	Neural thread protein.	117	44
3717	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	95	67
3718	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	108	81
3719	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	132	55
3720	M64923	Bos taurus	C10 protein	194	94
3721	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	115	75
3722	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	118	95
3723	AF302773	Homo sapiens	ninein-Lm isoform	157	57
3724	AK024455	Homo sapiens	FLJ00047 protein	134	59
3725	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	161	80
3726	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	121	52
3727	AF220264	Homo sapiens	MOST-1	86	88
3728	L27428	Homo sapiens	reverse transcriptase	316	62
3729	U83303	Homo sapiens	line-1 reverse transcriptase	112	46
3730	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	145	68
3731	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	118	56
3732	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	131	65
3733	AF090930	Homo sapiens	PRO0478	148	71
3734	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	72
3735	U93569	Homo sapiens	putative p150	270	59
3736	U93568	Homo sapiens	putative p150	151	38
3737	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	124	82
3738	X92485	Plasmodium vivax	pva1	101	44
3739	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	146	51
3740	AF090944	Homo sapiens	PRO0663	124	56
3741	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	94	47
3742	AF118086	Homo sapiens	PRO1992	124	61
3743	AF083929	Mus musculus	ES18	108	35
3744	L34685	Arabidopsis	cell wall protein	120	34

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		thaliana			
3745	AF090931	Homo sapiens	PRO0483	117	54
3746	AF090930	Homo sapiens	PRO0478	136	75
3747	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	154	59
3748	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	92	44
3749	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	98	42
3750	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	165	73
3751	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	87
3752	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	58
3753	U93574	Homo sapiens	putative p150	157	60
3754	X56015	Citridia oncopelti	NADH dehydrogenase subunit 5	103	30
3755	M80613	Homo sapiens	putative	114	26
3756	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	119	54
3757	D38112	Homo sapiens	NADH dehydrogenase subunit 2	210	89
3758	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	91	58
3759	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	110	46
3760	M13100	Rattus norvegicus	unknown protein	119	46
3761	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	135	52
3762	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	84
3763	M11900	Mus musculus	15-kDa proline-rich salivary protein	125	40
3764	U63542	Homo sapiens	FAP protein	131	72
3765	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	143	76
3766	X92485	Plasmodium vivax	pva1	119	54
3767	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	81	56
3768	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	98	65
3769	AB005216	Homo sapiens	Nck, Ash and phospholipase C gamma-binding protein NAP4	487	90
3770	AF026211	Caenorhabditis elegans	Similar to cuticular collagen	102	37
3771	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	91	55
3772	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	128	76
3773	AK024455	Homo sapiens	FLJ00047 protein	138	66
3774	AF090895	Homo sapiens	PRO0117	152	60
3775	AF130051	Homo sapiens	PRO0898	122	78
3776	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	100	63
3777	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	187	75
3778	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	130	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3779	X55685	Lycopersicon esculentum	extensin (class I)	132	38
3780	L27428	Homo sapiens	reverse transcriptase	116	53
3781	Y71066	Homo sapiens	Human membrane transport protein, MTRP-11.	188	86
3782	AL390114	Leishmania major	extremely cysteine/valine rich protein	122	67
3783	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	462	75
3784	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	127	67
3785	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	129	36
3786	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	152	78
3787	S80119	Rattus sp.	reverse transcriptase homolog	143	40
3788	AF090942	Homo sapiens	PRO0657	134	67
3789	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	63
3790	AF116661	Homo sapiens	PRO1438	128	45
3791	K03205	Homo sapiens	salivary proline-rich protein precursor	130	38
3792	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	127	74
3793	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	101	48
3794	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	175	46
3795	K03205	Homo sapiens	salivary proline-rich protein precursor	117	40
3796	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	185	88
3797	D38112	Homo sapiens	cytochrome c oxidase subunit 3	610	84
3798	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	156	56
3799	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	71	52
3800	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	127	77
3801	AF130079	Homo sapiens	PRO2852	164	54
3802	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	118	45
3803	U42580	Paramecium bursaria Chlorella virus 1	Pro-rich, PAPK (20X); similar to Arabidopsis anter-specific Pro-rich protein, corresponds to Swiss-Prot Accession Number P40602	101	36
3804	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	173	87
3805	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	126	72
3806	D38112	Homo sapiens	NADH dehydrogenase subunit 4	225	85
3807	U88587	Nicotiana glauca	120 kDa style glycoprotein	118	38
3808	D38112	Homo sapiens	cytochrome c oxidase subunit 1	129	82
3809	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	67
3810	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	213	97
3811	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	106	63
3812	AF169974	Homo sapiens	serine racemase	153	56
3813	L27428	Homo sapiens	reverse transcriptase	175	43
3814	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	109	43

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3815	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	176	78
3816	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	112	65
3817	AF119901	Homo sapiens	PRO2831	113	55
3818	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	99	89
3819	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	91	66
3820	X92485	Plasmodium vivax	pval	108	46
3821	AK024455	Homo sapiens	FLJ00047 protein	79	59
3822	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	178	87
3823	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	99	50
3824	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	86	94
3825	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	138	53
3826	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	88
3827	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	77	61
3828	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	139	51
3829	K03208	Homo sapiens	salivary proline-rich protein precursor	161	41
3830	U44838	Glycine max	extensin	108	47
3831	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	136	71
3832	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	205	84
3833	AL163912	Arabidopsis thaliana	glycine-rich protein atGRP-7	117	37
3834	AF130089	Homo sapiens	PRO2550	138	45
3835	G02552	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	92	76
3836	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	70
3837	X56010	Sorghum bicolor	hydroxyproline-rich glycoprotein	98	37
3838	X68249	Xenopus laevis	Proline rich protein	92	66
3839	U12690	Homo sapiens	cytochrome oxidase subunit II	262	92
3840	R63235	Homo sapiens	CNS neural thread protein HB4.	186	100
3841	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	103	64
3842	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	116	62
3843	AF164614	Homo sapiens	envelope protein	508	77
3844	AF130051	Homo sapiens	PRO0898	130	73
3845	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	144	74
3846	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	119	68
3847	M13100	Rattus norvegicus	unknown protein	129	46
3848	X97675	Homo sapiens	plakophilin 2b	145	67
3849	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	65
3850	K03206	Homo sapiens	salivary proline-rich protein precursor	114	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3851	U93574	Homo sapiens	putative p150	165	82
3852	AF090931	Homo sapiens	PRO0483	97	78
3853	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	279	80
3854	U93570	Homo sapiens	putative p150	135	38
3855	M13100	Rattus norvegicus	unknown protein	100	57
3856	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	166	63
3857	Y48576	Homo sapiens	Human breast tumour-associated protein 37.	117	49
3858	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	147	45
3859	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	150	71
3860	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	165	69
3861	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	131	83
3862	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	171	81
3863	AK000241	Homo sapiens	unnamed protein product	100	48
3864	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	121	80
3865	AK024455	Homo sapiens	FLJ00047 protein	124	69
3866	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	87	64
3867	AF116712	Homo sapiens	PRO2738	92	48
3868	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	165	62
3869	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	128	62
3870	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	94	75
3871	AK024455	Homo sapiens	FLJ00047 protein	83	72
3872	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	147	44
3873	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	113	51
3874	AF090930	Homo sapiens	PRO0478	120	63
3875	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	145	70
3876	D88674	Homo sapiens	antizyme inhibitor	147	75
3877	AF263744	Homo sapiens	erbB2-interacting protein ERBIN	212	37
3878	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	140	82
3879	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	82	35
3880	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	144	60
3881	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	122	60
3882	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	134	75
3883	M81321	Macaca fascicularis	proline-rich protein	101	41
3884	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	109	56
3885	AF013214	Bos taurus	acidic ribosomal phosphoprotein PO	177	94
3886	G00403	Homo sapiens	Human secreted protein, SEQ ID NO:	162	77

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4484.		
3887	Y59860	Homo sapiens	Human normal uterus tissue derived protein 23.	137	72
3888	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	147	72
3889	M64792	Rattus norvegicus	salivary proline-rich protein	104	40
3890	AF156228	Drosophila melanogaster	salivary gland secretion protein	104	35
3891	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	90	47
3892	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	138	38
3893	D38112	Homo sapiens	NADH dehydrogenase subunit 5	146	65
3894	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	34
3895	X02873	Daucus carota	put. precursor	104	48
3896	AF090942	Homo sapiens	PRO0657	135	50
3897	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	77
3898	X92485	Plasmodium vivax	pval	111	62
3899	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	107	70
3900	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	94	93
3901	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	163	83
3902	AF090942	Homo sapiens	PRO0657	134	65
3903	AF220264	Homo sapiens	MOST-1	74	59
3904	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	131	53
3905	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	129	85
3906	AK025047	Homo sapiens	unnamed protein product	127	73
3907	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	135	86
3908	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	134	72
3909	X77816	Rattus norvegicus	PR-Vbeta1	104	62
3910	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	114	70
3911	AK024455	Homo sapiens	FLJ00047 protein	135	61
3912	U93567	Homo sapiens	putative p150	233	63
3913	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	96	40
3914	X94976	Brassica napus	cell wall-plasma membrane linker protein	104	36
3915	P92219	Homo sapiens (human)	CRI protein.	125	73
3916	X92485	Plasmodium vivax	pval	94	64
3917	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	105	52
3918	AF118086	Homo sapiens	PRO1992	130	87
3919	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	125	80
3920	G00412	Homo sapiens	Human secreted protein, SEQ ID NO:	162	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4493.		
3921	AF090930	Homo sapiens	PRO0478	128	64
3922	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	75
3923	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	130	65
3924	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	134	71
3925	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	102	58
3926	D63487	Homo sapiens	The KIAA0153 gene product is related to a putative C.elegans gene encoded in cosmid F42A8.	141	100
3927	U21123	Drosophila melanogaster	ena polypeptide	117	37
3928	X58438	Mus musculus	proline rich protein	136	36
3929	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	152	71
3930	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	132	73
3931	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	86	48
3932	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	110	65
3933	X92485	Plasmodium vivax	pval	116	36
3934	X97675	Homo sapiens	plakophilin 2b	129	82
3935	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	84	58
3937	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	107	56
3938	AF090895	Homo sapiens	PRO0117	166	68
3939	K02550	Oncorhynchus mykiss	70-kilodalton heat shock protein	104	38
3940	AK024455	Homo sapiens	FLJ00047 protein	112	74
3941	L26953	Homo sapiens	chromosomal protein	92	67
3942	U63542	Homo sapiens	FAP protein	135	75
3943	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	139	80
3944	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	141	67
3945	AK024455	Homo sapiens	FLJ00047 protein	123	76
3946	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	92	52
3947	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	103	56
3948	AF252293	Homo sapiens	PAR3	161	44
3949	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	125	47
3950	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	59
3951	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	174	87
3952	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	152	75
3953	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	168	64
3954	R95913	Homo sapiens	Neural thread protein.	110	54
3955	AF130089	Homo sapiens	PRO2550	122	63
3956	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3957	Y36203	Homo sapiens	Human secreted protein #75.	121	75
3958	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	177	61
3959	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	131	69
3960	U93563	Homo sapiens	putative p150	227	62
3961	D86853	Catharanthus roseus	extensin	100	40
3962	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	101	41
3963	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	107	80
3964	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	121	42
3965	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	66
3966	M11901	Rattus norvegicus	proline-rich salivary protein	101	34
3967	AF229126	Homo sapiens	acetylcholinesterase collagen-like tail subunit isoform VII	108	36
3968	AJ006770	Cicer arietinum	extensin	86	29
3969	AF130089	Homo sapiens	PRO2550	128	82
3970	U93563	Homo sapiens	putative p150	99	48
3971	AK000496	Homo sapiens	unnamed protein product	134	71
3972	Z70684	Caenorhabditis elegans	F28D1.8	108	42
3973	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	137	72
3974	AK024455	Homo sapiens	FLJ00047 protein	132	65
3975	AK024455	Homo sapiens	FLJ00047 protein	128	85
3976	X01918	Drosophila melanogaster	salivary gland glue protein	99	40
3977	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	136	46
3978	AF229067	Homo sapiens	PADI-H protein.	107	87
3979	M64793	Rattus norvegicus	salivary proline-rich protein	189	48
3980	S80119	Rattus sp.	reverse transcriptase homolog	134	49
3981	AF090901	Homo sapiens	PRO0195	106	94
3982	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	111	42
3983	X92485	Plasmodium vivax	pva1	102	39
3984	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	127	64
3985	AB012162	Homo sapiens	APCL protein	190	42
3986	AF016099	Mus musculus	endonuclease/reverse transcriptase	139	65
3987	U93570	Homo sapiens	putative p150	170	71
3988	D38112	Homo sapiens	NADH dehydrogenase subunit 5	202	73
3989	D38112	Homo sapiens	NADH dehydrogenase subunit 5	244	85
3990	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	420	92
3991	D38112	Homo sapiens	NADH dehydrogenase subunit 4	272	85
3992	L38908	Nicotiana tabacum	extensin	114	40
3993	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	64
3994	AF090944	Homo sapiens	PRO0663	99	39
3995	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	150	75
3996	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	574	87
3997	D38112	Homo sapiens	NADH dehydrogenase subunit 4	488	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3998	U52077	Homo sapiens	mariner transposase	475	70
3999	U93570	Homo sapiens	p40	111	34
4000	U15647	Mus musculus	reverse transcriptase	137	43
4001	AF116712	Homo sapiens	PRO2738	105	52
4002	AF113685	Homo sapiens	PRO0974	125	53
4003	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	78
4004	AF116715	Homo sapiens	PRO2829	115	73
4005	D38112	Homo sapiens	NADH dehydrogenase subunit 2	288	80
4006	D38112	Homo sapiens	cytochrome c oxidase subunit 1	614	86
4007	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	106	45
4008	U90268	Homo sapiens	Krit1	152	52
4009	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	472	96
4010	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	304	100
4011	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	472	98
4012	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	102	50
4013	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	124	73
4014	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	118	47
4015	U12690	Homo sapiens	cytochrome oxidase subunit II	522	81
4016	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	147	52
4017	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	57
4018	AB003476	Homo sapiens	gravin	549	91
4019	D38112	Homo sapiens	NADH dehydrogenase subunit 4	391	93
4020	U44949	Xenopus laevis	zona pellucida A glycoprotein homolog	143	32
4021	D38113	Pan troglodytes	cytochrome c oxidase subunit I	571	88
4022	D38113	Pan troglodytes	cytochrome c oxidase subunit I	554	87
4023	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	165	88
4024	AL390114	Leishmania major	extremely cysteine/valine rich protein	131	38
4025	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	583	86
4026	AF090895	Homo sapiens	PRO0117	104	49
4027	AF130056	Homo sapiens	PRO1367	80	60
4028	X97675	Homo sapiens	plakophilin 2b	157	83
4029	X67337	Homo sapiens	Human pre-mRNA cleavage factor I 68 kDa subunit	114	35
4030	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	110	74
4031	D38112	Homo sapiens	ATPase subunit 6	395	80
4032	S70718	Hemicentrotus pulcherrimus=sea urchins, tests, Peptide, 632 aa	fibrillar collagen alpha 120 and 140 chains	104	33
4033	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	355	66
4034	AC004497	Homo sapiens	MX2	464	58
4035	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	151	61
4036	AF117888	Homo sapiens	myosin-Ixa	113	34
4038	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	100	48
4039	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	153	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4040	D38112	Homo sapiens	NADH dehydrogenase subunit 4	338	86
4041	AF116661	Homo sapiens	PRO1438	136	53
4042	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	120	84
4043	D38112	Homo sapiens	cytochrome c oxidase subunit 3	493	85
4044	M90516	Homo sapiens	glutamine:fructose-6-phosphate amidotransferase	261	72
4045	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	102	64
4046	AF130089	Homo sapiens	PRO2550	143	78
4047	AF090942	Homo sapiens	PRO0657	119	41
4048	R95913	Homo sapiens	Neural thread protein.	138	47
4049	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	111	59
4050	X77962	Tetrahymena thermophila	fibrillarin	105	49
4051	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	144	71
4052	X02794	Friend murine leukemia virus	Pr65	107	37
4053	Y00994	Homo sapiens	Human CSR3 protein sequence.	109	38
4054	AL121585	Homo sapiens	ba504H3.1 (SNX5 (sorting nexin 5))	299	74
4055	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	314	80
4056	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	65	54
4057	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	67
4058	AF205385	Pan troglodytes	NADH dehydrogenase subunit 5	202	89
4059	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	100
4060	U63542	Homo sapiens	FAP protein	142	73
4061	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	158	50
4062	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	123	44
4063	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	76	65
4064	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	165	46
4065	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	147	93
4066	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	76
4067	AB035523	Gallus gallus	avenaIII	101	48
4068	AC079829	Arabidopsis thaliana	Pto kinase interactor, putative	105	43
4069	AF210651	Homo sapiens	NAG18	97	77
4070	M64793	Rattus norvegicus	salivary proline-rich protein	111	43
4071	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	158	65
4072	K02576	Homo sapiens	salivary proline-rich protein 1	131	43
4073	AF038007	Homo sapiens	FIC1	153	96
4074	M33228	Trypanosoma brucei	ATPase 6	103	37
4075	U54788	Mus musculus	Wiskott-Aldrich Syndrome Protein	119	46
4076	M81321	Macaca fascicularis	proline-rich protein	104	36
4077	X52235	Homo sapiens	ORFII	192	39
4078	G00328	Homo sapiens	Human secreted protein, SEQ ID NO:	126	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4409.		
4079	AB026542	Homo sapiens	WASP-family protein	98	41
4080	L17318	Rattus norvegicus	proline-rich proteoglycan	105	42
4081	AF130051	Homo sapiens	PRO0898	117	42
4082	AF130089	Homo sapiens	PRO2550	85	79
4083	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	117	48
4084	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	89	40
4085	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	163	80
4086	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	144	74
4087	AF085691	Homo sapiens	multidrug resistance-associated protein 3A	197	49
4088	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	109	62
4089	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	139	51
4090	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	103	65
4091	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	159	68
4092	X92485	Plasmodium vivax	pva1	95	38
4093	U93569	Homo sapiens	p40	205	40
4094	L16864	African swine fever virus	cd2 homologue	98	45
4095	X71413	Homo sapiens	ELE1	675	98
4096	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	149	60
4097	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	116	70
4098	AF090930	Homo sapiens	PRO0478	149	78
4099	AF090942	Homo sapiens	PRO0657	124	56
4100	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	139	62
4101	L26953	Homo sapiens	chromosomal protein	104	54
4102	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	128	70
4103	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	94	58
4104	U73199	Mus musculus	Rho-guanine nucleotide exchange factor	370	56
4105	AF090931	Homo sapiens	PRO0483	104	90
4106	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	133	72
4107	AF118082	Homo sapiens	PRO1902	145	49
4108	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	116	50
4109	U93564	Homo sapiens	p40	539	91
4110	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	144	54
4111	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	138	65
4112	AF217536	Homo sapiens	truncated mevalonate kinase	91	73
4113	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	120	36
4114	M17522	Paracoccus	cytochrome c1 precursor (EC 1.10.2.2)	101	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		denitrificans			
4115	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	121	59
4116	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	148	73
4117	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	80	85
4118	X04758	Homo sapiens	pro- alpha (V)collagen (AA 1099)	106	39
4119	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	122	47
4120	AF130089	Homo sapiens	PRO2550	132	68
4121	AF090942	Homo sapiens	PRO0657	136	48
4122	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	115	66
4123	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	72	48
4124	X92485	Plasmodium vivax	pva1	104	54
4125	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	59
4126	AK024455	Homo sapiens	FLJ00047 protein	86	61
4127	AF119855	Homo sapiens	PRO1847	99	68
4128	S80119	Rattus sp.	reverse transcriptase homolog	129	39
4129	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	156	62
4130	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	135	72
4131	R86406	Homo sapiens	Human matrix metalloproteinase MMPm1a.	108	83
4132	L16461	Chlamydomonas reinhardtii	structural wali protein	87	37
4133	Y30713	Homo sapiens	Amino acid sequence of a human secreted protein.	232	95
4134	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	121	69
4135	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	135	70
4136	K02576	Homo sapiens	salivary proline-rich protein 1	134	42
4137	Y15173	Human papillomavirus type 75	E4 protein	101	38
4138	AF130089	Homo sapiens	PRO2550	130	35
4139	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	38
4140	Y36203	Homo sapiens	Human secreted protein #75.	120	48
4141	AF130089	Homo sapiens	PRO2550	139	36
4142	S80119	Rattus sp.	reverse transcriptase homolog	170	47
4143	U54636	Staphylococcus aureus	protein A	135	35
4144	AL390114	Leishmania major	extremely cysteine/valine rich protein	157	55
4145	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	112	54
4146	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	117	37
4147	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	98	61
4148	AF130051	Homo sapiens	PRO0898	124	88
4149	G00673	Homo sapiens	Human secreted protein, SEQ ID NO:	133	67

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4754.		
4150	Z29481	Homo sapiens	3-hydroxyanthranilic acid dioxygenase	244	62
4151	M81321	Macaca fascicularis	proline-rich protein	172	50
4152	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	129	66
4153	AF119851	Homo sapiens	PRO1722	128	62
4154	AB037826	Homo sapiens	KIAA1405 protein	194	60
4155	M12099	Mus musculus	proline-rich protein	124	37
4156	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	46
4157	M11901	Rattus norvegicus	proline-rich salivary protein	124	41
4158	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	134	83
4159	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	141	74
4160	M76546	Helianthus annuus	hydroxyproline-rich protein	135	39
4161	U35730	Mus musculus	jerky	116	31
4162	Z81525	Caenorhabditis elegans	contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=35.5, E-value=4e-07, N=2	130	50
4163	AF113685	Homo sapiens	PRO0974	129	45
4164	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	168	71
4165	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	137	70
4166	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	175	72
4167	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	86	45
4168	AB000505	Daucus carota	unnamed protein product	101	43
4169	U87607	Rattus norvegicus	putative RNA binding protein 1	113	30
4170	AF119900	Homo sapiens	PRO2822	154	59
4171	AE001381	Plasmodium falciparum	hypothetical protein	106	33
4172	AE000034	Mycoplasma pneumoniae	bifunctional threonine dehydrogenase; galactosyltransferase	100	28
4173	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	100	47
4174	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	142	68
4175	AK024455	Homo sapiens	FLJ00047 protein	116	60
4176	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	94	44
4177	AK024455	Homo sapiens	FLJ00047 protein	102	59
4178	AY007557	Mycobacterium avium subsp. paratuberculosis	fibronectin-attachment protein FAP-P	98	42
4179	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	115	69
4180	M12100	Mus musculus	proline-rich protein MP-3	132	44
4181	AF090930	Homo sapiens	PRO0478	138	63
4182	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	152	75
4183	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4184	K03205	Homo sapiens	salivary proline-rich protein precursor	150	43
4185	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	128	51
4186	AF090944	Homo sapiens	PRO0663	124	49
4187	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	93	62
4188	D38112	Homo sapiens	ATPase subunit 6	439	78
4189	AF130051	Homo sapiens	PRO0898	89	57
4190	AF090930	Homo sapiens	PRO0478	137	83
4191	K03205	Homo sapiens	salivary proline-rich protein precursor	100	35
4192	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	212	91
4193	Y13247	Homo sapiens	FB19 protein	142	46
4194	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	268	93
4195	AF124729	Mus musculus	acinusS	140	42
4196	AJ277425	Globodera pallida	putative cuticular collagen	156	43
4197	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	77
4198	Z70684	Caenorhabditis elegans	F28D1.8	97	45
4199	M64793	Rattus norvegicus	salivary proline-rich protein	119	36
4200	X62379	Mus musculus	formin, isoform IV	115	48
4201	D38113	Pan troglodytes	NADH dehydrogenase subunit 4	224	93
4202	M14820	Trypanosoma brucei	ORF2 bases 1807-2850; first start codon at 2032; putative	103	29
4203	U93572	Homo sapiens	p40	182	34
4204	D82026	Silene latifolia	glycine-rich protein	98	49
4205	AF003151	Caenorhabditis elegans	contains similarity to an RNA recognition motif	107	40
4206	L07545	Leishmania tarentolae	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression	101	35
4207	K03205	Homo sapiens	salivary proline-rich protein precursor	104	38
4208	AF229126	Homo sapiens	acetylcholinesterase collagen-like tail subunit isoform VII	96	75
4209	AF090895	Homo sapiens	PRO0117	142	68
4210	X92485	Plasmodium vivax	pva1	104	35
4211	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	173	73
4212	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	151	69
4213	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	122	43
4214	AF090944	Homo sapiens	PRO0663	97	39
4215	X12544	Homo sapiens	3 HLA-DR B protein precursor (AA - 29 to 267)	111	60
4216	M69065	human herpesvirus 2	ORF1	89	38
4217	AF090895	Homo sapiens	PRO0117	133	78
4218	B01372	Homo sapiens	Neuron-associated protein.	135	46
4219	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	71	47
4220	U93567	Homo sapiens	p40	170	35
4221	D00570	Mus musculus	open reading frame (251 AA)	108	28
4222	X97675	Homo sapiens	plakophilin 2b	122	47
4223	AF270937	Plutella xylostella	PxORF73 peptide	99	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		granulovirus			
4224	AF130089	Homo sapiens	PRO2550	144	69
4225	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	125	82
4226	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	99	62
4227	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	172	59
4228	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	161	74
4229	AL049537	Homo sapiens	dJ1164110.1 (brefeldin A-inhibited guanine nucleotide-exchange protein 2)	212	90
4230	AF118086	Homo sapiens	PRO1992	150	69
4231	M81321	Macaca fascicularis	proline-rich protein	130	41
4232	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	138	68
4233	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	132	56
4234	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	110	52
4235	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	124	32
4236	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	119	42
4237	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	368	56
4238	R95913	Homo sapiens	Neural thread protein.	139	55
4239	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	146	63
4240	X97675	Homo sapiens	plakophilin 2b	108	78
4241	Y36156	Homo sapiens	Human secreted protein #28.	137	65
4242	AK000385	Homo sapiens	unnamed protein product	131	33
4243	AJ252253	human herpesvirus 2	glycoprotein G-2	107	36
4244	Y99447	Homo sapiens	Human PRO1556 (UNQ764) amino acid sequence SEQ ID NO:372.	597	100
4245	Y05398	Homo sapiens	Human TIE ligand NL8 protein sequence.	424	84
4246	L00016	Homo sapiens	urf4	222	90
4247	AF134579	Zea mays	arabinogalactan protein	134	39
4248	Z34465	Zea mays	extensin-like protein	123	33
4249	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	128	62
4250	J02695	Plasmodium yoelii	circumsporozoite protein	110	33
4251	AK024455	Homo sapiens	FLJ00047 protein	136	65
4252	U02570	Homo sapiens	CDC42 GTPase-activating protein	566	93
4253	D38112	Homo sapiens	cytochrome c oxidase subunit 1	449	85
4254	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	111	63
4255	M61143	Bovine herpesvirus 1	latency-related open reading frame 2; putative	101	42
4256	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	43
4257	Y06294	Homo sapiens	Human transcription regulator MOP6 partial sequence.	410	79
4258	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	112	61
4259	D90252	Human papillomavirus type 5b	E4 protein	110	32

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4260	X90569	Homo sapiens	elastic titin	660	95
4261	AF090930	Homo sapiens	PRO0478	114	71
4262	AF132209	Homo sapiens	prepro-major basic protein homolog	422	72
4263	AF043102	Pneumocystis carinii	surface glycoprotein A	121	29
4264	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	132	55
4265	AF090895	Homo sapiens	PRO0117	159	62
4266	AF090930	Homo sapiens	PRO0478	143	50
4267	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	119	34
4268	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	106	61
4269	D23660	Homo sapiens	ribosomal protein	493	73
4270	AF130089	Homo sapiens	PRO2550	119	39
4271	U93564	Homo sapiens	putative p150	121	37
4272	AB033615	Mus musculus	phospholipase C-L2	485	79
4273	AF006082	Homo sapiens	Arp2	488	85
4274	Y12293	Mus musculus	lun	104	33
4275	X54289	Bos taurus	cGMP-dependent protein kinase (isoform I beta)	561	81
4276	AF119855	Homo sapiens	PRO1847	155	71
4277	J01415	Homo sapiens	MTND4	372	63
4278	AB021078	Plasmid Colb-p9	ybbA	101	30
4279	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	110	73
4280	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	110	73
4281	AF119851	Homo sapiens	PRO1722	110	60
4282	D38116	Pan paniscus	NADH dehydrogenase subunit I	346	92
4283	Y15908	Homo sapiens	DIA-12C protein	109	52
4284	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	122	76
4285	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	121	42
4286	AK024455	Homo sapiens	FLJ00047 protein	135	57
4287	Y11525	Homo sapiens	CCAAT/enhancer binding protein alpha	100	32
4288	AF033122	Homo sapiens	non-p53 regulated PA26-T1 nuclear protein	128	81
4289	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	111	39
4290	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	140	58
4291	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	132	34
4292	X60432	Zea mays	prolin rich protein	118	42
4293	U09367	Homo sapiens	zinc finger protein ZNF136	461	60
4294	AF038960	Homo sapiens	SKD1 homolog	146	82
4295	AL390114	Leishmania major	extremely cysteine/valine rich protein	128	54
4296	U66561	Homo sapiens	kruppel-related zinc finger protein	512	89
4297	AF043706	Caenorhabditis elegans	contains similarity to granulins	104	55
4298	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	65
4299	AF152510	Homo sapiens	protocadherin gamma A3 short form protein	520	87

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4300	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	142	72
4301	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	109	50
4302	AL035440	Arabidopsis thaliana	putative protein	103	31
4303	L05500	Homo sapiens	adenylyl cyclase	655	96
4304	AF116712	Homo sapiens	PRO2738	140	54
4305	D13757	Homo sapiens	amidophosphoribosyltransferase	182	92
4306	L20450	Mus musculus	DNA-binding protein	470	64
4307	AF213386	Mus musculus	ATP-binding cassette protein	175	97
4308	X76850	Mus musculus	MAP kinase-activated protein kinase 2	154	69
4309	S80119	Rattus sp.	reverse transcriptase homolog	123	55
4310	X67337	Homo sapiens	Human pre-mRNA cleavage factor 1 68 kDa subunit	110	32
4311	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	58
4312	Z46236	Ovis aries	keratinocyte growth factor	210	75
4313	AB020700	Homo sapiens	KIAA0893 protein	569	87
4314	AF124727	Homo sapiens	acinusS	498	88
4315	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	88	32
4316	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	122	53
4317	AF119900	Homo sapiens	PRO2822	135	58
4318	U74612	Homo sapiens	hepatocyte nuclear factor-3/fork head homolog 11A	104	70
4319	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	117	51
4320	AB026054	Homo sapiens	brain finger protein	412	90
4321	AF090944	Homo sapiens	PRO0663	133	71
4322	AF165513	Homo sapiens	vacuolar protein sorting 45 isoform	712	97
4323	Y99418	Homo sapiens	Human PRO1317 (UNQ783) amino acid sequence SEQ ID NO:277.	532	97
4324	AF163772	Leishmania major	7138.7	142	37
4325	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	128	59
4326	W40054	Homo sapiens	P300/CBP-associated transcriptional cofactor P/CAF C-terminus.	175	94
4327	AF217411	Homo sapiens	neuroligin 3 isoform HNL3	549	84
4328	U94836	Homo sapiens	ERPROT 213-21	175	87
4329	Y20763	Homo sapiens	Human neurofilament-M mutant protein fragment 45.	501	87
4330	AB037745	Homo sapiens	KIAA1324 protein	1014	99
4331	M91563	Rattus norvegicus	NMDA receptor subtype 2C	116	39
4332	G03704	Homo sapiens	Human secreted protein, SEQ ID NO: 7785.	286	76
4333	AC006841	Arabidopsis thaliana	Mutator-like transposase	130	70
4334	AP000373	Arabidopsis thaliana	jasmonate inducible protein; myrosinase binding protein-like	130	53
4335	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	377	90
4336	AJ277426	Globodera pallida	putative cuticular collagen	112	37

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4337	U16802	Rattus norvegicus	Ca2+-dependent activator protein; calcium-dependent actin-binding protein	560	79
4338	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	118	56
4339	AB024520	Homo sapiens	notch4	93	33
4340	AF128406	Homo sapiens	nuclear prelamin A recognition factor	241	100
4341	W19771	Homo sapiens	Beta-1 integrin modulator B171.	169	100
4342	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2 Antigen)	666	88
4343	D50312	Homo sapiens	uKATP-1	542	80
4344	U84487	Homo sapiens	CX3C chemokine precursor	371	78
4345	U93569	Homo sapiens	putative p150	111	47
4346	AL161755	Streptomyces coelicolor A3(2)	putative serine/threonine protein kinase	102	30
4347	AK026162	Homo sapiens	unnamed protein product	377	98
4348	AF221759	Homo sapiens	Mam1	314	47
4349	AF165926	Homo sapiens	NUPI55	147	84
4351	U50185	Rattus norvegicus	PP-1M	144	52
4352	D50455	Rattus norvegicus	phospholipase C delta4	196	70
4353	X54131	Homo sapiens	protein-tyrosine phosphatase	261	87
4354	AF151850	Homo sapiens	CGI-92 protein	255	92
4355	G03996	Homo sapiens	Human secreted protein, SEQ ID NO: 8077.	105	95
4356	U93564	Homo sapiens	putative p150	171	72
4357	AP001507	Bacillus halodurans	unknown conserved protein	159	34
4358	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	153	60
4359	AF072697	Mus musculus	SHYC	177	97
4360	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	69
4361	M98776	Homo sapiens	keratin 1	449	77
4362	AK024436	Homo sapiens	FLJ00026 protein	671	91
4363	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	155	49
4364	D13896	Rattus norvegicus	cytoplasmic dynein heavy chain	327	92
4365	X79389	Homo sapiens	glutathione transferase T1	164	96
4366	AB006458	Mus musculus	alpha-D-mannosidase	177	56
4367	X01060	Homo sapiens	put. transferrin receptor (aa 1-760)	160	96
4368	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	103	54
4369	AL353715	Homo sapiens	bK3184A7.3.1 (helicase-like protein NHL)	485	100
4370	AF001631	Oryctolagus cuniculus	glucose-regulated protein GRP94	118	92
4371	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	113	80
4372	AL121741	Schizosaccharomyces pombe	putative negative regulator of vesicle formation	200	41
4373	M96982	Homo sapiens	U2 snRNP auxiliary factor small subunit	279	70
4374	U47741	Homo sapiens	CREB-binding protein	123	96
4375	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	127	75
4376	Y12781	Homo sapiens	transducin (beta) like 1 protein	1056	90

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4377	W69424	Homo sapiens	Human secreted protein bg140 1.	183	97
4378	AL096700	Homo sapiens	d1499B10.2 (phosphorylase kinase, alpha 2 (liver) (PYK))	639	86
4379	AF177390	Manduca sexta	antennal specific membrane protein AMP	378	51
4380	X97675	Homo sapiens	plakophilin 2b	156	75
4381	R33713	Homo sapiens	Pg1101.	104	100
4382	AB015473	Arabidopsis thaliana	gene_id:MCM23.1~unknown protein	113	61
4383	AF116715	Homo sapiens	PRO2829	133	50
4384	AL357472	Homo sapiens	VPS33B	676	99
4385	AF090931	Homo sapiens	PRO0483	155	58
4386	U92645	Gecarcinus lateralis	alpha-1-tubulin	511	75
4387	Y36095	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 480.	202	90
4388	M64923	Bos taurus	C10 protein	218	95
4389	X98264	Homo sapiens	M-phase phosphoprotein 4	197	100
4390	AK000264	Homo sapiens	unnamed protein product	239	73
4391	M12937	Homo sapiens	ferritin heavy subunit	662	84
4392	P92219	Homo sapiens (human)	CR1 protein.	116	80
4393	X16135	Homo sapiens	L protein (AA 1-558)	759	99
4394	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	148	58
4395	AC005591	Homo sapiens	PkB-like	170	97
4396	AF161426	Homo sapiens	HSPC308	313	77
4397	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	146	61
4398	AF104921	Homo sapiens	succinyl-CoA synthetase alpha subunit	679	88
4399	AF257330	Homo sapiens	COBW-like protein	586	90
4400	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	116	65
4401	AF119851	Homo sapiens	PRO1722	101	79
4402	M55542	Homo sapiens	guanylate binding protein isoform I	230	76
4403	Y07752	Voivox carteri	pherophorin-S	459	88
4404	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	113	44
4405	U07786	Sus scrofa	beta actin	519	90
4406	A06977	Homo sapiens	albumin	586	88
4407	L20755	Cuscuta reflexa	hybrid proline-rich protein;cytokinin-induced;haustoria	112	41
4408	AB002299	Homo sapiens	KIAA0301	612	98
4409	AB001424	Mus musculus	KIF17	104	47
4410	M88108	Homo sapiens	p62	574	92
4411	AL121673	Homo sapiens	bA305P22.2 (novel protein)	415	71
4412	AF064553	Mus musculus	NSD1 protein	224	64
4413	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	107	36
4414	A06977	Homo sapiens	albumin	505	82
4415	A06977	Homo sapiens	albumin	596	90
4416	Y87116	Homo sapiens	Human secreted protein sequence SEQ ID NO:155.	123	50
4417	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	103	85
4418	G03053	Homo sapiens	Human secreted protein, SEQ ID NO: 7134.	100	54
4419	AF049606	Mus musculus	transcription factor NF-ATc isoform b	114	90

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4420	Z11190_cdl	Homo sapiens	11-DEC-1998 Interleukin-3 coding sequence from b2HFLS20W cDNA library.	354	97
4421	W64469	Homo sapiens	Human secreted protein from clone CW795 2.	203	100
4422	M12523	Homo sapiens	albumin Venezia	350	94
4423	AF130077	Homo sapiens	PRO2619	561	89
4424	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	161	64
4425	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	393	91
4426	A09561	synthetic construct	human serum albumin	651	96
4427	AL133215	Homo sapiens	bA108L7.5 (novel protein similar to Plasmodium POM1 and C. elegans F46G11.1 (Tr:Q20485))	392	100
4428	W33663	Homo sapiens	Human puromycin-sensitive aminopeptidase (PSA)-68.	172	96
4429	AB021654	Homo sapiens	DD2/bile acid-binding protein/AKR1C2/3alpha-hydroxysteroid dehydrogenase type 3	184	81
4430	W63683	Homo sapiens	Human secreted protein 3.	114	42
4431	AY008763	Homo sapiens	sentrin/SUMO-specific protease	447	96
4432	U52965	Homo sapiens	ENX-1	176	94
4433	AF180470	Mus musculus	Kiaa0575	423	77
4434	X17206	Homo sapiens	put. LLRep3 protein (AA 1-221)	581	99
4435	Y70929	Homo sapiens	Human zll4 splice variant protein.	621	100
4436	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	135	71
4437	A06977	Homo sapiens	albumin	610	97
4438	A00279	synthetic construct	Human serum albumin	621	94
4439	L29028	Chlamydomonas eugametos	amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 .. 109, 128 .. 130, 132 .. 134, 158 .. 160, 163 .. 165; amino acid feature: Rod protein domain, aa 169 .. 340; amino acid feature: globular protein domain, aa 32 .. 168	105	36
4440	AK024455	Homo sapiens	FLJ00047 protein	112	65
4441	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	133	69
4442	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	142	60
4443	AF113685	Homo sapiens	PRO0974	101	54
4444	W03627	Homo sapiens	Human follicle stimulating hormone GPR N-terminal sequence.	181	42
4445	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	132	76
4446	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	141	54
4447	L02867	Homo sapiens	paraneoplastic antigen	136	78
4448	D38435	Homo sapiens	homologue of yeast PMS1	108	66
4449	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	122	65
4450	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	68
4451	AF220264	Homo sapiens	MOST-1	101	40
4452	AF130079	Homo sapiens	PRO2852	97	59
4453	AF116715	Homo sapiens	PRO2829	139	69

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4454	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	144	53
4455	AF130087	Homo sapiens	PRO2411	108	73
4456	AF279891	Homo sapiens	dead box protein 15	108	58
4457	L08258	Strongylocentrotus purpuratus	kinesin light chain isoform 4	176	94
4458	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	116	78
4460	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	146	74
4461	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	156	52
4462	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	118	72
4463	AF119900	Homo sapiens	PRO2822	144	80
4464	M15530	Homo sapiens	B-cell growth factor	92	76
4465	Y17833	Human endogenous retrovirus K	env protein	107	62
4466	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	132	78
4467	AF090895	Homo sapiens	PRO0117	112	79
4468	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	146	64
4469	X97675	Homo sapiens	plakophilin 2b	119	78
4470	AF118081	Homo sapiens	PRO1900	119	74
4471	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	121	60
4472	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	63
4473	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	205	73
4474	AF130114	Homo sapiens	PRO2459	121	67
4475	AF178534	Homo sapiens	taln	213	67
4476	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	122	92
4477	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	99	66
4478	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	142	62
4479	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	153	55
4480	AF217374	Acanthaster planci	cytochrome oxidase subunit 1	130	100
4481	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	110	57
4482	Y20983	Homo sapiens	Human glial fibrillary acidic protein GFAP wild type fragment 9.	110	63
4483	AF221552	Oryza sativa	proline-rich protein RiP-15	119	33
4484	L25941	Homo sapiens	integral nuclear envelope inner membrane protein	110	84
4485	AF130089	Homo sapiens	PRO2550	161	81
4486	U39742	Caenorhabditis elegans	coded for by C. elegans cDNA yk25e5.3; coded for by C. elegans cDNA yk25e5.5; similar to repeat guanylate kinase domain of D. melanogaster lethal(1) discs large-1 tumor suppressor protein (SP:DLG1_DROME, P31007) and R. norvegicus postsynaptic density protein	98	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4487	Y86248	Homo sapiens	95 (PSD-95) (SP:PSD9 RAT. P31016) Human secreted protein HCHPF68, SEQ ID NO:163.	89	81
4488	X97675	Homo sapiens	plakophilin 2b	127	88
4489	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	105	71
4490	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	160	64
4491	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	77
4492	U83280	Leishmania donovani	39 kDa antigen	107	76
4493	AF023142	Homo sapiens	pre-mRNA splicing SR protein rA4	141	40
4494	K02576	Homo sapiens	salivary proline-rich protein 1	119	40
4495	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	98	45
4496	AF130089	Homo sapiens	PRO2550	132	75
4497	AF090930	Homo sapiens	PRO0478	160	76
4498	AF119900	Homo sapiens	PRO2822	158	55
4499	AF116661	Homo sapiens	PRO1438	126	44
4500	AF116661	Homo sapiens	PRO1438	118	42
4501	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	113	48
4502	M81321	Macaca fascicularis	proline-rich protein	154	44
4503	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	96
4504	D44596	Saccharomyces cerevisiae	Mdjlp heat shock protein	93	42
4505	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	76
4506	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	207	93
4507	U93564	Homo sapiens	p40	520	86
4508	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	135	55
4509	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	77
4510	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	146	66
4511	L27428	Homo sapiens	reverse transcriptase	143	87
4512	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	80
4513	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	97	75
4514	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	60
4515	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	73
4516	AF130051	Homo sapiens	PRO0898	141	86
4517	U12690	Homo sapiens	cytochrome oxidase subunit II	185	94
4518	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	130	100
4519	AK024455	Homo sapiens	FLJ00047 protein	152	68
4520	AF210651	Homo sapiens	NAG18	161	88
4521	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	140	68
4522	AF217374	Acanthaster planci	cytochrome oxidase subunit I	131	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4523	U72520	Mus musculus	mena protein	102	42
4524	J01415	Homo sapiens	cytochrome oxidase subunit 3	129	75
4525	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	108	84
4526	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	139	76
4527	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	89
4528	AF090931	Homo sapiens	PRO0483	91	88
4529	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	111	51
4530	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	130	92
4531	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	123	64
4532	L26953	Homo sapiens	chromosomal protein	102	79
4533	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	88	54
4534	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	122	40
4535	AF090944	Homo sapiens	PRO0663	113	53
4536	U15647	Mus musculus	expressed in select embryonal carcinoma cells and testicular cells; similar to Swiss-Prot Accession Number P11260	119	35
4537	L13858	Homo sapiens	guanine nucleotide exchange factor	150	81
4538	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	138	68
4539	AF090930	Homo sapiens	PRO0478	104	53
4540	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	112	64
4541	K02401	Homo sapiens	chorionic somatomammotropin	672	96
4542	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	171	67
4543	J04208	Homo sapiens	inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	455	92
4544	K02401	Homo sapiens	chorionic somatomammotropin	397	88
4545	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	155	66
4546	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	161	68
4547	R24056	Homo sapiens	hGH variant #8 - 172Arg 174Thr 176Tyr 178His.	117	62
4548	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	111	68
4549	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	124	65
4550	AF119855	Homo sapiens	PRO1847	152	68
4551	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	153	70
4552	M59217	Homo sapiens	alpha-1 type XIII collagen	98	57
4553	R83119	Homo sapiens	Human cisplatin resistance protein.	136	96
4554	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	72
4555	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	91	60
4556	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	70
4557	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y	101	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			isoform		
4558	AF130089	Homo sapiens	PRO2550	150	85
4559	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	161	56
4560	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	81	64
4561	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	115	55
4562	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	106	82
4563	AF090931	Homo sapiens	PRO0483	145	73
4564	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	358	77
4565	AF130089	Homo sapiens	PRO2550	175	85
4566	Z93244	Homo sapiens	bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	125	61
4567	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	142	56
4568	AF130089	Homo sapiens	PRO2550	125	75
4569	AF130089	Homo sapiens	PRO2550	172	82
4570	AF225961	Rattus norvegicus	RhoGEF glutamate transport modulator GTRAP48	149	78
4571	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	143	64
4572	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	157	70
4573	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	91	73
4574	X92485	Plasmodium vivax	pva1	111	52
4575	U93567	Homo sapiens	p40	151	71
4576	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	90	57
4577	AC007508	Arabidopsis thaliana	F1K23.4	143	42
4578	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	145	53
4579	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	175	73
4580	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	142	76
4581	AF130079	Homo sapiens	PRO2852	117	70
4582	AF090930	Homo sapiens	PRO0478	109	57
4583	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	134	79
4584	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	149	62
4585	AF118090	Homo sapiens	PRO2044	175	97
4586	AL080243	Homo sapiens	E1A binding protein p300; match: proteins: Sw:Q09472 Sw:Q92793 Sw:P45481 Wp:CE00571 Wp:CE21117 Tr:O01368 Wp:CE08856 Wp:CE00570 Wp:CE08453 Tr:O44076	144	93
4587	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	140	62
4588	AJ131245	Homo sapiens	Sec24B protein	131	81
4589	W02105	Homo sapiens	Human L-asparaginase.	559	100
4590	L26953	Homo sapiens	chromosomal protein	146	71
4591	M16976	Glycine max	N-75	125	36

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4592	AF119851	Homo sapiens	PRO1722	118	61
4593	AF090931	Homo sapiens	PRO0483	99	85
4594	M20789	Homo sapiens	alpha-1 type I collagen	103	41
4595	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	97	72
4596	AF130089	Homo sapiens	PRO2550	124	71
4597	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	143	65
4598	AF118082	Homo sapiens	PRO1902	122	64
4599	AK023034	Homo sapiens	unnamed protein product	156	100
4600	AF118082	Homo sapiens	PRO1902	148	62
4601	AF119855	Homo sapiens	PRO1847	130	50
4602	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	99	77
4603	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	162	65
4604	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	135	54
4605	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	123	75
4606	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	127	74
4607	V00672	Pan troglodytes	reading frame protein 4	194	72
4608	X86791	Sus scrofa	beta-globin	156	87
4609	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	130	88
4610	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	90
4611	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	149	68
4612	AB029309	Homo sapiens	Npw38-binding protein NpwBP	120	38
4613	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	53
4614	AK024372	Homo sapiens	unnamed protein product	124	63
4615	AC005360	Homo sapiens	FAA	175	91
4616	D38113	Pan troglodytes	ATPase subunit 6	204	69
4617	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	122	45
4618	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	118	81
4619	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	99	90
4620	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	125	50
4621	S79410	Mus musculus	nuclear localization signal binding protein	107	45
4622	AF126163	Homo sapiens	HLA3 protein	124	75
4623	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	109	69
4624	U38184	Trypanosoma cruzi	ATPase subunit 6	102	45
4625	U01849	Trypanosoma brucei	ORF1	97	36
4626	G03058	Homo sapiens	Human secreted protein, SEQ ID NO: 7139.	95	57
4627	M33228	Trypanosoma brucei	ATPase 6	126	37
4628	AF118086	Homo sapiens	PRO1992	113	60
4629	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	149	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4630	X12544	Homo sapiens	3 HLA-DR B protein precursor (AA - 29 to 267)	108	48
4631	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	111	46
4632	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	124	60
4633	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	151	60
4634	J01415	Homo sapiens	cytochrome oxidase subunit 3	138	100
4635	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	135	56
4636	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	189	100
4637	X67320	Rattus norvegicus	H1d-Histone	122	40
4638	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	181	76
4639	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	96	73
4640	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	136	54
4641	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	70
4642	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	190	56
4643	M29580	Homo sapiens	zinc finger protein 7 (ZFP7)	103	38
4645	U47741	Homo sapiens	CREB-binding protein	207	94
4646	AL035461	Homo sapiens	dJ967N21.5 (novel MCM2/3/5 family member)	213	80
4647	G03435	Homo sapiens	Human secreted protein, SEQ ID NO: 7516.	76	60
4648	AF227948	Homo sapiens	HBV pX associated protein-8; XAP-8	402	86
4649	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	143	86
4650	U93574	Homo sapiens	putative p150	121	33
4651	A02739	synthetic construct	chloramphenicol acetyltransferase	622	99
4652	AF190449	Mus musculus	putative transcription factor ALF-4	274	83
4653	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	108	76
4654	X15187	Homo sapiens	precursor polypeptide (AA -21 to 782)	763	98
4655	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	91
4656	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	169	77
4657	B01372	Homo sapiens	Neuron-associated protein.	135	83
4658	AK024455	Homo sapiens	FLJ00047 protein	151	60
4659	AC004850	Homo sapiens	vacuolar assembly protein VPS41 homolog (S53)	187	92
4660	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	181	92
4661	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446	138	58
4662	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	154	78
4663	M69180	Homo sapiens	nonmuscle myosin heavy chain-A	106	84
4664	AF130089	Homo sapiens	PRO2550	117	65
4665	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4666	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	62
4667	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	111	78
4668	AF113695	Homo sapiens	PRO1365	82	71
4669	AF003540	Homo sapiens	Krueppel family zinc finger protein	111	64
4670	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	49
4671	AL109638	Homo sapiens	dJ776F14.1 (ortholog of mouse P47)	110	100
4672	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	62
4673	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	138	60
4674	X51591	Homo sapiens	beta-myosin heavy chain (1151 AA)	442	97
4675	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	148	76
4676	D86971	Homo sapiens	no similarities to reported gene products	133	100
4677	K02576	Homo sapiens	salivary proline-rich protein 1	142	43
4678	AF044205	Gossypium hirsutum	proline-rich protein precursor	117	39
4679	D38116	Pan paniscus	NADH dehydrogenase subunit 4	243	98
4680	AF113685	Homo sapiens	PRO0974	117	74
4681	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	193	90
4682	L26163	Mus musculus	histone H1e	111	37
4683	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	145	78
4684	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	112	53
4685	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	110	60
4686	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	153	72
4687	D38112	Homo sapiens	NADH dehydrogenase subunit 6	165	100
4688	W50922	Homo sapiens	Amino acid sequence of a heterogenous ribonucleotide protein.	139	100
4689	Y00281	Homo sapiens	precursor	789	100
4690	AF210651	Homo sapiens	NAG18	142	65
4691	L26953	Homo sapiens	chromosomal protein	124	72
4692	L26953	Homo sapiens	chromosomal protein	124	72
4693	U12690	Homo sapiens	cytochrome oxidase subunit II	166	80
4694	L27428	Homo sapiens	reverse transcriptase	144	87
4695	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	165	74
4696	W29474	Homo sapiens	Human histone H1 isoform HIS-1.	93	41
4697	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	126	56
4698	S79410	Mus musculus	nuclear localization signal binding protein	138	62
4699	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	141	54
4700	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	162	70
4701	AF003540	Homo sapiens	Krueppel family zinc finger protein	112	88
4702	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	159	59
4703	AF241242	Mus musculus	T-cell-specific T-box transcription factor T-bet	294	75
4704	Y86248	Homo sapiens	Human secreted protein HCHPF68,	152	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SEQ ID NO:163.		
4705	AF038963	Homo sapiens	RNA helicase	102	70
4706	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	148	63
4707	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	145	70
4708	AF289099	Maackia amurensis	ENOD2f	113	42
4709	AF130087	Homo sapiens	PRO2411	124	57
4710	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	188	86
4711	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	86
4712	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	78
4713	AF273133	Ochotona macrotis	NADH dehydrogenase subunit 4	154	76
4714	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	104	48
4715	Z18361	Ovis aries	trichohyalin	120	33
4716	AF130089	Homo sapiens	PRO2550	152	75
4717	AF119851	Homo sapiens	PRO1722	143	60
4718	K03205	Homo sapiens	salivary proline-rich protein precursor	145	45
4719	K02401	Homo sapiens	chorionic somatomammotropin	619	96
4720	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	114	52
4721	J03756	Homo sapiens	hGH-V2	515	74
4722	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	194	93
4723	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	128	56
4724	D49490	Homo sapiens	protein disulfide isomerase-related protein (PDIR)	213	55
4725	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	138	66
4726	K02401	Homo sapiens	chorionic somatomammotropin	657	98
4727	D87459	Homo sapiens	Similar to Volvox carteri extensin (S22697)	162	80
4728	AL359782	Trypanosoma brucei	possible (hvh-6) u1102, variant a dna, complete virion genome.	99	34
4729	AF090944	Homo sapiens	PRO0663	151	63
4730	M32305	Human papillomavirus type 47	E1/E4 fusion protein	106	40
4731	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	133	57
4732	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	76
4733	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	114	43
4734	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	72
4735	M76546	Helianthus annuus	hydroxyproline-rich protein	113	43
4736	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	99	59
4737	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	92	47
4738	AP000616	Oryza sativa	similar to RING-H2 finger protein	133	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			RHA1a (AF078683)		
4739	AF044205	Gossypium hirsutum	proline-rich protein precursor	105	42
4740	S78854	Oryctolagus cuniculus	alpha-tropomyosin	159	87
4741	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	151	79
4742	B01372	Homo sapiens	Neuron-associated protein.	159	85
4743	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	122	100
4744	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	82
4745	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	78
4746	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	164	80
4747	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	100
4748	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	117	53
4749	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	208	93
4750	AF155232	Pisum sativum	extensin	172	40
4751	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	76
4752	AF130079	Homo sapiens	PRO2852	104	70
4753	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	154	50
4754	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	167	50
4755	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	138	100
4756	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	163	66
4757	M11901	Rattus norvegicus	proline-rich salivary protein	102	45
4758	D38112	Homo sapiens	NADH dehydrogenase subunit 5	242	94
4759	AF046935	Homo sapiens	PCF11p homolog	244	94
4760	M76546	Helianthus annuus	hydroxyproline-rich protein	165	41
4761	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	115	60
4762	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	178	84
4763	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	134	84
4764	R95913	Homo sapiens	Neural thread protein.	136	70
4765	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	139	69
4766	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	102	56
4767	U63159	Mus musculus	transaldolase	218	100
4768	AF230279	Caenorhabditis elegans	SWI3-like protein; PSA-1	106	38
4769	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	116	56
4770	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	136	67
4771	X92485	Plasmodium	pva1	85	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
4772	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	95	80
4773	AC002398	Homo sapiens	F25965_3	96	39
4774	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	75
4775	AF120151	Homo sapiens	cytokine receptor-like molecule 9	112	100
4776	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	141	74
4777	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	108	75
4778	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	117	55
4779	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	101	55
4780	AB007860	Homo sapiens	KIAA0400	119	88
4781	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	122	88
4782	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	98	84
4783	M22334	Homo sapiens	unknown protein	611	93
4784	Y36203	Homo sapiens	Human secreted protein #75.	350	76
4785	K02401	Homo sapiens	chorionic somatomammotropin	188	97
4786	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	152	64
4787	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	102	67
4788	M38451	Homo sapiens	growth hormone	264	94
4789	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	77
4790	K02401	Homo sapiens	chorionic somatomammotropin	250	96
4791	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	127	88
4792	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	125	78
4793	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	131	51
4794	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	124	57
4795	M18095	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	103	34
4796	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	131	69
4797	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	160	77
4798	AL132841	Caenorhabditis elegans	Y15E3A.3	120	51
4799	AL009146	Drosophila melanogaster	alternatively spliced form	79	94
4800	S74221	Homo sapiens	IK factor=cytokine down-regulating HLA class II	108	80
4801	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	121	100
4802	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	94	90
4803	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	101	90

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4804	R95913	Homo sapiens	Neural thread protein.	139	71
4805	X61045	Hydra sp.	mini-collagen	126	68
4806	X12544	Homo sapiens	3 HLA-DR B protein precursor (AA - 29 to 267)	114	56
4807	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	160	84
4808	D38112	Homo sapiens	NADH dehydrogenase subunit 6	277	94
4809	L26953	Homo sapiens	chromosomal protein	90	60
4810	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	76
4811	L26953	Homo sapiens	chromosomal protein	121	62
4812	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	124	71
4813	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	78	46
4814	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	100	78
4815	AF152961	Homo sapiens	chromatin-specific transcription elongation factor FACT 140 kDa subunit	152	96
4816	U93569	Homo sapiens	putative p150	334	82
4817	AB014575	Homo sapiens	KIAA0675 protein	125	67
4818	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	114	90
4819	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	129	45
4820	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	134	48
4821	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	129	61
4822	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	137	83
4823	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	126	55
4824	AF113685	Homo sapiens	PRO0974	110	54
4825	U63542	Homo sapiens	FAP protein	136	70
4826	X83413	Human herpesvirus 6	U88	130	54
4827	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	152	76
4828	U76609	Homo sapiens	ribosomal L5 protein	134	89
4829	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	110	57
4830	AC006161	Arabidopsis thaliana	putative CENP-B/ARS-binding protein-like protein	141	31
4831	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	143	71
4832	U94189	Rattus norvegicus	Duo	158	79
4833	J04031	Homo sapiens	MDMCSF (EC 1.5.1.5; EC 3.5.4.9; EC 6.3.4.3)	193	97
4834	Y13397	Homo sapiens	Amino acid sequence of protein PRO334.	654	97
4835	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	107	53
4836	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	464	93
4837	AF272833	Homo sapiens	misato	413	87
4838	AF130089	Homo sapiens	PRO2550	132	71
4839	G00333	Homo sapiens	Human secreted protein, SEQ ID NO:	116	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4840	G00437	Homo sapiens	4414. Human secreted protein, SEQ ID NO: 4518.	89	80
4841	W77354	Homo sapiens	Human telomere repeat binding factor 2 truncated protein.	106	100
4842	AF090942	Homo sapiens	PRO0657	160	75
4843	AF090944	Homo sapiens	PRO0663	202	80
4844	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	167	81
4845	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	166	74
4846	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	228	97
4847	U12690	Homo sapiens	cytochrome oxidase subunit II	198	95
4848	AB023485	Mus musculus	transcription factor CA150b	118	42
4849	Z70684	Caenorhabditis elegans	F28D1.8	98	42
4850	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	106	45
4851	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	179	92
4852	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	145	82
4853	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	123	77
4854	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	112	55
4855	U66464	Homo sapiens	hematopoietic progenitor kinase	110	81
4856	AC011708	Arabidopsis thaliana	putative RING zinc finger protein	121	43
4857	M81321	Macaca fascicularis	proline-rich protein	126	35
4858	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	104	40
4859	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	75
4860	X65165	Volvox carteri	extensin	248	55
4861	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	106	79
4862	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	185	92
4863	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	75
4864	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
4865	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	63
4866	AB023229	Homo sapiens	KIAA1012 protein	208	92
4867	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	144	80
4868	L26953	Homo sapiens	chromosomal protein	126	70
4869	U63542	Homo sapiens	FAP protein	134	40
4870	D86853	Catharanthus roseus	extensin	102	48
4871	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	69
4872	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	55
4873	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	156	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4874	Y17832	Human endogenous retrovirus K	env protein	219	67
4875	AF217517	Homo sapiens	uncharacterized bone marrow protein BM041	81	38
4876	L27428	Homo sapiens	reverse transcriptase	105	91
4877	M64792	Rattus norvegicus	salivary proline-rich protein	146	46
4878	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	99	38
4879	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	105	77
4880	R58816	Homo sapiens	Human c-myc far upstream element (FUSE) binding protein (FBP) variant from PBL clone 31-10.	87	39
4881	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	150	67
4882	AF175223	Drosophila melanogaster	SANT domain protein SMRTER	84	89
4883	AF174482	Homo sapiens	polycomb 3	136	57
4884	Y54324	Homo sapiens	Amino acid sequence of a human gastric cancer antigen protein.	147	66
4885	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	141	71
4886	U55376	Caenorhabditis elegans	F16H11.2 gene product	95	100
4887	AF261918	Homo sapiens	disintegrin metalloproteinase with thrombospondin repeats	262	72
4888	J02459	bacteriophage lambda	K (tail component;199)	610	100
4889	Y95435	Homo sapiens	Human calcium channel SOC-2/CRAC-1.	219	89
4890	B01372	Homo sapiens	Neuron-associated protein.	134	80
4891	X64712	Gallus gallus	collagen-alpha-3 type IX	112	41
4892	K02401	Homo sapiens	chorionic somatomammotropin	556	87
4893	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	108	55
4894	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	62
4895	L26953	Homo sapiens	chromosomal protein	93	81
4896	AJ277740	Homo sapiens	RPB11b1beta protein	102	66
4897	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	145	87
4898	AL359782	Trypanosoma brucei	possible (bhv-6) u1102, variant a dna, complete virion genome.	131	67
4899	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	153	64
4900	U90304	Homo sapiens	iroquois-class homeodomain protein IRX-2a	109	41
4901	D29956	Homo sapiens	This gene is similar to the oncogene(X63547)	120	73
4902	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	116	70
4903	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	102	82
4904	AF119900	Homo sapiens	PRO2822	157	57
4905	U93565	Homo sapiens	putative p150	146	55
4906	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	120	67
4907	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	160	76
4908	Y86248	Homo sapiens	Human secreted protein HCHPF68,	136	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SEQ ID NO:163.		
4909	AF155232	Pisum sativum	extensin	98	43
4910	U15647	Mus musculus	reverse transcriptase	196	50
4911	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	144	56
4912	AF225419	Homo sapiens	HSCARG	248	61
4913	M76546	Helianthus annuus	hydroxyproline-rich protein	110	47
4914	AL117382	Homo sapiens	dJ881L22.2 (novel protein)	312	100
4915	AB037814	Homo sapiens	KIAA1393 protein	192	68
4916	D38112	Homo sapiens	NADH dehydrogenase subunit 4	169	89
4917	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	90
4918	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078583)	116	86
4919	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	132	100
4920	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	183	65
4921	AF090944	Homo sapiens	PRO0663	141	57
4922	AF090931	Homo sapiens	PRO0483	159	55
4923	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	81
4924	U09500	Homo sapiens	cytochrome b	276	94
4925	AB002377	Homo sapiens	KIAA0379 protein	304	98
4926	M22334	Homo sapiens	unknown protein	201	62
4927	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	65
4928	AF130089	Homo sapiens	PRO2550	116	82
4929	U21123	Drosophila melanogaster	ena polypeptide	94	41
4930	W75159	Homo sapiens	Human secreted protein encoded by gene 45 clone HTD554.	294	82
4931	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	96	74
4932	G02460	Homo sapiens	Human secreted protein, SEQ ID NO: 6541.	101	57
4933	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	142	70
4934	AF130087	Homo sapiens	PRO2411	137	80
4935	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	132	56
4936	AB032604	Mus musculus	MIWI (piwi)	313	50
4937	X74987	Homo sapiens	2'-5' oligoadenylate binding protein	144	96
4938	AF054658	Homo sapiens	kappa 1 immunoglobulin light chain variable region	120	87
4939	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	134	67
4940	U22230	Felis catus	ribosomal protein S17	118	100
4941	AB028956	Homo sapiens	KIAA1033 protein	527	88
4942	G00429	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	281	86
4943	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	71
4944	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	108	95
4945	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	170	76
4946	AF090895	Homo sapiens	PRO0117	125	65
4947	D13866	Homo sapiens	alpha-catenin	575	100
4948	L01664	Homo sapiens	lysophospholipase	166	96

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4949	AF118085	Homo sapiens	PRO1975	572	96
4950	AK024455	Homo sapiens	FLJ00047 protein	95	81
4951	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	58
4952	AB011142	Homo sapiens	KIAA0570 protein	120	88
4953	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	39
4954	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	69
4955	AK024455	Homo sapiens	FLJ00047 protein	119	64
4956	AF116715	Homo sapiens	PRO2829	142	75
4957	M31520	Homo sapiens	ribosomal protein S24	158	100
4958	D38113	Pan troglodytes	ATPase subunit 8	98	64
4959	AF130089	Homo sapiens	PRO2550	156	75
4960	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	136	95
4961	S61950	Oryctolagus cuniculus	alpha 2(I) procollagen, alpha 2(I) {C-terminal}	159	93
4962	AF070540	Homo sapiens	putative nuclear protein	513	93
4963	S61950	Oryctolagus cuniculus	alpha 2(I) procollagen, alpha 2(I) {C-terminal}	159	93
4964	AF146191	Homo sapiens	FRG1	343	92
4965	Y16624	Homo sapiens	Human phosphoprotein 32 (pp32) protein sequence.	114	100
4966	X67813	Canis familiaris	signal recognition particle, 72 kDa subunit	127	100
4967	S79410	Mus musculus	nuclear localization signal binding protein	127	63
4968	U83303	Homo sapiens	line-1 reverse transcriptase	117	69
4969	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	101	80
4970	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	173	69
4971	D38112	Homo sapiens	ATPase subunit 6	112	91
4972	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	209	97
4973	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	162	80
4974	AL050399	Arabidopsis thaliana	putative proline-rich protein	75	91
4975	L11668	Bos taurus	cyclophilin-40	134	100
4976	M55169	Homo sapiens	tripeptidyl peptidase II	385	90
4977	AF090944	Homo sapiens	PRO0663	154	88
4978	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	102	62
4979	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	128	70
4980	G00721	Homo sapiens	Human secreted protein, SEQ ID NO: 4802.	104	95
4981	R54656	Homo sapiens	Prostaglandin I2 production stimulating protein B.	101	100
4982	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	124	38
4983	AF273053	Homo sapiens	CTCL tumor antigen se89-1	281	96
4984	M15530	Homo sapiens	B-cell growth factor	117	58
4985	D13641	Homo sapiens	mitochondrial outer membrane protein 19	534	94
4986	L11316	Mus musculus	ect2	528	92
4987	X51755	Homo sapiens	open reading frame (458 AA)	108	90
4988	M61877	Homo sapiens	erythroid alpha spectrin	129	87

SEQ ID NO:	Accession No.	Species	Description:	Smith-Waterman Score	% Identity
4989	X57316	Saccharomyces cerevisiae	carboxypeptidase s	134	50
4990	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	151	78
4991	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	173	61
4992	M34019	Bos taurus	beta-adrenergic receptor kinase	172	100
4993	L26953	Homo sapiens	chromosomal protein	135	86
4994	X97675	Homo sapiens	plakophilin 2b	124	63
4995	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	153	77
4996	AF130089	Homo sapiens	PRO2550	175	48
4997	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	95	68
4998	Y86214	Homo sapiens	Nuclear transport protein clone hfb341 protein sequence.	312	98
4999	G03681	Homo sapiens	Human secreted protein, SEQ ID NO: 7762.	100	95
5000	AF152961	Homo sapiens	chromatin-specific transcription elongation factor FACT 140 kDa subunit	127	96
5001	U70063	Homo sapiens	acid ceramidase	315	96
5002	AF041373	Rattus norvegicus	clathrin assembly protein short form	163	63
5003	AK001841	Homo sapiens	unnamed protein product	468	83
5004	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	143	61
5005	S79410	Mus musculus	nuclear localization signal binding protein	116	47
5006	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	107	55
5007	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	151	76
5008	Z15005	Homo sapiens	CENP-E	281	84
5009	AF130089	Homo sapiens	PRO2550	122	75
5010	AL049698	Homo sapiens	dJ470B24.1.1 (myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6) (isoform 1))	77	33
5011	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	90	62
5012	AL023780	Schizosaccharomyces pombe	DNA binding protein	145	36
5013	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	93	46
5014	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	104	43
5015	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	55
5016	U15647	Mus musculus	expressed in select embryonal carcinoma cells and testicular cells; similar to Swiss-Prot Accession Number P11260	119	35
5017	B10545	Homo sapiens	Human aspartate protease psn-like4 protein.	649	98
5018	AF089745	Homo sapiens	FK506-binding protein	656	98
5019	AF081484	Homo sapiens	alpha-tubulin isoform 1	634	97
5020	AF081484	Homo sapiens	alpha-tubulin isoform 1	603	92
5021	AF081484	Homo sapiens	alpha-tubulin isoform 1	623	94
5022	AF081484	Homo sapiens	alpha-tubulin isoform 1	671	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5023	AF130089	Homo sapiens	PRO2550	109	71
5024	AB013452	Homo sapiens	ATPasell	208	77
5025	R27654	Homo sapiens	Human calcium channel 27980/16.	183	100
5026	Y36156	Homo sapiens	Human secreted protein #28.	114	64
5027	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	74
5028	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	149	59
5029	S74728	Homo sapiens	antiquitin=26g turgor protein homolog	652	98
5030	L41498	Homo sapiens	longation factor 1-alpha }	592	87
5031	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase	454	70
5032	AJ223948	Homo sapiens	RNA helicase	574	84
5033	AF021935	Rattus norvegicus	myotonic dystrophy kinase-related Cdc42-binding kinase	670	97
5034	AF150755	Mus musculus	microtubule-actin crosslinking factor	526	80
5035	AF150755	Mus musculus	microtubule-actin crosslinking factor	602	89
5036	AF081484	Homo sapiens	alpha-tubulin isoform 1	598	89
5037	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	708	96
5038	AE003621	Drosophila melanogaster	CG13384 gene product	279	45
5039	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	107	68
5040	AF047469	Homo sapiens	arsenite translocating ATPase	650	94
5041	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	109	41
5042	AJ007798	Homo sapiens	stromal antigen 3, (STAG3)	288	100
5043	L26953	Homo sapiens	chromosomal protein	124	67
5044	AB005047	Homo sapiens	SH3 binding protein	105	88
5045	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	143	78
5046	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	164	83
5047	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	121	63
5048	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	153	64
5049	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	120	59
5050	Z25535	Homo sapiens	nuclear pore complex protein hnup153	115	88
5051	J03176	Bradyrhizobium japonicum	cytochrome b/c1 precursor	97	35
5052	X85995	Homo sapiens	immunoglobulin light chain	200	100
5053	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	164	76
5054	B01372	Homo sapiens	Neuron-associated protein.	109	80
5055	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	209	54
5056	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	110	51
5057	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	93	39
5058	X92474	Homo sapiens	ch-TOG	147	100
5059	L27428	Homo sapiens	reverse transcriptase	264	75
5060	S79410	Mus musculus	nuclear localization signal binding protein	119	44
5061	L25616	Homo sapiens	CG1 protein	119	77
5062	G03790	Homo sapiens	Human secreted protein, SEQ ID NO:	99	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7871.		
5063	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	164	59
5064	AF118082	Homo sapiens	PRO1902	175	53
5065	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	84	51
5066	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	100
5067	AF155232	Pisum sativum	extensin	137	45
5068	X63005	Mus musculus	proline-rich protein	98	35
5069	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	307	56
5070	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	173	89
5071	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	153	68
5072	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	164	73
5073	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	109	73
5074	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	121	80
5075	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	113	72
5076	U12690	Homo sapiens	cytochrome oxidase subunit II	151	88
5077	AF090944	Homo sapiens	PRO0663	138	78
5078	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	150	74
5079	X97675	Homo sapiens	plakophilin 2b	179	93
5080	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	123	76
5081	AF240630	Mus musculus	IQ motif containing GTPase activating protein 1	176	59
5082	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	100	54
5083	S79410	Mus musculus	nuclear localization signal binding protein	99	59
5084	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	101	57
5085	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	118	77
5086	AB047600	Macaca fascicularis	hypothetical protein	93	69
5087	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	88	80
5088	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	112	57
5089	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	87	61
5090	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	74	61
5091	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	83	78
5092	AF065484	Homo sapiens	sorting nexin 1A	172	81
5093	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	139	90
5094	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	78
5095	U02313	Mus musculus	protein kinase	147	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5096	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	129	67
5097	U64849	Caenorhabditis elegans	Contains similarity to Pfam domain: PF00646 (F-box), Score=28.7, E-value=4.3e-05, N=1	197	39
5098	AF006010	Homo sapiens	progesterone induced protein	174	86
5099	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	119	55
5100	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	132	82
5101	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	159	77
5102	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	99	70
5103	J02459	bacteriophage lambda	J (tail: host specificity; 1132)	485	96
5104	J02459	bacteriophage lambda	H (tail component; 853)	823	98
5105	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID: g8148)	106	42
5106	AF130089	Homo sapiens	PRO2550	121	35
5107	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	135	81
5108	P92219	Homo sapiens (human)	CR1 protein.	123	88
5109	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	83	78
5110	U41751	Mus musculus	E124	560	83
5111	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	69
5112	AF130089	Homo sapiens	PRO2550	164	88
5113	G03084	Homo sapiens	Human secreted protein, SEQ ID NO: 7165.	160	72
5114	AF052831	Trypanosoma cruzi	unknown	107	70
5115	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna; complete virion genome.	128	68
5116	X55684	Lycopersicon esculentum	extensin (class I)	60	29
5117	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	124	64
5118	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	60
5119	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	112	79
5120	X65718	Prunus dulcis	extensin	94	33
5121	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
5122	AJ007714	Homo sapiens	lysine-ketoglutarate reductase /saccharopine dehydrogenase	154	96
5123	AJ007714	Homo sapiens	lysine-ketoglutarate reductase /saccharopine dehydrogenase	158	80
5124	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	109	44
5125	AF130089	Homo sapiens	PRO2550	112	46
5126	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	60
5127	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	99	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5128	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	143	57
5129	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	140	55
5130	J02459	bacteriophage lambda	H (tail component, 853)	378	100
5131	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	78
5132	J04088	Homo sapiens	DNA topoisomerase II (EC 5.99.1.3)	163	96
5133	AL132841	Caenorhabditis elegans	Y15E3A.3	147	85
5134	D90827	Escherichia coli	Serine/Threonine protein phosphatase (EC 3.1.3.16)	329	46
5135	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	159	62
5136	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	161	91
5137	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	136	96
5138	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	129	67
5139	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	93	31
5140	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	141	46
5141	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	166	67
5142	AF003535	Homo sapiens	ORF2-like protein	168	50
5143	AF259792	Homo sapiens	SW11Lbeta protein	684	98
5144	Y36203	Homo sapiens	Human secreted protein #75.	130	63
5145	AF130089	Homo sapiens	PRO2550	151	76
5146	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	52
5147	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	129	85
5148	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	101	67
5149	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	118	56
5150	AF130051	Homo sapiens	PRO0898	80	72
5151	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	165	63
5152	X56832	Homo sapiens	muscle specific enolase	573	90
5153	X76930	Homo sapiens	hepatocyte nuclear factor 4	544	91
5154	U12919	Mus musculus	adenylyl cyclase type VII	156	75
5155	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	91	76
5156	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	133	50
5157	Y08387	Homo sapiens	mu-adaptin-related protein 2	252	86
5158	R13556	Homo sapiens	Protein encoded downstream of hhcm oncoprotein.	126	66
5159	AF090942	Homo sapiens	PRO0657	139	77
5160	AF090942	Homo sapiens	PRO0657	120	70
5161	D67066	Bos taurus	N-WASP	135	42
5162	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	115	73
5163	AF044496	Canis familiaris	acidic ribosomal phosphoprotein P0	112	78
5164	W48351	Homo sapiens	Human breast cancer related protein	106	58

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
5165	AJ250095	Bordetella bronchiseptica	pertactin (P.68)	119	64
5166	U96411	Mus musculus	otogelin; MLEMP	609	90
5167	AF116238	Homo sapiens	pseudouridine synthase 1	237	87
5168	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	151	78
5169	AL050342	Homo sapiens	dJ655K7.1 (novel protein)	263	100
5170	AK024455	Homo sapiens	FLJ00047 protein	177	72
5171	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	94	100
5172	L38908	Nicotiana tabacum	extensin	101	47
5173	AF055904	Myxococcus xanthus	unknown	107	36
5174	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	143	59
5175	Y00337	Homo sapiens	Human secreted protein encoded by gene 81.	123	86
5176	AJ010957	Hippopotamus amphibius	NADH1	212	90
5177	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	84	76
5178	U83280	Leishmania donovani	39 kDa antigen	128	90
5179	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	183	45
5180	L27428	Homo sapiens	reverse transcriptase	106	46
5181	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	144	45
5182	R83119	Homo sapiens	Human cisplatin resistance protein.	142	96
5183	R95330	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 1TU).	475	71
5184	AF090930	Homo sapiens	PRO0478	121	57
5185	AF193613	Homo sapiens	cell recognition molecule Caspr2	338	50
5186	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	102	36
5187	AL031118	Homo sapiens	dJ153G14.3 (novel C2H2 type Zinc Finger protein)	465	62
5188	AF183144	Mus musculus	left-right dynein	199	83
5189	J02459	bacteriophage lambda	J (tail:host specificity;1132)	748	95
5190	AF193613	Homo sapiens	cell recognition molecule Caspr2	229	50
5191	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	135	65
5192	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	84
5193	Y00311	Homo sapiens	Human secreted protein encoded by gene 54.	112	49
5194	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	126	56
5195	AF104261	Mus musculus	Pax transcription activation domain interacting protein PTIP	487	72
5196	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	132	65
5197	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	80
5198	X55777	Homo sapiens	52kD protein	106	30
5199	AF092170	Homo sapiens	polycystic kidney disease 2 related	122	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5200	AF092170	Homo sapiens	protein	138	96
5201	G03798	Homo sapiens	polycystic kidney disease 2 related protein	107	67
5202	AP000616	Oryza sativa	Human secreted protein, SEQ ID NO: 7879.	110	81
5203	R95913	Homo sapiens	similar to RING-H2 finger protein RHA1a (AF078683)	96	61
5204	G02507	Homo sapiens	Neural thread protein.	83	55
5205	AF319476	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	705	100
5206	G02832	Homo sapiens	GKAP42	78	62
5207	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	119	75
5208	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	166	50
5209	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	139	39
5210	AF090931	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	94	90
5211	G00357	Homo sapiens	PRO0483	114	74
5212	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	116	70
5213	U53209	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	124	95
5214	G02485	Homo sapiens	transformer-2 alpha	130	58
5215	Y02671	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	151	49
5216	L26953	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	95	52
5217	G02532	Homo sapiens	chromosomal protein	149	66
5218	AF220264	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	151	65
5219	G03133	Homo sapiens	MOST-1	125	53
5220	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	138	65
5221	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	129	66
5222	AF194537	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	120	60
5223	G00376	Homo sapiens	NAG13	115	60
5224	Y14482	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	144	58
5225	AF000996	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	164	70
5226	G00332	Homo sapiens	ubiquitous TPR motif, Y isoform	125	73
5227	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	164	69
5228	M34451	Caenorhabditis elegans	Human secreted protein, SEQ ID NO: 7519.	100	41
5229	X16396	Homo sapiens	collagen (rol-6)	306	88
5230	AL359782	Trypanosoma brucei	precursor polypeptide (AA -29 to 315) possible (hiv-6) u1102, variant a dna, complete virion genome.	112	69
5231	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	157	75
5232	D86982	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	201	100
5233	AF116712	Homo sapiens	similar to human ankryrin 1(S08275)	135	49
5234	AL049758	Homo sapiens	PRO2738	184	70
			dJ437M21.1 (novel protein)		

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5235	AB014527	Homo sapiens	KIAA0627 protein	164	100
5236	AF194537	Homo sapiens	NAG13	183	64
5237	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	170	43
5238	AF135439	Mus musculus	formin binding protein 11	230	100
5239	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	137	69
5240	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	63
5241	AF116661	Homo sapiens	PRO1438	152	58
5242	L27428	Homo sapiens	reverse transcriptase	193	53
5243	AF130089	Homo sapiens	PRO2550	141	60
5244	AF118086	Homo sapiens	PRO1992	135	71
5245	AJ228863	Mus musculus	CLIP-115	195	97
5246	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	81
5247	AC007887	Arabidopsis thaliana	F15O4.29	76	93
5248	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	151	75
5249	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	66
5250	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	70
5251	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	80
5252	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	54
5253	AF090944	Homo sapiens	PRO0663	177	62
5254	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	132	57
5255	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	129	74
5256	D38112	Homo sapiens	NADH dehydrogenase subunit 2	157	91
5257	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	160	78
5258	U16296	Homo sapiens	TIAM1 protein	133	100
5259	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	92	93
5260	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	324	78
5261	AK024455	Homo sapiens	FLJ00047 protein	100	50
5262	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	217	100
5263	AB047600	Macaca fascicularis	hypothetical protein	125	57
5264	U83246	Homo sapiens	copine I	199	86
5265	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	72
5266	U91329	Homo sapiens	kinesin-like motor protein KIF1C	132	93
5267	J00672	Oryctolagus cuniculus	beta-myosin	109	100
5268	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	74	43
5269	AF119851	Homo sapiens	PRO1722	96	61
5270	AF090930	Homo sapiens	PRO0478	113	91
5271	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	123	62
5272	B01372	Homo sapiens	Neuron-associated protein.	122	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5273	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	116	78
5274	AF090931	Homo sapiens	PRO0483	144	67
5275	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	117	68
5276	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	111	58
5277	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	67
5278	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	67
5279	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	69
5280	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	196	45
5281	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	115	73
5282	A18812	Brassica napus	extensin	120	38
5283	Z68747	Homo sapiens	imogen 38	291	75
5284	X77816	Rattus norvegicus	PR-Vbeta1	97	37
5285	AF130089	Homo sapiens	PRO2550	181	73
5286	AF130089	Homo sapiens	PRO2550	147	67
5287	AF090942	Homo sapiens	PRO0657	90	50
5288	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	116	74
5289	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	64
5290	D86972	Homo sapiens	similar to E.coli hypothetical 29.6 KD protein(P1:YIGW_ECOLI)	111	100
5291	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	145	57
5292	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	65
5293	Y08061	Homo sapiens	Human c-myc protein fragment.	213	76
5294	AF090895	Homo sapiens	PRO0117	134	52
5295	AF017635	Homo sapiens	DCHT	145	100
5296	G02558	Homo sapiens	Human secreted protein, SEQ ID NO: 6639.	136	60
5297	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	67
5298	AK024455	Homo sapiens	FLJ00047 protein	67	80
5299	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	164	75
5300	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	55
5301	R14643	Homo sapiens	Gamma interferon receptor.	107	82
5302	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	238	90
5303	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	205	68
5304	AF130089	Homo sapiens	PRO2550	100	77
5305	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	117	44
5306	X92485	Plasmodium vivax	pva1	128	61
5307	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	77	57
5308	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	140	42
5309	Y91577	Homo sapiens	Human secreted protein sequence	489	78

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded by gene 2 SEQ ID NO:250.		
5310	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	65
5311	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	129	65
5312	AF119851	Homo sapiens	PRO1722	97	65
5313	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	160	90
5314	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	113	81
5315	AF071310	Mus musculus	OPA-containing protein 1	228	53
5316	AF090942	Homo sapiens	PRO0657	162	70
5317	U83303	Homo sapiens	line-1 reverse transcriptase	109	83
5318	AF090894	Homo sapiens	PRO0113	125	63
5319	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	129	66
5320	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	75
5321	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	138	81
5322	L27428	Homo sapiens	reverse transcriptase	139	52
5323	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	109	83
5324	AF118082	Homo sapiens	PRO1902	107	70
5325	M81321	Macaca fascicularis	proline-rich protein	114	37
5326	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	112	79
5327	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	99	72
5328	AF090930	Homo sapiens	PRO0478	152	73
5329	L27428	Homo sapiens	reverse transcriptase	267	65
5330	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	140	82
5331	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	164	54
5332	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	135	52
5333	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	124	76
5334	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	97	56
5335	AP000060	Aeropyrum pernix	103aa long hypothetical protein	71	50
5336	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	75
5337	Z93784	Homo sapiens	dJ398C22.1 (novel protein, ortholog of mouse brain protein E46)	280	68
5338	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	132	64
5339	AF210651	Homo sapiens	NAG18	160	56
5340	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	133	80
5341	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	151	75
5342	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	105	50
5343	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	103	75
5344	G03021	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	132	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7102.		
5345	Y87103	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	92	48
5346	AL121891	Homo sapiens	dJ1187M17.2 (K1AA0552 protein)	148	43
5347	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	130	33
5348	AF090944	Homo sapiens	PRO0663	205	72
5349	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	135	37
5350	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	101	37
5351	AF265578	Homo sapiens	orphan neurotransmitter transporter NTT5	121	39
5352	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	105	75
5353	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	167	69
5354	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	97	60
5355	G00590	Homo sapiens	Human secreted protein, SEQ ID NO: 4671.	113	80
5356	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	123	67
5357	W88609	Homo sapiens	Secreted protein encoded by gene 76 clone HKIXL73.	94	79
5358	AC004450	Arabidopsis thaliana	putative extensin	110	37
5359	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	79
5360	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	199	74
5361	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	97
5362	AB017437	Gallus gallus	avena	98	44
5363	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	93
5364	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	181	70
5365	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	159	68
5366	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	94	60
5367	X52022	Homo sapiens	collagen type VI, alpha 3 chain	150	33
5368	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	120	77
5369	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	145	75
5370	X97675	Homo sapiens	plakophilin 2b	170	85
5371	AF130079	Homo sapiens	PRO2852	103	95
5372	L26953	Homo sapiens	chromosomal protein	117	54
5373	AF210651	Homo sapiens	NAG18	137	67
5374	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	106	76
5375	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	70
5376	AL109819	Arabidopsis thaliana	extensin-like protein	123	34
5377	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	127	79
5378	AF036170	Dictyostelium	homeobox-containing protein Wariar	93	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		discoideum			
5379	AF130089	Homo sapiens	PRO2550	134	75
5380	AF161384	Homo sapiens	HSPC266	663	96
5381	AF130051	Homo sapiens	PRO0898	147	77
5382	AF090944	Homo sapiens	PRO0663	118	83
5383	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	129	55
5384	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	110	68
5385	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	165	53
5386	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	145	96
5387	U54788	Mus musculus	Wiskott-Aldrich Syndrome Protein	108	51
5388	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	104	89
5389	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	125	70
5390	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	103	72
5391	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	119	85
5392	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	120	65
5393	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	131	78
5394	G01552	Homo sapiens	Human secreted protein, SEQ ID NO: 5633.	159	90
5395	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	110	65
5396	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	85	59
5397	X86681	Homo sapiens	HNP36 protein	248	71
5398	L27428	Homo sapiens	reverse transcriptase	133	62
5399	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	132	54
5400	AL080196	Homo sapiens	hypothetical protein	164	96
5401	D38112	Homo sapiens	NADH dehydrogenase subunit 5	119	75
5402	AF090944	Homo sapiens	PRO0663	99	64
5403	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	93	58
5404	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	103	37
5405	W05278	Homo sapiens	Tumour necrosis factor-related gene product CL6.5.40.	137	80
5406	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	102	69
5407	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	102	69
5408	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	142	69
5409	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	139	63
5410	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	65	47
5411	AF181626	Drosophila melanogaster	BcDNA.GH03694	171	53
5412	U93565	Homo sapiens	putative p150	195	70
5413	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	170	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5414	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	61
5415	X83572	Homo sapiens	ARSD	133	100
5416	D86853	Catharanthus roseus	extensin	113	41
5417	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	139	60
5418	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	175	77
5419	R32010	Homo sapiens	Rp15-TIA-1.	140	83
5420	D67066	Bos taurus	N-WASP	153	41
5421	U42391	Homo sapiens	myosin-IXb	203	100
5422	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	74
5423	AF220264	Homo sapiens	MOST-1	94	78
5424	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	128	63
5425	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	131	57
5426	AF130089	Homo sapiens	PRO2550	120	58
5427	Z70204	Caenorhabditis elegans	contains similarity to Pfam domain: PF00628 (PHD-finger), Score=63.1, E-value=1.9e-15, N=1-cDNA EST EMBL:T00556 comes from this gene-cDNA EST yk3447.5 comes from this gene	131	55
5428	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	158	51
5429	AF130089	Homo sapiens	PRO2550	112	73
5430	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	161	52
5431	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	131	72
5432	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	152	79
5433	AF090942	Homo sapiens	PRO0657	109	67
5434	AE003588	Drosophila melanogaster	CG2839 gene product	141	50
5435	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	154	79
5436	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	128	41
5437	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	63
5438	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	117	84
5439	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	112	76
5440	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	42
5441	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	64
5442	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	193	56
5443	X07495	Homo sapiens	translated region (AA 1-264)	108	41
5444	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	135	62
5445	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	130	41
5446	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	136	71

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5447	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	123	62
5448	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	101	45
5449	U13866	unidentified cloning vector	non-functional lacZ alpha peptide	106	57
5450	X01469	Plasmodium falciparum	histidine-rich protein	162	56
5451	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	130	88
5452	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	155	68
5453	AF119900	Homo sapiens	PRO2822	162	63
5454	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	120	51
5455	AC007204	Homo sapiens	BC273239.1	1485	69
5456	L27428	Homo sapiens	reverse transcriptase	122	41
5457	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	141	39
5458	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	68
5459	AF090930	Homo sapiens	PRO0478	144	64
5460	AF130089	Homo sapiens	PRO2550	124	60
5461	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	135	69
5462	X97675	Homo sapiens	plakophilin 2b	103	72
5463	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	137	69
5464	AF229067	Homo sapiens	PADI-H protein	146	65
5465	AF116715	Homo sapiens	PRO2829	83	71
5466	AF090930	Homo sapiens	PRO0478	146	52
5467	U93574	Homo sapiens	putative p150	203	52
5468	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	89	50
5469	AF191838	Homo sapiens	TANK binding kinase TBK1	121	95
5470	AF130079	Homo sapiens	PRO2852	146	69
5471	AF090944	Homo sapiens	PRO0663	90	66
5472	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	106	63
5473	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	60
5474	AF064553	Mus musculus	NSD1 protein	269	100
5475	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	132	65
5476	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	130	86
5477	U11271	Homo sapiens	thromboxane A2 receptor	118	67
5478	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	143	60
5479	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	113	75
5480	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	119	74
5481	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	103	85
5482	AF238235	Entamoeba histolytica	diaphanous protein	108	35
5483	AF090930	Homo sapiens	PRO0478	120	55
5484	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5485	M61883	Sus scrofa	apomucin	252	55
5486	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	107	77
5487	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	110	46
5488	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	88	62
5489	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	124	47
5490	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	220	71
5491	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	65
5492	M76546	Helianthus annuus	hydroxyproline-rich protein	116	38
5493	AF118086	Homo sapiens	PRO1992	135	82
5494	AF090930	Homo sapiens	PRO0478	105	74
5495	Y94451	Homo sapiens	Human inflammation associated protein #8.	170	61
5496	G03465	Homo sapiens	Human secreted protein, SEQ ID NO: 7546.	72	65
5497	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	152	78
5498	X56123	Mus musculus	talin	594	88
5499	AL035652	Homo sapiens	dJ1J6.1 (topoisomerase (DNA) I)	105	86
5500	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
5501	Y45389	Homo sapiens	Human secreted protein fragment encoded from gene 31.	161	93
5502	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	119	60
5503	X03145	Homo sapiens	pot. ORF 1	215	79
5504	AF240630	Mus musculus	IQ motif containing GTPase activating protein 1	180	61
5505	AL390212	Homo sapiens	dJ29M10B.1.2 (protein kinase C binding protein 1 (isoform 2))	1282	93
5506	AF118086	Homo sapiens	PRO1992	146	61
5507	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	116	74
5508	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	165	50
5509	D38112	Homo sapiens	NADH dehydrogenase subunit 5	211	95
5510	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	114	69
5511	AF090944	Homo sapiens	PRO0663	125	58
5512	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	125	53
5513	Y36156	Homo sapiens	Human secreted protein #28.	110	68
5514	AF118086	Homo sapiens	PRO1992	128	76
5515	Z22866	Mus musculus	skelemin	218	95
5516	Z22866	Mus musculus	skelemin	218	95
5517	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	127	71
5518	AL133380	Homo sapiens	dJ862P8.3 (Similar to MAP3K10 (mitogen-activated protein kinase kinase kinase 10))	603	77
5519	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	187	78
5520	AF090901	Homo sapiens	PRO0195	115	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5521	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	180	53
5522	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	155	73
5523	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	149	100
5524	X97675	Homo sapiens	plakophilin 2b	153	70
5525	D37793	Mus musculus	synaptotagmin II/1P4BP	651	84
5526	M32319	Homo sapiens	HLA protein allele B51	754	94
5527	AF130051	Homo sapiens	PRO0898	93	64
5528	X92485	Plasmodium vivax	pval	88	66
5529	AJ131890	Homo sapiens	DNA polymerase lambda	205	100
5530	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	132	68
5531	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	87	59
5532	AF090931	Homo sapiens	PRO0483	133	75
5533	AF090942	Homo sapiens	PRO0657	122	66
5534	RI3556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	145	56
5535	D38112	Homo sapiens	NADH dehydrogenase subunit 5	569	91
5536	K02401	Homo sapiens	chorionic somatomammotropin	375	98
5537	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	136	68
5538	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	130	44
5539	S62928	Homo sapiens	PRBIM protein precursor	104	40
5540	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	127	70
5541	AE000463	Escherichia coli K12	putative glycosidase	254	100
5542	J02459	bacteriophage lambda	H (tail component;853)	761	100
5543	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	119	58
5544	U59185	Homo sapiens	putative monocarboxylate transporter	233	87
5545	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	187	65
5546	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	556	84
5547	X92485	Plasmodium vivax	pval	110	67
5548	AB023233	Homo sapiens	KIAA1016 protein	246	97
5549	U16359	Rattus norvegicus	nitric oxide synthase	95	64
5550	AC002044	Homo sapiens	Alpha-fetoprotein enhancer binding protein (3' partial)	111	38
5551	AF026802	Homo sapiens	alpha-3 type IX collagen	117	47
5552	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	85	88
5553	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	91	88
5554	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	104	71
5555	AF130089	Homo sapiens	PRO2550	172	86
5556	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	105	72
5557	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	160	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5558	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	131	68
5559	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	112	67
5560	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	159	73
5561	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	141	67
5562	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	150	71
5563	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	146	80
5564	AF090942	Homo sapiens	PRO0657	157	73
5565	M64793	Rattus norvegicus	salivary proline-rich protein	169	43
5566	AL035526	Arabidopsis thaliana	extensin-like protein	103	40
5567	AF130089	Homo sapiens	PRO2550	132	67
5568	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	129	83
5569	X67337	Homo sapiens	Human pre-mRNA cleavage factor 1 68 kDa subunit	153	42
5570	AF068266	Homo sapiens	EHT protein	169	91
5571	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	113	42
5572	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	68
5573	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	71
5574	L20450	Mus musculus	DNA-binding protein	283	61
5575	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	95
5576	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	140	71
5577	Y20648	Homo sapiens	Human neurofilament-L wild type protein fragment 38.	66	37
5578	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	112	41
5579	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	142	74
5580	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	142	77
5581	AF153606	Homo sapiens	angiopoietin-related protein	737	95
5582	AF090930	Homo sapiens	PRO0478	149	77
5583	X52493	Glycine max	DNA-directed RNA polymerase	140	46
5584	M76546	Helianthus annuus	hydroxyproline-rich protein	101	51
5585	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	66	47
5586	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	130	72
5587	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	148	56
5588	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	148	66
5589	AC006014	Homo sapiens	similar to KIAA0618 and nuclear envelope protein POM 121; alternatively spliced product; similar to PID:g3327050 and P52591 (PID:g1709213)	108	84
5590	R13556	Homo sapiens	Protein encoded downstream of hhc_M	122	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5591	AB001684	Chlorella vulgaris	oncoprotein. ORF74	61	47
5592	AF090930	Homo sapiens	PRO0478	123	70
5593	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	120	57
5594	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	124	59
5595	L26953	Homo sapiens	chromosomal protein	116	62
5596	L26953	Homo sapiens	chromosomal protein	115	67
5597	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	157	55
5598	Y71213	Homo sapiens	Human irritable bowel disease related polypeptide IMX39.	131	44
5599	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	125	45
5600	AF130089	Homo sapiens	PRO2550	142	62
5601	AY014404	Homo sapiens	kinesin-like protein RBKIN2	297	98
5602	AF210651	Homo sapiens	NAG18	113	71
5603	AF090931	Homo sapiens	PRO0483	129	71
5604	X01060	Homo sapiens	put. transferrin receptor (aa 1-760)	226	80
5605	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	455	75
5606	M64793	Rattus norvegicus	salivary proline-rich protein	119	42
5607	A31039	Nicotiana glauca	PRP3	92	36
5608	AF090944	Homo sapiens	PRO0663	147	64
5609	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	64	46
5610	X01065	Cairina moschata	histone H5	88	40
5611	U03413	Dictyostelium discoideum	calcium binding protein	104	40
5612	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	144	37
5613	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	127	65
5614	G01218	Homo sapiens	Human secreted protein, SEQ ID NO: 5299.	196	97
5615	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	122	68
5616	AB029309	Homo sapiens	Npw38-binding protein NpwBP	312	78
5617	X03145	Homo sapiens	pot. ORF III	101	80
5618	AF090930	Homo sapiens	PRO0478	159	78
5619	D88461	Rattus rattus	N-WASP	107	40
5620	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	104	38
5621	Y36156	Homo sapiens	Human secreted protein #28.	134	50
5622	AF090894	Homo sapiens	PRO0113	119	65
5623	AF130089	Homo sapiens	PRO2550	130	69
5624	AF130089	Homo sapiens	PRO2550	140	78
5625	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	162	49
5626	AF130089	Homo sapiens	PRO2550	152	80
5627	AF151837	Homo sapiens	CGI-79 protein	127	78
5628	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	122	84
5629	AJ237981	Vitis vinifera	putative proline-rich cell wall protein	93	50
5630	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	110	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5631	AF130089	Homo sapiens	PRO2550	151	62
5632	U47661	Lupinus luteus	proline-rich protein PRP2 precursor	67	28
5633	Y08061	Homo sapiens	Human c-myc protein fragment.	93	61
5634	AL133215	Homo sapiens	bA108L7.6 (semaphorin 4G (sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain))	323	100
5635	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	138	67
5636	AF090942	Homo sapiens	PRO0657	184	67
5637	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	95	80
5638	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	139	83
5639	AF119900	Homo sapiens	PRO2822	143	62
5640	AL390114	Leishmania major	extremely cysteine/valine rich protein	151	61
5641	Y36243	Homo sapiens	Human secreted protein encoded by gene 20.	118	72
5642	AF090895	Homo sapiens	PRO0117	140	56
5643	Y51611	Homo sapiens	Human HSGT1 protein.	611	96
5644	AF162692	Homo sapiens	putative voltage-gated calcium channel gamma-4 subunit	172	73
5645	Z98883	Homo sapiens	c407A10.1 (GPII (N-acetylglucosaminyl transferase component))	229	100
5646	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	117	80
5647	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	159	78
5648	AF217517	Homo sapiens	uncharacterized bone marrow protein BM041	97	49
5649	AF210651	Homo sapiens	NAG18	149	58
5650	AK000385	Homo sapiens	unnamed protein product	125	36
5651	U02313	Mus musculus	protein kinase	143	96
5652	AF090944	Homo sapiens	PRO0663	95	43
5653	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	61
5654	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	100	58
5655	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	157	70
5656	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	100
5657	M64793	Rattus norvegicus	salivary proline-rich protein	123	47
5658	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	159	46
5659	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	163	60
5660	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	46
5661	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	125	71
5662	D87744	Mus musculus	DRPLA protein	89	40
5663	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	65
5664	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	87	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5665	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	71	44
5666	A18812	Brassica napus	extensin	98	41
5667	AF130089	Homo sapiens	PRO2550	128	74
5668	AF090930	Homo sapiens	PRO0478	136	54
5669	X52634	Mus musculus	tlm protein	169	59
5670	AB001684	Chlorella vulgaris	ORF49b	70	62
5671	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	153	66
5672	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	78
5673	AF090942	Homo sapiens	PRO0657	150	60
5674	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	78
5675	M22332	Homo sapiens	unknown protein	121	43
5676	W40353	Homo sapiens	Human unspecified protein from US5702907.	128	72
5677	AL049868	Homo sapiens	dJ927M24.2 (K1AA1219)	403	95
5678	U31785	Human papillomavirus type 36	putative	103	44
5679	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	101	73
5680	AF068229	Homo sapiens	lysyl hydroxylase 3	148	92
5681	Y00358	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	209	81
5682	AB008515	Homo sapiens	RanBPM	142	100
5683	AB010692	Arabidopsis thaliana	contains similarity to endo-beta-N-acetylglucosaminidase-gene_id:K18I2.3.27	148	45
5684	J02459	bacteriophage lambda	J (tail:host specificity;1132)	746	100
5685	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	194	69
5686	AB049054	Homo sapiens	brain link protein-1	160	100
5687	AF229067	Homo sapiens	PADI-H protein	144	68
5688	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	120	70
5689	AP001313	Arabidopsis thaliana	contains similarity to pherophorin-gene_id:TSM7.14	106	47
5690	M76976	Drosophila melanogaster	dorsal-ventral patterning protein	167	37
5691	L24559	Homo sapiens	DNA polymerase alpha	175	100
5692	AF071777	Mus musculus	IRE1	604	85
5693	AF061741	Homo sapiens	retinal short-chain dehydrogenase/reductase retSDR1	704	99
5694	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	178	66
5695	AF092092	Homo sapiens	AP-3 adaptor complex mu3A subunit	653	92
5696	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	106	86
5697	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	132	75
5698	M64793	Rattus norvegicus	salivary proline-rich protein	116	40
5699	AF161361	Homo sapiens	HSPC098	128	56
5700	U21123	Drosophila melanogaster	ena polypeptide	106	57

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5701	AF119901	Homo sapiens	PRO2831	113	76
5702	K02576	Homo sapiens	salivary proline-rich protein 1	101	49
5703	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	105	78
5704	AF130089	Homo sapiens	PRO2550	122	75
5705	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	136	72
5706	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	113	75
5707	AF229067	Homo sapiens	PADI-H protein	134	81
5708	W40353	Homo sapiens	Human unspecified protein from US5702907.	129	65
5709	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	137	81
5710	AK024455	Homo sapiens	FLJ00047 protein	108	54
5711	Y76381	Homo sapiens	Fragment of human secreted protein encoded by gene 75.	247	93
5712	AF116715	Homo sapiens	PRO2829	118	75
5713	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	154	71
5714	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	141	79
5715	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	91	80
5716	AF090944	Homo sapiens	PRO0663	136	56
5717	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	153	65
5718	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	109	70
5719	AF130089	Homo sapiens	PRO2550	140	86
5720	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	144	67
5721	AF130089	Homo sapiens	PRO2550	146	58
5722	AF118086	Homo sapiens	PRO1992	130	58
5723	D21230	Homo sapiens	alpha 1(XV) collagen chain	390	78
5724	AL049569	Homo sapiens	dJ37C10.5 (KIAA0445)	266	93
5725	X04412	Homo sapiens	plasma gelsolin	761	95
5726	A21853	synthetic construct	serine protease inhibitor	206	100
5727	Y16610	Homo sapiens	paraplegin	218	95
5728	AF132021	Homo sapiens	myosin X	613	87
5729	AL163491	Arabidopsis thaliana	putative protein	236	46
5730	L19704	Homo sapiens	alternative first exon	561	86
5731	D83703	Homo sapiens	peroxisome assembly factor-2	240	84
5732	AB007936	Homo sapiens	KIAA0467 protein	189	77
5733	L38622	Mus musculus	mSin3B gene product	280	94
5734	AF051944	Gallus gallus	Xin	460	68
5735	B07857	Homo sapiens	Amino acid sequence of Smad1 interactor protein clone S1+12-5.	172	67
5736	Z14020	Nicotiana tabacum	Pistil extensin like protein, partial CDS only	105	44
5737	L17308	Gossypium hirsutum	proline-rich cell wall protein	145	34
5738	Y76141	Homo sapiens	Human secreted protein encoded by gene 18.	109	72
5739	AF178534	Homo sapiens	talin	583	82
5740	D13435	Homo sapiens	PIG-F	143	100
5741	AC005578	Homo sapiens	F20887_1, partial CDS	584	86

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5742	AC005578	Homo sapiens	F20887_1, partial CDS	470	85
5743	AJ010479	Homo sapiens	kinesin-like protein	102	23
5744	M19419	Mus musculus	proline-rich salivary protein	107	42
5745	U29377	Caenorhabditis elegans	lysine-rich	97	44
5746	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	90	67
5747	D84223	Homo sapiens	leucyl tRNA synthetase	165	83
5748	J04990	Homo sapiens	cathepsin G	165	100
5749	Y36203	Homo sapiens	Human secreted protein #75.	122	77
5750	V00488	Homo sapiens	alpha globin	181	94
5751	M18642	Homo sapiens	lactoferrin	122	96
5752	W15286	Homo sapiens	Soluble type I insulin-like growth factor receptor.	481	87
5753	Z98595	Schizosaccharomyces pombe	coronin-like protein	192	38
5754	AL035683	Homo sapiens	dJ1063B2.1 (Beta-1,4-galactosyltransferase)	239	100
5755	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	170	61
5756	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	105	61
5757	D49490	Homo sapiens	protein disulfide isomerase-related protein (PDIR)	669	96
5758	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	175	72
5759	X61451	Mus musculus	F41	130	100
5760	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	91	61
5761	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	130	76
5762	AF130079	Homo sapiens	PRO2852	126	61
5763	AF143946	Homo sapiens	transcriptional activator SRCAP	288	40
5764	M80627	Homo sapiens	helix-loop-helix protein	127	88
5765	AF038007	Homo sapiens	FIC1	290	47
5766	G01881	Homo sapiens	Human secreted protein, SEQ ID NO: 5962.	427	97
5767	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	172	75
5768	B12884	Homo sapiens	Human alpha-bradeion protein sequence.	465	70
5769	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	347	100
5770	AB033168	Mus musculus	nuclear protein ZAP	115	39
5771	X83575	Cricetulus griseus	CHO1 antigen	113	57
5772	AF135422	Homo sapiens	GDP-mannose pyrophosphorylase A	764	91
5773	L38644	Rattus norvegicus	karyopherin beta	121	68
5774	AB020746	Arabidopsis thaliana	protein kinase-like protein	107	33
5775	Y17920	Drosophila melanogaster	CALO protein	128	31
5776	AK000309	Homo sapiens	unnamed protein product	988	98
5777	AF010404	Homo sapiens	ALR	469	97
5778	AB045131	Homo sapiens	NADPH-dependent retinol dehydrogenase/reductase	126	92
5779	AF197927	Homo sapiens	AF5q31 protein	530	95
5780	X79198	Homo sapiens	host cell factor	119	74
5781	X69838	Homo sapiens	G9a	157	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5782	Y94450	Homo sapiens	Human inflammation associated protein #7.	227	44
5783	AF216804	Rattus norvegicus	nuclear matrix transcription factor	1539	98
5784	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	638	91
5785	AF000149	Mus musculus	ATP-binding cassette transporter	292	41
5786	D89974	Homo sapiens	glycosylphosphatidyl inositol-anchored protein GPI-80	490	78
5787	AF090942	Homo sapiens	PRO0657	132	63
5788	X56932	Homo sapiens	23 kD highly basic protein	286	100
5789	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	114	63
5790	Z97211	Schizosaccharomyces pombe	kinesin-like protein	346	60
5791	AF134707	Homo sapiens	disintegrin and metalloproteinase domain 19	144	95
5792	Z19550	Homo sapiens	N-acetylglucosaminidase beta-1,6-N-acetylglucosaminyltransferase	547	76
5793	AF090930	Homo sapiens	PRO0478	103	80
5794	Y59879	Homo sapiens	Human normal uterus tissue derived protein 42.	407	97
5795	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	149	72
5796	AF077208	Homo sapiens	HSPC022	682	100
5797	D42138	Homo sapiens	PIG-B	597	86
5798	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	151	75
5799	M29487	Homo sapiens	integrin alpha subunit precursor	160	80
5800	D87438	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	354	85
5801	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	195	97
5802	AB030176	Homo sapiens	peptidylarginine deiminase type II	107	100
5803	D38441	Homo sapiens	acylamino acid-releasing enzyme	156	71
5804	Y55939	Homo sapiens	Human GEK2 protein.	157	96
5805	X89626	Bos taurus	240K protein of rod photoreceptor cng-channel	92	42
5806	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	177	38
5807	Y86275	Homo sapiens	Human secreted protein HSRGW16, SEQ ID NO:190.	436	77
5808	D50577	Mesocricetus auratus	carboxylesterase precursor	328	55
5809	AF272148	Homo sapiens	KRAB zinc finger protein	593	68
5810	W57260	Homo sapiens	Human semaphorin Y.	651	96
5811	AF202893	Mus musculus	Klf21b	491	82
5812	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	219	38
5813	AB017114	Homo sapiens	AD 3	142	57
5814	AC007954	Homo sapiens	unknown	678	100
5815	AF124726	Homo sapiens	acinusL	790	93
5816	AB015330	Homo sapiens	HRJHFB2007	167	36
5817	AB020684	Homo sapiens	KIAA0877 protein	699	57
5818	Z15025	Homo sapiens	Bat2	172	49
5819	X95761	Mus musculus	new:Rhobin	549	79
5820	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	166	68
5821	X55126	Mus musculus	Zfp-29	633	93
5822	Y99366	Homo sapiens	Human PRO1475 (UNQ746) amino	452	98

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			acid sequence SEQ ID NO:88.		
5823	AB040801	Homo sapiens	SREB3	611	95
5824	M27878	Homo sapiens	DNA binding protein	462	64
5825	Y13620	Homo sapiens	BCL9	140	40
5826	AF152510	Homo sapiens	protocadherin gamma A3 short form protein	525	92
5827	M23451	Achlya ambisexualis	steroid receptor	337	61
5828	AJ011305	Homo sapiens	guanine nucleotide exchange factor, delta subunit	132	100
5829	Y85565	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/2) sequence.	710	96
5830	U03277	Drosophila melanogaster	cloned by ability to arrest the cell cycle when expressed in the fission yeast Schizosaccharomyces pombe	258	46
5831	AF193342	Mus musculus	GCN2alpha	469	85
5832	AF279265	Homo sapiens	putative anion transporter 1	240	91
5833	AK023998	Homo sapiens	unnamed protein product	687	97
5834	AK023998	Homo sapiens	unnamed protein product	674	96
5835	AF071059	Mus musculus	zinc finger RNA binding protein	243	100
5836	AF178534	Homo sapiens	talin	463	62
5837	J04569	Homo sapiens	glial fibrillary acidic protein	102	55
5838	AF068625	Mus musculus	DNA cytosine-5 methyltransferase 3A	130	89
5839	AB037739	Homo sapiens	KIAA1318 protein	644	97
5840	R86865	Homo sapiens	Human protocadherin pc3.	660	96
5841	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	117	84
5842	X51486	Gallus gallus	cNFI-A1 protein (AA 1-522)	590	86
5843	U65785	Homo sapiens	150 kDa oxygen-regulated protein ORP150	200	95
5844	U16126	Homo sapiens	EAA4	679	97
5845	AL035071	Homo sapiens	dJ1085F17.1.3 (ortholog of mouse DNMT3B (DNA Cytosine-5 Methyltransferase 3B3) (isoform 3))	717	100
5846	Y13620	Homo sapiens	BCL9	505	81
5847	AC004812	Homo sapiens	similar to human HsGCN1 U77700 (PID:g2282576); similar to yeast translation activator GCN1 (PID:g462168)	316	100
5848	M77246	Rattus norvegicus	beta-chain clathrin associated protein complex AP-2	611	89
5849	AF007833	Homo sapiens	kruppel-related zinc finger protein hcKrox	569	79
5850	AF056617	Homo sapiens	BWSCR2 associated zinc-finger protein BAZ1	175	32
5851	D38548	Homo sapiens	The ha0936 gene product is novel.	409	65
5852	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	166	55
5853	D87071	Homo sapiens	similar to C.elegans protein encoded in cosmid T20D3 (Z68220).	188	76
5854	M64979	Homo sapiens	glial factor-1	557	83
5855	G01480	Homo sapiens	Human secreted protein, SEQ ID NO: 5561.	400	82
5856	X06345	Xenopus laevis	lamin A (AA 1-265)	109	68
5857	AB017499	Oryctolagus cuniculus	Lipoprotein Receptor Related Protein 5	196	40
5858	D43633	Oryzias latipes	G protein-coupled seven-transmembrane receptor	281	50
5859	AF067165	Homo sapiens	zinc finger protein 3	669	87

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5860	AL031118	Homo sapiens	dJ153G14.3 (novel C2H2 type Zinc Finger protein)	218	38
5861	U13897	Homo sapiens	homolog of Drosophila discs large protein, isoform 1	130	35
5862	M74002	Homo sapiens	arginine-rich nuclear protein	80	23
5863	X67855	Oryctolagus cuniculus	brain calcium channel BII-1	147	66
5864	U35376	Homo sapiens	repressor transcriptional factor	475	67
5865	AF251038	Homo sapiens	GAP-like protein	325	58
5866	L46815	Mus musculus	DNA binding protein Rc	409	66
5867	S68944	Rattus sp.	Na+/Cl(-)-dependent neurotransmitter transporter	582	95
5868	X97675	Homo sapiens	plakophilin 2b	159	93
5869	AF152478	Homo sapiens	protocadherin alpha 13 short form protein	680	100
5870	AF118082	Homo sapiens	PRO1902	130	48
5871	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	149	49
5872	A61971	unidentified	MCSP	621	82
5873	Z54206	Bovine herpesvirus 1	UL51	104	33
5874	AF069765	Homo sapiens	signal recognition particle 72	674	97
5875	AF179428	Homo sapiens	DNA polymerase zeta catalytic subunit variant 1	692	100
5876	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	119	48
5877	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	446	98
5878	L08811	Drosophila melanogaster	adherin	264	42
5879	D86983	Homo sapiens	similar to D.melanogaster peroxidase(U11052)	429	100
5880	AF152508	Homo sapiens	protocadherin gamma A2 short form protein	664	100
5881	AF152508	Homo sapiens	protocadherin gamma A2 short form protein	660	98
5882	AF190018	Mus musculus	K-Cl cotransporter	199	88
5883	AB023229	Homo sapiens	KIAA1012 protein	107	83
5884	U53420	Rattus norvegicus	sodium-calcium exchanger form 3	595	98
5885	AF039019	Homo sapiens	zinc finger DNA binding protein 89 kDa	608	92
5886	AF207661	Homo sapiens	sodium bicarbonate cotransporter-like protein	701	100
5887	AF130051	Homo sapiens	PRO0898	115	74
5888	AF152508	Homo sapiens	protocadherin gamma A2 short form protein	720	100
5889	AF251079	Homo sapiens	heptacellular carcinoma novel gene-3 protein	741	98
5890	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	118	51
5891	AF157326	Homo sapiens	TIP120 protein	571	85
5892	AF129170	Homo sapiens	apolipoprotein E receptor 2	630	99
5893	X05561	Homo sapiens	alpha-1 chain precursor (AA -27 to 917) (2953 is 2nd base in codon)	197	45
5894	AJ238374	Homo sapiens	putative protein TH1	641	96
5895	X63526	Homo sapiens	homologue to elongation factor 1-gamma from A.salina	709	97
5896	Y11651	Homo sapiens	phosphate cyclase	521	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5897	Y18448	Homo sapiens	Bassoon protein	681	100
5898	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	138	63
5899	AF152473	Homo sapiens	protocadherin alpha C1 short form protein	733	100
5900	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	133	66
5901	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	522	99
5902	X12928	Triticum aestivum	HMW glutenin subunit 5 (AA 1-848)	169	25
5903	X61048	Hydra sp.	mini-collagen	88	33
5904	AF118082	Homo sapiens	PRO1902	247	60
5905	A00279	synthetic construct	Human serum albumin	482	84
5906	T14722_cd1	Homo sapiens	01-DEC-1992 Human CD27 antigen cDNA.	431	94
5907	Y73475	Homo sapiens	Human secreted protein clone ye7_1 protein sequence SEQ ID NO:172.	271	94
5908	AF175265	Homo sapiens	vacuolar sorting protein 35	645	92
5909	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	125	50
5910	G00360	Homo sapiens	Human secreted protein, SEQ ID NO: 4441.	115	58
5911	W88762	Homo sapiens	Polypeptide fragment encoded by gene 20.	152	50
5912	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	154	68
5913	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	209	71
5914	AB046048	Macaca fascicularis	unnamed portein product	143	49
5915	S80644	Sus scrofa	glutaminase; GA	338	85
5916	AF213393	Mus musculus	ATP-binding cassette protein	92	95
5917	X52622	Mus musculus	integrase (409 AA)	425	45
5918	U49973	Homo sapiens	ORF2: function unknown	114	64
5919	S71403	Mus musculus	m33-A isoform	120	42
5920	AF090931	Homo sapiens	PRO0483	94	89
5921	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	99	36
5922	AJ006770	Cicer arietinum	extensin	96	32
5923	AJ250193	Mus musculus	muscle protein 637	730	72
5924	AF229067	Homo sapiens	PADI-H protein	278	63
5925	X92485	Plasmodium vivax	pva1	99	50
5926	G03714	Homo sapiens	Human secreted protcin, SEQ ID NO: 7795.	84	66
5927	AF130089	Homo sapiens	PRO2550	114	64
5928	J00126	Homo sapiens	MHC factor B	237	100
5929	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	251	79
5930	AF090895	Homo sapiens	PRO0117	63	62
5931	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	147	37
5932	U83857	Homo sapiens	Aac11	209	80
5933	AF068294	Homo sapiens	HDCMB45P	144	50
5934	X92485	Plasmodium vivax	pva1	135	69
5935	L07545	Leishmania tarentolae	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to	127	36

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gel compression		
5936	R95913	Homo sapiens	Neural thread protein.	276	58
5937	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	130	65
5938	Y16781	Homo sapiens	Human secreted protein (clone bh157.7).	1258	100
5939	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	167	68
5940	U93570	Homo sapiens	putative p150	103	41
5941	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	189	74
5942	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	110	47
5943	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	122	90
5944	AF130089	Homo sapiens	PRO2550	101	48
5945	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	162	86
5946	X92485	Plasmodium vivax	pval	104	70
5947	M29622	Mus musculus	open reading frame 2	132	64
5948	AF130089	Homo sapiens	PRO2550	131	60
5949	AF130089	Homo sapiens	PRO2550	151	60
5950	AF130079	Homo sapiens	PRO2852	117	52
5951	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	185	62
5952	U49973	Homo sapiens	ORF2: function unknown	160	62
5953	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	145	55
5954	M22332	Homo sapiens	unknown protein	169	41
5955	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	133	72
5956	U70935	Peromyscus maniculatus	reverse transcriptase	100	36
5957	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	105	63
5958	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	112	48
5959	Z49944	Canis familiaris	CDC42 GTP-binding protein	120	40
5960	AF118082	Homo sapiens	PRO1902	158	61
5961	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	91	65
5962	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	121	62
5963	AF118082	Homo sapiens	PRO1902	113	60
5964	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	65
5965	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	120	57
5966	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	306	77
5967	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	80	41
5968	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	109	75
5969	AF119855	Homo sapiens	PRO1847	162	72
5970	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	146	46
5971	M19155	Plasmodium falciparum	S-antigen precursor	122	37
5972	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	121	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5973	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	107	60
5974	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	83	68
5975	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	111	47
5976	U93572	Homo sapiens	p40	112	33
5977	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	58
5978	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	120	70
5979	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	106	54
5980	M64792	Rattus norvegicus	salivary proline-rich protein	105	31
5981	X66285	Mus musculus	HC1 ORF	86	36
5982	M64793	Rattus norvegicus	salivary proline-rich protein	110	43
5983	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	131	60
5984	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	110	60
5985	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	107	47
5986	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	160	77
5987	AF130079	Homo sapiens	PRO2852	272	77
5988	U93570	Homo sapiens	putative p150	87	46
5989	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	202	89
5990	AF130089	Homo sapiens	PRO2550	238	74
5991	AF118082	Homo sapiens	PRO1902	119	41
5992	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	60
5993	L27428	Homo sapiens	reverse transcriptase	110	60
5994	S79410	Mus musculus	nuclear localization signal binding protein	98	45
5995	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	90
5996	X58236	Homo sapiens	36/8-8 fusion protein with epitope for anti-lectin antibody	78	68
5997	Y08061	Homo sapiens	Human c-myc protein fragment.	97	63
5998	AP002460	Arabidopsis thaliana	gene_id:F1D9.26-unknown protein	100	38
5999	U93569	Homo sapiens	p40	103	52
6000	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	100	63
6001	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	121	51
6002	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	64
6003	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	105	40
6004	AF130089	Homo sapiens	PRO2550	122	63
6005	R5913	Homo sapiens	Neural thread protein.	235	56
6006	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	173	58
6007	X92485	Plasmodium vivax	pva1	96	53

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6008	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	236	62
6009	Y17832	Human endogenous retrovirus K	env protein	103	66
6010	AF119900	Homo sapiens	PRO2822	91	50
6011	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	155	55
6012	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	201	91
6013	Y36156	Homo sapiens	Human secreted protein #28.	253	70
6014	AF130079	Homo sapiens	PRO2852	119	36
6015	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	63
6016	AF130089	Homo sapiens	PRO2550	110	40
6017	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	57
6018	AF116661	Homo sapiens	PRO1438	147	69
6019	AF130089	Homo sapiens	PRO2550	169	71
6020	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	208	60
6021	AF119851	Homo sapiens	PRO1722	147	65
6022	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	139	47
6023	AF130089	Homo sapiens	PRO2550	142	66
6024	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	76
6025	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	103	48
6026	D86853	Catharanthus roseus	extensin	97	46
6027	AF130089	Homo sapiens	PRO2550	95	47
6028	X92485	Plasmodium vivax	pval	102	61
6029	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	149	53
6030	G00643	Homo sapiens	Human secreted protein, SEQ ID NO: 4724.	96	76
6031	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	144	44
6032	AB011483	Arabidopsis thaliana	contains similarity to root cap protein-gene id:MUF9.16	117	37
6033	X92485	Plasmodium vivax	pval	85	40
6034	AF118082	Homo sapiens	PRO1902	112	58
6035	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	121	59
6036	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	65
6037	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	107	71
6038	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	140	65
6039	X92485	Plasmodium vivax	pval	84	78
6040	AF130051	Homo sapiens	PRO0898	107	69
6041	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	113	58
6042	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	209	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6043	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	98	56
6044	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	126	43
6045	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	65
6046	Y36156	Homo sapiens	Human secreted protein #28.	93	62
6047	AF130079	Homo sapiens	PRO2852	205	83
6048	R95913	Homo sapiens	Neural thread protein.	148	45
6049	D38112	Homo sapiens	cytochrome c oxidase subunit 3	234	86
6050	D38113	Pan troglodytes	NADH dehydrogenase subunit 5	403	61
6051	M11901	Rattus norvegicus	proline-rich salivary protein	96	42
6052	AF130089	Homo sapiens	PRO2550	348	73
6053	AF119851	Homo sapiens	PRO1722	109	68
6054	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	168	66
6055	AF161356	Homo sapiens	HSPC093	83	58
6056	X92485	Plasmodium vivax	pval	155	55
6057	G04000	Homo sapiens	Human secreted protein, SEQ ID NO: 8081.	520	100
6058	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	148	65
6059	W03626	Homo sapiens	Human thyrotropin GPR N-terminal sequence.	163	53
6060	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	300	68
6061	U93563	Homo sapiens	putative p150	389	37
6062	AF090895	Homo sapiens	PRO0117	66	78
6063	X92485	Plasmodium vivax	pval	110	86
6064	AF130089	Homo sapiens	PRO2550	166	71
6065	M22332	Homo sapiens	unknown protein	188	48
6066	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	101	52
6067	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	107	41
6068	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	99	75
6069	M22332	Homo sapiens	unknown protein	153	80
6070	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	82
6071	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	123	73
6072	AF130079	Homo sapiens	PRO2852	143	60
6073	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	132	55
6074	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	158	65
6075	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	157	68
6076	AF116712	Homo sapiens	PRO2738	102	41
6077	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	102	69
6078	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	109	60
6079	AF118082	Homo sapiens	PRO1902	196	61
6080	AF118082	Homo sapiens	PRO1902	165	59
6081	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	153	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6082	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	188	71
6083	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	109	60
6084	V00672	Pan (troglodytes	reading frame protein 4	185	85
6085	AF130051	Homo sapiens	PRO0898	307	67
6086	AF130079	Homo sapiens	PRO2852	96	72
6087	D38112	Homo sapiens	NADH dehydrogenase subunit 1	171	82
6088	AF090895	Homo sapiens	PRO0117	110	67
6089	U43360	Peromyscus maniculatus	reverse transcriptase	101	46
6090	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	114	36
6091	Y02925	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	111	46
6092	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	137	54
6093	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	176	59
6094	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	199	50
6095	U70935	Peromyscus maniculatus	reverse transcriptase	216	44
6096	X71442	Rattus norvegicus	ORF 1; putative	109	53
6097	AF119855	Homo sapiens	PRO1847	88	71
6098	L27428	Homo sapiens	reverse transcriptase	104	45
6099	AF090895	Homo sapiens	PRO0117	119	61
6100	U52077	Homo sapiens	mariner transposase	295	67
6101	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	156	73
6102	M22332	Homo sapiens	unknown protein	132	44
6103	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	140	56
6104	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	64	47
6105	M64791	Rattus norvegicus	salivary proline-rich protein	123	41
6106	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	139	69
6107	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	75	58
6108	AF068294	Homo sapiens	HDCMB45P	141	43
6109	AF118086	Homo sapiens	PRO1992	160	77
6110	M63819	Plasmodium falciparum	malaria antigen	62	46
6111	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	130	65
6112	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	282	70
6113	AF119851	Homo sapiens	PRO1722	156	63
6114	AF229067	Homo sapiens	PADI-H protein	134	48
6115	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	143	44
6116	D38112	Homo sapiens	cytochrome c oxidase subunit 1	201	80
6117	AF285567	Microcebus griseorufus	cytochrome b	185	58
6118	AL138656	Arabidopsis thaliana	extensin precursor-like protein	141	28
6119	X92485	Plasmodium vivax	pval	165	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6120	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	164	84
6121	M13100	Rattus norvegicus	unknown protein	176	49
6122	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	177	50
6123	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	83	71
6124	AF130089	Homo sapiens	PRO2550	109	85
6125	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	129	70
6126	AF144054	Homo sapiens	apoptosis related protein APR-4	149	54
6127	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	138	70
6128	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	236	77
6129	U93564	Homo sapiens	putative p150	152	53
6130	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	129	57
6131	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	56
6132	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	195	67
6133	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	92	42
6134	AK000496	Homo sapiens	unnamed protein product	158	59
6135	X92485	Plasmodium vivax	pva1	146	55
6136	Y36203	Homo sapiens	Human secreted protein #75.	133	57
6137	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	148	68
6138	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	106	36
6139	AF130051	Homo sapiens	PRO0898	77	65
6140	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	222	73
6141	AF119851	Homo sapiens	PRO1722	107	63
6142	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	117	57
6143	R95913	Homo sapiens	Neural thread protein.	114	70
6144	AF068294	Homo sapiens	HDCMB45P	123	56
6145	AF118082	Homo sapiens	PRO1902	113	32
6146	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	105	42
6147	Y30731	Homo sapiens	Amino acid sequence of a human secreted protein.	938	100
6148	U93574	Homo sapiens	putative p150	99	47
6149	AF090894	Homo sapiens	PRO0113	145	55
6150	AF130079	Homo sapiens	PRO2852	125	49
6151	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	48
6152	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	89	60
6153	Y01398	Homo sapiens	Secreted protein encoded by gene 16 clone HNGFR75.	90	82
6154	X92485	Plasmodium vivax	pva1	110	42
6155	S79410	Mus musculus	nuclear localization signal binding protein	118	48
6156	G01495	Homo sapiens	Human secreted protein, SEQ ID NO:	170	89

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6157	X92485	Plasmodium vivax	5576. pval	157	52
6158	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	108	58
6159	U36794	Coturnix japonica	Cytochrome oxidase subunit I	70	73
6160	AF118082	Homo sapiens	PRO1902	119	66
6161	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	154	64
6162	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	107	37
6163	M22332	Homo sapiens	unknown protein	125	51
6164	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	163	59
6165	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	235	64
6166	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	108	36
6167	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	139	59
6168	D38112	Homo sapiens	cytochrome c oxidase subunit 3	562	85
6169	D38113	Pan troglodytes	NADH dehydrogenase subunit 4	296	51
6170	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	95	85
6171	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	329	73
6172	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	136	53
6173	K03206	Homo sapiens	salivary proline-rich protein precursor	104	36
6174	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	75
6175	U93569	Homo sapiens	p40	192	40
6176	X70343	Nicotiana sylvestris	extensin	94	35
6177	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	140	81
6178	AF119855	Homo sapiens	PRO1847	114	43
6179	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	98	68
6180	X03717	Homo sapiens	pot. unidentified reading frame	112	42
6181	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	204	76
6182	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	110	73
6183	D38112	Homo sapiens	NADH dehydrogenase subunit 3	240	88
6184	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	102	47
6185	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	99	49
6186	Y36156	Homo sapiens	Human secreted protein #28.	196	75
6187	AF169387	Mus musculus	alpha 3 collagen IV	111	38
6188	AF194537	Homo sapiens	NAGI3	138	37
6189	X91836	Vigna unguiculata	extensin class 1 protein	167	33
6190	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	175	63
6191	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	123	46
6192	X92485	Plasmodium	pval	115	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
6193	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	345	65
6194	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	82	54
6195	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	214	56
6196	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	87	79
6197	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	118	41
6198	X62691	Homo sapiens	ribosomal protein homologous to yeast S24	215	73
6199	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	100	46
6200	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	143	73
6201	V00711	Mus musculus	cytochrome oxidase I	435	92
6202	U93572	Homo sapiens	putative p150	99	63
6203	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	109	45
6204	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	163	39
6205	M15530	Homo sapiens	B-cell growth factor	113	60
6206	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	128	50
6207	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	181	72
6208	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	75
6209	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	120	62
6210	Y36203	Homo sapiens	Human secreted protein #75.	169	81
6211	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	52
6212	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	123	48
6213	D86854	Catharanthus roseus	extensin	120	44
6214	G02754	Homo sapiens	Human secreted protein, SEQ ID NO: 6835.	117	100
6215	W33698	Homo sapiens	AL-2-long (AL-2l) protein.	262	100
6216	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	102	62
6217	U40342	Mus musculus	ninein	77	72
6218	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	174	49
6219	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	234	54
6220	X92485	Plasmodium vivax	pva1	107	46
6221	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	104	40
6222	X86029	Vigna unguiculata	extensin-like protein	140	35
6223	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	216	59
6224	AF068294	Homo sapiens	HDCMB45P	164	60
6225	Y50797	Homo sapiens	Human calmodulin/NEF protein binding inhibitor 2.	135	50
6226	AE003859	Xylella fastidiosa	hypothetical protein	139	41
6227	G00637	Homo sapiens	Human secreted protein, SEQ ID NO:	103	58

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4718.		
6228	AF130089	Homo sapiens	PRO2550	126	43
6229	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	190	88
6230	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	77
6231	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	79
6232	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	78
6233	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	164	67
6234	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	288	94
6235	AF113685	Homo sapiens	PRO0974	114	46
6236	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	150	40
6237	AL096844	Streptomyces coelicolor A3(2)	putative integral membrane protein	88	39
6238	AF130079	Homo sapiens	PRO2852	167	50
6239	AF130089	Homo sapiens	PRO2550	365	85
6240	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	212	69
6241	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	102	54
6242	AF109907	Homo sapiens	S164	146	90
6243	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	132	52
6244	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	52
6245	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	113	32
6246	AF130089	Homo sapiens	PRO2550	154	77
6247	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	91	40
6248	Y36156	Homo sapiens	Human secreted protein #28.	105	43
6249	AF116661	Homo sapiens	PRO1438	131	60
6250	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	68
6251	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	70	73
6252	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	106	42
6253	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	247	68
6254	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	75
6255	V00662	Homo sapiens	cytochrome oxidase I	355	78
6256	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	131	65
6257	D38112	Homo sapiens	cytochrome c oxidase subunit I	176	86
6258	AF061340	Artibeus jamaicensis	cytochrome c oxidase subunit III	308	63
6259	AF016099	Mus musculus	endonuclease/reverse transcriptase	114	43
6260	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	179	78
6261	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	192	75
6262	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	71
6263	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	114	37
6264	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	88	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6265	U49974	Homo sapiens	mariner transposase	206	71
6266	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	71	72
6267	AF097473	Mus musculus	ORF1	86	40
6268	X70343	Nicotiana sylvestris	extensin	95	33
6269	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	84
6270	L27428	Homo sapiens	reverse transcriptase	132	48
6271	AF118082	Homo sapiens	PRO1902	153	53
6272	U12690	Homo sapiens	cytochrome oxidase subunit II	222	91
6273	X03145	Homo sapiens	pot. ORF V	89	35
6274	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	90	71
6275	U93572	Homo sapiens	p40	83	43
6276	AF058700	Bos taurus	ubiquitin-S27a fusion protein	148	70
6277	AF016099	Mus musculus	endonuclease/reverse transcriptase	96	65
6278	AF130079	Homo sapiens	PRO2852	179	86
6279	AF161356	Homo sapiens	HSPC093	108	57
6280	X77816	Rattus norvegicus	PR-Vbeta1	109	51
6281	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	130	58
6282	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	81	69
6283	AF068294	Homo sapiens	HDCMB45P	98	37
6284	AF116715	Homo sapiens	PRO2829	112	68
6285	X92485	Plasmodium vivax	pva1	92	64
6286	U93570	Homo sapiens	p40	90	38
6287	Y36203	Homo sapiens	Human secreted protein #75.	225	62
6288	Z11793	Homo sapiens	selenoprotein P	220	65
6289	X92485	Plasmodium vivax	pva1	125	70
6290	X52634	Mus musculus	tlm protein	114	45
6291	M11901	Rattus norvegicus	proline-rich salivary protein	94	36
6292	AF116661	Homo sapiens	PRO1438	144	46
6293	L27428	Homo sapiens	reverse transcriptase	81	44
6294	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	152	51
6295	AF130089	Homo sapiens	PRO2550	137	35
6296	L27428	Homo sapiens	reverse transcriptase	96	53
6297	B01372	Homo sapiens	Neuron-associated protein.	134	69
6298	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	110	38
6299	AF130089	Homo sapiens	PRO2550	110	61
6300	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	136	63
6301	AF220264	Homo sapiens	MOST-1	172	90
6302	AF130079	Homo sapiens	PRO2852	311	71
6303	AF068294	Homo sapiens	HDCMB45P	136	53
6304	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	110	62
6305	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	113	45
6306	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	166	58

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6307	S85655	Homo sapiens	prohibitin	664	91
6308	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	155	64
6309	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	73
6310	AF119851	Homo sapiens	PRO1722	160	67
6311	L27428	Homo sapiens	reverse transcriptase	91	50
6312	AF130089	Homo sapiens	PRO2550	140	55
6313	AF130089	Homo sapiens	PRO2550	211	68
6314	X15917	Paramecium aurelia	ORF4 protein (AA 1-156)	97	38
6315	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	94	51
6316	Y36203	Homo sapiens	Human secreted protein #75.	124	65
6317	L27428	Homo sapiens	reverse transcriptase	117	56
6318	M11900	Mus musculus	15-kDa proline-rich salivary protein	105	41
6319	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	69
6320	U92673	Eurythmes sp. 'AUS-3F'	cytochrome oxidase I	59	37
6321	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	283	72
6322	AK000496	Homo sapiens	unnamed protein product	206	70
6323	AB047934	Macaca fascicularis	hypothetical protein	173	68
6324	AB023485	Mus musculus	transcription factor CA150b	131	43
6325	AF020262	Bos taurus	general protein transport factor p16	76	67
6326	U22376	Homo sapiens	alternatively spliced product using exon 13A	98	57
6327	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	115	60
6328	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	100	57
6329	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	67
6330	U43360	Peromyscus maniculatus	reverse transcriptase	82	63
6331	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	57
6332	K01664	Drosophila melanogaster	Bkm-like protein	112	37
6333	M69297	Homo sapiens	ORF 3	70	43
6334	U15647	Mus musculus	reverse transcriptase	146	53
6335	AF090894	Homo sapiens	PRO0113	107	48
6336	AF130089	Homo sapiens	PRO2550	359	75
6337	AJ271872	Nicotiana glauca	extensin	134	32
6338	AJ132694	Homo sapiens	small GTPase rac1b	99	100
6339	AF119851	Homo sapiens	PRO1722	123	60
6340	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	215	56
6341	U83774	Felis concolor	cytochrome oxidase I	193	80
6342	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	139	62
6343	X92485	Plasmodium vivax	pva1	104	81
6344	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	110	64
6345	U93572	Homo sapiens	p40	79	48
6346	X92485	Plasmodium	pva1	156	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
6347	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	104	85
6348	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	158	77
6349	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	89	64
6350	AF130089	Homo sapiens	PRO2550	187	69
6351	U56732	Rattus norvegicus	KRAB/zinc finger suppressor protein 1	161	64
6352	U70932	Peromyscus leucopus	reverse transcriptase	126	61
6353	X55687	Lycopersicon esculentum	extensin (class II)	89	44
6354	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	107	57
6355	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	88	76
6356	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	98	61
6357	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	165	51
6358	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	214	58
6359	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	75	88
6360	X07882	Homo sapiens	Po protein	151	47
6361	Z11592	Phytophthora parasitica	cytochrome c oxidase subunit 3	78	76
6362	AF090944	Homo sapiens	PRO0663	130	46
6363	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	39
6364	AF229067	Homo sapiens	PADI-H protein	155	75
6365	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	100	55
6366	AK024501	Homo sapiens	FLJ00110 protein	282	100
6367	AF118082	Homo sapiens	PRO1902	157	57
6368	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	151	63
6369	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	161	96
6370	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	124	63
6371	AF130079	Homo sapiens	PRO2852	297	77
6372	X92485	Plasmodium vivax	pva1	129	42
6373	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	122	63
6374	AF119851	Homo sapiens	PRO1722	251	65
6375	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	139	73
6376	X70343	Nicotiana sylvestris	extensin	104	35
6377	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	70	52
6378	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	97	69
6379	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	109	51
6380	Z38128	Mus musculus	histone H1	113	36
6381	U93573	Homo sapiens	p40	212	43

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6382	K02576	Homo sapiens	salivary proline-rich protein 1	109	40
6383	AL096744	Homo sapiens	hypothetical protein	164	49
6384	AF220264	Homo sapiens	MOST-1	119	56
6385	X92485	Plasmodium vivax	pva1	108	65
6386	X53581	Rattus norvegicus	ORF4	148	36
6387	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	116	52
6388	M13100	Rattus norvegicus	unknown protein	119	48
6389	AB047948	Macaca fascicularis	hypothetical protein	80	33
6390	X53581	Rattus norvegicus	ORF4	139	55
6391	AK025947	Homo sapiens	unnamed protein product	166	52
6392	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	244	75
6393	M22332	Homo sapiens	unknown protein	166	39
6394	AF229067	Homo sapiens	PADI-H protein	128	59
6395	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	80	70
6396	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	95	44
6397	M26361	Mus musculus	LINE/Ig H-chain fusion protein	97	61
6398	AF118082	Homo sapiens	PRO1902	93	48
6399	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	116	89
6400	U93570	Homo sapiens	putative p150	88	43
6401	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	147	61
6402	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	77	56
6403	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	156	47
6404	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	155	56
6405	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	88	39
6406	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	84	68
6407	G00560	Homo sapiens	Human secreted protein, SEQ ID NO: 4641.	244	90
6408	L27428	Homo sapiens	reverse transcriptase	108	42
6409	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	136	58
6410	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	106	44
6411	U70935	Peromyscus maniculatus	reverse transcriptase	154	40
6412	AF090931	Homo sapiens	PRO0483	99	85
6413	AL031186	Homo sapiens	bK984G1.1 (supported by FGENES)	249	78
6414	AF130089	Homo sapiens	PRO2350	100	55
6415	AB047963	Macaca fascicularis	hypothetical protein	165	57
6416	M22332	Homo sapiens	unknown protein	111	42
6417	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	140	50
6418	AF016099	Mus musculus	endonuclease/reverse transcriptase	147	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6419	D38112	Homo sapiens	NADH dehydrogenase subunit 1	194	84
6420	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	144	81
6421	U49973	Homo sapiens	ORF2: function unknown	91	62
6422	G02754	Homo sapiens	Human secreted protein, SEQ ID NO: 6835.	135	96
6423	AF072508	Homo sapiens	envelope protein	128	49
6424	AK000385	Homo sapiens	unnamed protein product	161	54
6425	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	148	54
6426	X92485	Plasmodium vivax	pval	103	75
6427	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	183	80
6428	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	97	46
6429	AF016099	Mus musculus	endonuclease/reverse transcriptase	100	51
6430	Y36203	Homo sapiens	Human secreted protein #75.	139	58
6431	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	112	47
6432	X92485	Plasmodium vivax	pval	83	72
6433	Y35984	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO: 233.	121	59
6434	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	66	43
6435	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	152	51
6436	D89501	Homo sapiens	similar to salivary proline-rich protein P-B	88	38
6437	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	113	58
6438	X99467	Medicago truncatula	ENOD20	110	37
6439	Y86574	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:491.	129	58
6440	X92485	Plasmodium vivax	pval	114	46
6441	AK024455	Homo sapiens	FLJ00047 protein	173	57
6442	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	85	51
6443	Y36203	Homo sapiens	Human secreted protein #75.	104	56
6444	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	138	50
6445	M24732	Homo sapiens	lamin-like protein	71	45
6446	AF119851	Homo sapiens	PRO1722	163	69
6447	AF126163	Homo sapiens	HHLA3 protein	98	53
6448	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	151	58
6449	AF200187	cercopithecine herpesvirus 15	EBNA2-like protein	125	38
6450	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	107	52
6451	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	114	54
6452	AF090942	Homo sapiens	PRO0657	129	65
6453	M19503	Homo sapiens	ORF1; putative	86	39
6455	X92485	Plasmodium vivax	pval	99	40

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6456	X86030	Vigna unguiculata	extensin-like protein	115	36
6457	Y08061	Homo sapiens	Human c-myc protein fragment.	113	61
6458	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	90	37
6459	AF119851	Homo sapiens	PRO1722	243	66
6460	J05497	Rattus norvegicus	snRNP-associated polypeptide N	101	31
6461	AF130089	Homo sapiens	PRO2550	183	76
6462	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	93	53
6463	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	122	72
6464	Y36156	Homo sapiens	Human secreted protein #28.	85	52
6465	AL160493	Leishmania major	probable (hbv-6) u1102, variant a DNA, complete virion genome	120	40
6466	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	94	36
6467	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	96	58
6468	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	121	67
6469	X92485	Plasmodium vivax	pva1	89	72
6470	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	128	56
6471	AF130089	Homo sapiens	PRO2550	155	83
6472	U93569	Homo sapiens	putative p150	131	42
6473	AF130079	Homo sapiens	PRO2852	111	54
6474	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	115	51
6475	AF220264	Homo sapiens	MOST-1	111	58
6476	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	137	45
6477	AF016099	Mus musculus	endonuclease/reverse transcriptase	106	35
6478	X92485	Plasmodium vivax	pva1	220	55
6480	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	112	61
6481	U49973	Homo sapiens	ORF2: function unknown	96	42
6482	U15647	Mus musculus	reverse transcriptase	111	61
6483	X92485	Plasmodium vivax	pva1	181	49
6484	L27428	Homo sapiens	reverse transcriptase	135	50
6485	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	144	52
6486	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	174	63
6487	U93569	Homo sapiens	p40	176	53
6488	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	72	42
6489	L26953	Homo sapiens	chromosomal protein	93	33
6490	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	125	57
6491	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	70
6492	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	251	75
6493	U15647	Mus musculus	reverse transcriptase	100	40

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6494	AK027208	Homo sapiens	unnamed protein product	109	68
6495	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	52
6496	AF130089	Homo sapiens	PRO2550	230	69
6497	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	237	62
6498	AF090894	Homo sapiens	PRO0113	140	68
6499	Y03000	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	138	84
6500	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	123	69
6501	M69297	Homo sapiens	ORF 3	87	58
6502	M22332	Homo sapiens	unknown protein	81	44
6503	X92485	Plasmodium vivax	pval	111	52
6504	AF090895	Homo sapiens	PRO0117	131	60
6505	Y73932	Homo sapiens	Human prostate tumor EST fragment derived protein #119.	97	69
6506	U93568	Homo sapiens	putative p150	122	32
6507	X86029	Vigna unguiculata	extensin-like protein	177	32
6508	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	282	60
6509	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	142	61
6510	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	93	35
6511	U52077	Homo sapiens	mariner transposase	372	73
6512	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	81	50
6513	AF090928	Homo sapiens	PRO0470	97	39
6514	AF134827	Monodelphis domestica	small nuclear ribonucleoprotein B'	108	47
6515	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	82	44
6516	AF068754	Homo sapiens	heat shock factor binding protein 1 HSBP1	118	69
6517	AF130089	Homo sapiens	PRO2550	207	69
6518	M22332	Homo sapiens	unknown protein	154	55
6519	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	95	39
6520	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	65	37
6521	AK023563	Homo sapiens	unnamed protein product	268	58
6522	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	181	61
6523	AF210651	Homo sapiens	NAG18	85	85
6524	AF130079	Homo sapiens	PRO2852	127	51
6525	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	113	51
6526	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	85	62
6527	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	115	48
6528	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	86	60
6529	R59842	Homo sapiens	ApoE4L1 protease.	92	58
6530	R59842	Homo sapiens	ApoE4L1 protease.	135	77
6531	W48351	Homo sapiens	Human breast cancer related protein	88	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2		
6532	AF119851	Homo sapiens	PRO1722	121	61
6533	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	85	35
6534	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	123	59
6535	R95913	Homo sapiens	Neural thread protein.	132	67
6536	AF130079	Homo sapiens	PRO2852	113	58
6537	AB047600	Macaca fascicularis	hypothetical protein	159	60
6538	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	279	68
6539	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	112	55
6540	AF130089	Homo sapiens	PRO2550	124	56
6541	U93574	Homo sapiens	putative p150	159	39
6542	AF118082	Homo sapiens	PRO1902	114	45
6543	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	78	50
6544	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	118	44
6545	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	138	62
6546	AF116661	Homo sapiens	PRO1438	162	59
6547	S62928	Homo sapiens	PKB1M protein precursor	116	48
6548	AB030192	Mus musculus	homologue of S70447 F1Fo-ATP synthase complex Fo membrane domain f subunit	174	63
6549	AK025116	Homo sapiens	unnamed protein product	136	56
6550	X92485	Plasmodium vivax	pva1	105	56
6551	AF130079	Homo sapiens	PRO2852	172	91
6552	U70935	Peromyscus maniculatus	reverse transcriptase	84	42
6553	S79410	Mus musculus	nuclear localization signal binding protein	100	55
6554	M76546	Helianthus annuus	hydroxyproline-rich protein	110	39
6555	AF130089	Homo sapiens	PRO2550	205	64
6556	AF130079	Homo sapiens	PRO2852	165	48
6557	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preproduct.	160	74
6558	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	133	49
6559	X92485	Plasmodium vivax	pva1	121	78
6560	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	76	45
6561	AF217374	Acanthaster planci	cytochrome oxidase subunit I	234	85
6562	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	61
6563	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO: 128.	134	84
6564	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	66	47
6565	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	180	49

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6566	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	96	57
6567	X92485	Plasmodium vivax	pval	96	58
6568	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	103	73
6569	AF119851	Homo sapiens	PRO1722	81	60
6570	AF289098	Cladrastis kentukea	ENOD2	110	36
6571	AF118086	Homo sapiens	PRO1992	115	65
6572	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	57
6573	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	89	41
6574	M22332	Homo sapiens	unknown protein	95	34
6575	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	98	64
6576	AK021848	Homo sapiens	unnamed protein product	131	41
6577	AF161356	Homo sapiens	HSPC093	155	57
6578	AF116909	Homo sapiens	unknown	75	76
6579	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	95	53
6580	AF130089	Homo sapiens	PRO2550	276	74
6581	K02576	Homo sapiens	salivary proline-rich protein 1	119	33
6582	U49973	Homo sapiens	ORF2: function unknown	94	62
6583	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	90	65
6584	AJ249395	Globodera pallida	NADH-ubiquinone oxidoreductase subunit 4	99	41
6585	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	75	62
6586	U49973	Homo sapiens	ORF2: function unknown	134	58
6587	Y08061	Homo sapiens	Human c-myc protein fragment.	112	47
6588	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	217	53
6589	K02576	Homo sapiens	salivary proline-rich protein 1	147	41
6590	U43627	Arabidopsis thaliana	extensin	103	31
6591	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	71	34
6592	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	177	66
6593	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	100	72
6594	M69297	Homo sapiens	ORF 3	137	43
6595	X68101	Rattus norvegicus	trg	372	89
6596	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	81	62
6597	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	99	43
6598	Z99714	Homo sapiens	bK1048E9.5 (novel protein)	1642	98
6599	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	162	59
6600	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	132	65
6601	AK000385	Homo sapiens	unnamed protein product	187	74
6602	AF130051	Homo sapiens	PRO0898	137	54
6603	S58722	Homo sapiens	X-linked retinopathy protein (C-	88	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			terminal, clone XEH.8c}		
6604	X61047	Hydra sp.	mini-collagen	116	45
6605	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	109	71
6606	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	212	66
6607	AF232673	Homo sapiens	B17 long form	1272	99
6608	AF118082	Homo sapiens	PRO1902	77	52
6609	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	132	74
6610	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	70	61
6611	Y36203	Homo sapiens	Human secreted protein #75.	140	62
6612	X92485	Plasmodium vivax	pval	157	72
6613	U52077	Homo sapiens	mariner transposase	260	67
6614	AF161392	Homo sapiens	HSPC274	138	45
6615	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	65
6616	AF119851	Homo sapiens	PRO1722	147	49
6617	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	101	63
6618	AL390114	Leishmania major	extremely cysteine/valine rich protein	117	39
6619	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	105	58
6620	U15647	Mus musculus	reverse transcriptase	106	38
6621	AF130089	Homo sapiens	PRO2550	171	52
6622	X92485	Plasmodium vivax	pval	139	44
6623	AF090895	Homo sapiens	PRO0117	161	58
6624	M63730	Homo sapiens	BPAG2	107	32
6625	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	183	61
6626	AF078860	Homo sapiens	PTD007	69	73
6627	AL080253	Arabidopsis thaliana	putative snRNP protein	101	37
6628	AK000385	Homo sapiens	unnamed protein product	140	57
6629	W60652	Homo sapiens	Human DVic-1 (alternative transcript).	218	51
6630	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	152	66
6631	AB046048	Macaca fascicularis	unnamed portein product	118	65
6632	X92485	Plasmodium vivax	pval	119	88
6633	X03145	Homo sapiens	pot. ORF V	98	39
6634	K02576	Homo sapiens	salivary proline-rich protein 1	165	41
6635	X59448	Drosophila melanogaster	dynamlin	111	39
6636	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	162	50
6637	AF130089	Homo sapiens	PRO2550	141	75
6638	AF118082	Homo sapiens	PRO1902	108	63
6639	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	144	60
6640	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	104	47
6641	AF118082	Homo sapiens	PRO1902	121	53
6642	AF118082	Homo sapiens	PRO1902	195	68
6643	R95913	Homo sapiens	Neural thread protein.	212	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6644	AF090928	Homo sapiens	PRO0470	81	65
6645	AF130079	Homo sapiens	PRO2852	151	69
6646	AF003535	Homo sapiens	ORF2-like protein	140	35
6647	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	169	61
6648	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	100	42
6649	M15530	Homo sapiens	B-cell growth factor	121	76
6650	AF090942	Homo sapiens	PRO0637	119	53
6651	AF118082	Homo sapiens	PRO1902	130	52
6652	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	143	87
6653	AF130089	Homo sapiens	PRO2550	143	63
6654	AF119851	Homo sapiens	PRO1722	285	70
6655	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	103	75
6656	AF119855	Homo sapiens	PRO1847	61	60
6657	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	107	36
6658	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	84	61
6659	AF119851	Homo sapiens	PRO1722	177	54
6660	X92485	Plasmodium vivax	pva1	104	55
6661	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	116	57
6662	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	68
6663	L22029	Glycine max	hydroxyproline-rich glycoprotein	115	35
6664	D00570	Mus musculus	open reading frame (251 AA)	126	35
6665	AF130051	Homo sapiens	PRO0898	129	77
6666	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	108	42
6667	G02851	Homo sapiens	Human secreted protein, SEQ ID NO: 6932.	71	41
6668	AF130079	Homo sapiens	PRO2852	110	59
6669	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	113	66
6670	G00527	Homo sapiens	Human secreted protein, SEQ ID NO: 4608.	98	73
6671	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	80	51
6672	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	113	36
6673	V01201	Simian sarcoma virus	coding sequence of pol	143	47
6674	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	159	78
6675	G00648	Homo sapiens	Human secreted protein, SEQ ID NO: 4729.	64	56
6676	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	96	48
6677	AF130089	Homo sapiens	PRO2550	100	75
6678	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	94	68
6679	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	105	71
6680	G03812	Homo sapiens	Human secreted protein, SEQ ID NO: 7893.	218	53
6681	G00352	Homo sapiens	Human secreted protein, SEQ ID NO:	115	53

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4433.		
6682	AF161356	Homo sapiens	HSPC093	163	47
6683	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	78	72
6684	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	87	42
6685	S79410	Mus musculus	nuclear localization signal binding protein	98	43
6686	U93564	Homo sapiens	p40	96	41
6687	AF119855	Homo sapiens	PRO1847	137	67
6688	U52077	Homo sapiens	mariner transposase	268	81
6689	X92485	Plasmodium vivax	pva1	97	58
6690	W48351	Homo sapiens	Human breast cancer related protein. BCRB2.	133	56
6691	M63274	Plasmodium falciparum	malaria antigen	61	46
6692	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	147	80
6693	M11901	Rattus norvegicus	proline-rich salivary protein	115	40
6694	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	131	50
6695	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	174	66
6696	AF068294	Homo sapiens	HDCMB45P	154	59
6697	X55685	Lycopersicon esculentum	extensin (class I)	112	41
6698	M83293	Simian immunodeficiency virus	vpx protein	85	41
6699	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	169	88
6700	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	121	58
6701	AF118080	Homo sapiens	PRO1880	127	59
6702	X92485	Plasmodium vivax	pva1	106	58
6703	AF161356	Homo sapiens	HSPC093	155	53
6704	X92485	Plasmodium vivax	pva1	164	54
6705	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	172	59
6706	AK025326	Homo sapiens	unnamed protein product	146	50
6707	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	112	43
6708	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	119	71
6709	AF176531	Mus musculus	F-box protein FBX16	324	60
6710	X92485	Plasmodium vivax	pva1	96	64
6711	AF130089	Homo sapiens	PRO2550	203	67
6712	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	150	59
6713	AF090944	Homo sapiens	PRO0663	114	43
6714	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	110	47
6715	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	131	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6716	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	103	65
6717	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	115	46
6718	G01222	Homo sapiens	Human secreted protein, SEQ ID NO: 5303.	54	100
6719	Y36203	Homo sapiens	Human secreted protein #75.	129	78
6720	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	64
6721	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	130	61
6722	Y36203	Homo sapiens	Human secreted protein #75.	167	72
6723	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	46
6724	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	133	42
6725	U80761	Homo sapiens	CTG26 alternate open reading frame	88	76
6726	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	218	61
6727	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	399	81
6728	U01877	Homo sapiens	p300 protein	119	27
6729	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	107	51
6730	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	130	58
6731	X66285	Mus musculus	HCl ORF	79	38
6732	K02576	Homo sapiens	salivary proline-rich protein 1	114	38
6733	AF057352	Homo sapiens	hepatocellular carcinoma autoantigen	148	81
6734	AF090895	Homo sapiens	PRO0117	152	57
6735	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	61
6736	X92485	Plasmodium vivax	pva1	92	89
6737	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	112	49
6738	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	278	72
6739	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	191	47
6740	AF118082	Homo sapiens	PRO1902	83	49
6741	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	83	43
6742	Y36708	Homo sapiens	Fragment of human secreted protein encoded by gene 62.	71	64
6743	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	177	70
6744	Y91475	Homo sapiens	Human secreted protein sequence encoded by gene 25 SEQ ID NO:148.	159	50
6745	X92485	Plasmodium vivax	pva1	112	39
6746	Z82268	Caenorhabditis elegans	predicted using Genefinder—contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=73.8, E-value=1.2e-18, N=2; PF01484 (Nematode cuticle collagen N-terminal domain), Score=37.5, E-value=1e-07, N=1—cDNA EST yk92f1.3 comes from this gene—cDNA EST yk55f6.5 comes from this gene—cDNA EST yk65b7.3 comes from this gene—cDNA EST	108	36

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			yk58f3.5 comes from this gene-cDNA EST yk72h5.5 comes from this gene-cDNA EST yk55c4.5 comes from this gene-cDNA EST yk58h1.5 comes from this gene-cDNA EST yk65a12.5 comes from this gene-cDNA EST yk94f4.5 comes from this gene		
6747	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	113	38
6748	R95913	Homo sapiens	Neural thread protein.	108	56
6749	U57747	Mus musculus	platelet-activating factor acetylhydrolase isoform Ib beta subunit	209	69
6750	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	159	65
6751	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	96	48
6752	AF090895	Homo sapiens	PRO0117	115	56
6753	AF217973	Homo sapiens	unknown	105	66
6754	AF119851	Homo sapiens	PRO1722	156	55
6755	AF119855	Homo sapiens	PRO1847	189	66
6756	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	163	55
6757	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	123	57
6758	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	156	70
6759	AF130051	Homo sapiens	PRO0898	98	68
6760	M36914	Zea mays	cell wall protein (put.); putative	75	28
6761	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	98	85
6762	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	88	62
6763	M19756	Homo sapiens	MHC HLA-Bw47 precursor	580	92
6764	AL359782	Trypanosoma brucei	possible (bhv-6) u1102, variant a dna, complete virion genome.	115	52
6765	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	321	51
6766	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	124	59
6767	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	303	64
6768	AF061340	Artibeus jamaicensis	cytochrome c oxidase subunit II	213	67
6769	T71265_cdl	Homo sapiens	19-JAN-1996 Neuronal apoptosis inhibitor protein (NAIP) cDNA.	188	59
6770	B01390	Homo sapiens	Neuron-associated protein.	92	55
6771	AF017777	Drosophila melanogaster	la costa	114	50
6772	Z34955	Sus scrofa	protein phosphatase 2A 65 kDa regulatory subunit, alpha isoform	331	93
6773	X61296	Rattus norvegicus	open reading frame 2	101	37
6774	AL117345	Homo sapiens	dJ416F21.2 (novel protein)	639	91
6775	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	110	61
6776	AJ007798	Homo sapiens	stromal antigen 3, (STAG3)	238	76
6777	AB029065	Mus musculus	Ser/Thr kinase KKIAMRE-beta	165	66
6778	M37400	Homo sapiens	aspartate aminotransferase	208	68
6779	AF130089	Homo sapiens	PRO2550	127	52
6780	AF130079	Homo sapiens	PRO2852	332	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6781	AL049748	Homo sapiens	dJ41P2.2 (RNA binding motif protein 9 (isoform 1))	264	60
6782	L11007	Rattus norvegicus	cyclin-dependent kinase 4	239	75
6783	AF319938	Thermus thermophilus	competence factor ComEA	115	36
6784	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	119	44
6785	L16864	African swine fever virus	cd2 homologue	152	34
6786	Y36203	Homo sapiens	Human secreted protein #75.	99	44
6787	AF130087	Homo sapiens	PRO2411	172	65
6788	AF208846	Homo sapiens	BM-004	664	100
6789	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	90	83
6790	AP000059	Aeropyrum pernix	120aa long hypothetical protein	81	43
6791	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	53
6792	Y12961	Homo sapiens	Amino acid sequence of a human secreted peptide.	175	65
6793	Y73442	Homo sapiens	Human secreted protein clone ya66_1 protein sequence SEQ ID NO:106.	565	93
6794	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	136	50
6795	AC004022	Homo sapiens	serum paraoxonase/arylesterase 3	137	93
6796	AF009668	multiple sclerosis associated retrovirus	polyprotein	194	60
6797	R59842	Homo sapiens	ApoE4L1 protease.	121	92
6798	U88167	Caenorhabditis elegans	contains similarity to C2 domains	171	73
6799	AF293024	Homo sapiens	steroid receptor RNA activator isoform 1	767	97
6800	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	65
6801	B01203	Homo sapiens	Human GTPase associated protein-28.	313	87
6802	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	125	47
6803	AF078036	Homo sapiens	RelA associated inhibitor; NF-kappaB subunit p65 binding protein	1275	95
6804	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	131	53
6805	Y57946	Homo sapiens	Human transmembrane protein HTMPN-70.	1128	100
6806	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	81	81
6807	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	52
6808	AB046048	Macaca fascicularis	unnamed poeitin product	273	63
6809	K02401	Homo sapiens	chorionic somatomammotropin	446	95
6810	AF130089	Homo sapiens	PRO2550	150	56
6811	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	123	65
6812	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	93	38
6813	AF090930	Homo sapiens	PRO0478	103	65
6814	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	138	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6815	B24423	Homo sapiens	Human PRO1244 protein sequence SEQ ID NO: 193.	484	95
6816	M11901	Rattus norvegicus	proline-rich salivary protein	105	43
6817	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	96	56
6818	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	102	48
6819	U82303	Homo sapiens	unknown	105	57
6820	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	113	45
6821	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	97	39
6822	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	146	86
6823	U52077	Homo sapiens	mariner transposase	192	78
6824	AC004237	Homo sapiens	KIF3	129	86
6825	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	138	66
6826	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	112	64
6827	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	108	68
6828	U49974	Homo sapiens	mariner transposase	103	86
6829	AF119851	Homo sapiens	PRO1722	115	53
6830	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	82	62
6831	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	94	73
6832	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	131	53
6833	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	74	50
6834	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	168	61
6835	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	140	60
6836	X92485	Plasmodium vivax	pval	99	58
6837	AB046048	Macaca fascicularis	unnamed protein product	147	42
6838	AB047600	Macaca fascicularis	hypothetical protein	134	52
6839	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	60
6840	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	126	73
6841	AF130089	Homo sapiens	PRO2550	167	63
6842	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	140	56
6843	AF090894	Homo sapiens	PRO0113	148	62
6844	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	119	51
6845	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	75	61
6846	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	65	44
6847	AF130089	Homo sapiens	PRO2550	160	76
6848	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	68
6849	AF116715	Homo sapiens	PRO2829	123	67
6850	Y01437	Homo sapiens	Secreted protein encoded by gene 55	142	96

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HLMBP18.		
6851	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	110	76
6852	AF068294	Homo sapiens	HDCMB45P	161	56
6853	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	111	57
6854	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	165	72
6855	AF130051	Homo sapiens	PRO0898	117	61
6856	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	138	72
6857	X55685	Lycopersicon esculentum	extensin (class I)	190	45
6858	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	164	69
6859	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	90	52
6860	AF119851	Homo sapiens	PRO1722	331	73
6861	G00418	Homo sapiens	Human secreted protein, SEQ ID NO: 4499.	130	67
6862	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	114	53
6863	X92485	Plasmodium vivax	pva1	105	63
6864	AF068294	Homo sapiens	HDCMB45P	206	61
6865	AF068294	Homo sapiens	HDCMB45P	128	46
6866	L00016	Homo sapiens	urf4	157	58
6867	X92485	Plasmodium vivax	pva1	95	89
6868	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	77
6869	AF130089	Homo sapiens	PRO2550	162	67
6870	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	257	65
6871	X71972	Mus musculus	ribosomal protein S24	211	85
6872	M28016	Homo sapiens	cytochrome b	72	93
6873	M24069	Homo sapiens	DNA-binding protein A	1662	79
6874	AF130051	Homo sapiens	PRO0898	163	76
6875	AF006061	Homo sapiens	placental growth hormone isoform hGH-V3	263	90
6876	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	94	80
6877	AF130079	Homo sapiens	PRO2852	130	76
6878	S80905	Homo sapiens	Con1	148	38
6879	X55683	Lycopersicon esculentum	extensin (class I)	70	35
6880	U16359	Rattus norvegicus	nitric oxide synthase	106	94
6881	AK025047	Homo sapiens	unnamed protein product	167	50
6882	X92485	Plasmodium vivax	pva1	110	63
6883	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	185	46
6884	AK024455	Homo sapiens	FLJ00047 protein	81	64
6885	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	113	47
6886	AF014008	Bos taurus	myocardial vascular inhibition factor	158	96
6887	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	183	83
6888	Y45382	Homo sapiens	Human secreted protein fragment	199	49

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded from gene 28.		
6889	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	140	67
6890	AF130051	Homo sapiens	PRO0898	135	65
6891	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	147	65
6892	X72963	Nicotiana tabacum	pAP8 product	80	44
6893	AF073957	Homo sapiens	CXC chemokine BRAK	399	82
6894	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	160	80
6895	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	70
6896	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	178	85
6897	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	142	62
6898	AF118082	Homo sapiens	PRO1902	144	53
6899	AF130051	Homo sapiens	PRO0898	187	72
6900	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	121	85
6901	AF130089	Homo sapiens	PRO2550	100	63
6902	Z29446	Hepatitis C virus	core region	60	36
6903	AF107406	Homo sapiens	GW128	71	63
6904	W03627	Homo sapiens	Human follicle stimulating hormone GPR N-terminal sequence.	173	64
6905	AF130089	Homo sapiens	PRO2550	88	65
6906	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	78	84
6907	U93569	Homo sapiens	p40	145	48
6908	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	186	50
6909	AF130089	Homo sapiens	PRO2550	244	77
6910	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	119	38
6911	AF130089	Homo sapiens	PRO2550	139	47
6912	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409	146	60
6913	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	131	70
6914	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	106	74
6915	AF161361	Homo sapiens	HSPC098	79	66
6916	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	207	60
6917	AF130051	Homo sapiens	PRO0898	258	61
6918	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	108	65
6919	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	58
6920	G02635	Homo sapiens	Human secreted protein, SEQ ID NO: 6716.	168	80
6921	AF116661	Homo sapiens	PRO1438	71	48
6922	AF090940	Homo sapiens	PRO0644	72	85
6923	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	186	70
6924	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	89	55
6925	AF229067	Homo sapiens	PADI-H protein	122	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6926	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	105	37
6927	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	173	60
6928	X56603	Mus musculus	mouse 57-KD Calcium-binding protein (MCaBP)	103	52
6929	AF119851	Homo sapiens	PRO1722	148	76
6930	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	61
6931	AF077208	Homo sapiens	HSPC022	155	72
6932	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	111	62
6933	M22332	Homo sapiens	unknown protein	154	77
6934	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	146	60
6935	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	63
6936	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	124	50
6937	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	77
6938	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	111	68
6939	AF118082	Homo sapiens	PRO1902	120	54
6940	AF090942	Homo sapiens	PRO0657	149	72
6941	M22332	Homo sapiens	unknown protein	96	51
6942	AF130087	Homo sapiens	PRO2411	132	58
6943	M15530	Homo sapiens	B-cell growth factor	97	52
6944	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	87	52
6945	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	73	66
6946	Z10561_cdl	Homo sapiens	12-MAR-1998 DNA encoding G protein-coupled receptor protein designated SREB2.	330	96
6947	W53869	Homo sapiens	Gravin polypeptide fragment, residues 1526-1780.	170	89
6948	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	164	86
6949	AF118086	Homo sapiens	PRO1992	117	86
6950	AF090928	Homo sapiens	PRO0470	115	58
6951	AF130089	Homo sapiens	PRO2550	124	69
6952	Y38397	Homo sapiens	Human secreted protein encoded by gene No. 12.	94	64
6953	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	132	55
6954	X92485	Plasmodium vivax	pva1	108	64
6955	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	117	85
6956	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	93	53
6957	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	106	50
6958	AF130089	Homo sapiens	PRO2550	127	67
6959	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	119	49
6960	J02459	bacteriophage lambda	U (tail component;131)	492	92
6961	G03133	Homo sapiens	Human secreted protein, SEQ ID NO:	180	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7214.		
6962	Z66490	Salmo trutta	slow myotomal muscle tropomyosin	182	72
6963	AF130089	Homo sapiens	PRO2550	108	73
6964	W21733	Homo sapiens	NIP-1 encoded by clone 59.	131	69
6965	AF161356	Homo sapiens	HSPC093	58	48
6966	AB047934	Macaca fascicularis	hypothetical protein	146	58
6967	X92485	Plasmodium vivax	pva1	116	55
6968	AF118082	Homo sapiens	PRO1902	85	65
6969	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	176	63
6970	AF116712	Homo sapiens	PRO2738	101	56
6971	X96667	Homo sapiens	beta-galactoside alpha-2,3-sialyltransferase	172	97
6972	Y86574	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:491.	150	82
6973	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	176	58
6974	AF162149	Mycoplasma bovis	variable surface lipoprotein	143	40
6975	W17971	Homo sapiens	RAC protein kinase C-terminal binding protein C-terminal region.	135	81
6976	AF130089	Homo sapiens	PRO2550	345	78
6977	AF130089	Homo sapiens	PRO2550	195	63
6978	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	75
6979	M60510	Mus musculus	beta-D-galactosidase fusion protein	96	47
6980	AF118086	Homo sapiens	PRO1992	131	64
6981	AF130089	Homo sapiens	PRO2550	132	64
6982	L27428	Homo sapiens	reverse transcriptase	128	35
6983	U93566	Homo sapiens	p40	98	31
6984	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	138	78
6985	L27428	Homo sapiens	reverse transcriptase	133	67
6986	AF090895	Homo sapiens	PRO0117	139	62
6987	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	212	60
6988	Y36203	Homo sapiens	Human secreted protein #75.	189	73
6989	AF116712	Homo sapiens	PRO2738	87	42
6990	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	63
6991	AF090930	Homo sapiens	PRO0478	154	52
6992	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	102	76
6993	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	151	48
6994	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	113	47
6995	J02974	Acanthamoeba castellanii	myosin IB heavy chain	120	43
6996	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	151	69
6997	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	153	60
6998	Y12961	Homo sapiens	Amino acid sequence of a human secreted peptide.	114	66
6999	AF113685	Homo sapiens	PRO0974	88	58
7000	AF130089	Homo sapiens	PRO2550	146	58

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7001	U93565	Homo sapiens	putative p150	96	46
7002	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	146	57
7003	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	206	92
7004	AF130089	Homo sapiens	PRO2550	104	50
7005	AL137472	Homo sapiens	hypothetical protein	179	55
7006	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	379	98
7007	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	121	38
7008	AF119851	Homo sapiens	PRO1722	136	63
7009	AF218028	Homo sapiens	unknown	104	52
7010	AF130079	Homo sapiens	PRO2852	129	60
7011	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	110	54
7012	X03145	Homo sapiens	pot. ORF VI	130	65
7013	AF090944	Homo sapiens	PRO0663	171	75
7014	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	122	65
7015	M26460	Homo sapiens	retinoblastoma 1	113	37
7016	X92485	Plasmodium vivax	pva1	112	56
7017	X92485	Plasmodium vivax	pva1	144	57
7018	AF130079	Homo sapiens	PRO2852	224	74
7019	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	129	43
7020	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	58
7021	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	106	69
7022	AF090901	Homo sapiens	PRO0195	103	88
7023	AF116661	Homo sapiens	PRO1438	120	47
7024	AP002460	Arabidopsis thaliana	gene_id: FID9.26-unknown protein	325	60
7025	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	126	63
7026	AF119900	Homo sapiens	PRO2822	111	70
7027	AF130051	Homo sapiens	PRO0898	133	44
7028	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	179	68
7029	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	72	60
7030	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	130	50
7031	J03941	Mus musculus	ferritin heavy chain	124	57
7032	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	157	59
7033	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	120	65
7034	Y36156	Homo sapiens	Human secreted protein #28.	164	48
7035	U80761	Homo sapiens	CTG26 alternate open reading frame	116	48
7036	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	130	52
7037	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	113	55
7038	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	78	68
7039	AF130089	Homo sapiens	PRO2550	121	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7040	AF119855	Homo sapiens	PRO1847	158	65
7041	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	116	62
7042	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	117	54
7043	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	123	80
7044	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	63
7045	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	86	44
7046	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	80	72
7047	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	100	57
7048	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	152	66
7049	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	94	72
7050	AF176323	Macropus eugenii	small nuclear ribonucleoprotein B'	103	41
7051	AF255446	Cryptocodinium cohnii	DipI-associated protein C	127	38
7052	M64792	Rattus norvegicus	salivary proline-rich protein	149	42
7053	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	69
7054	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	109	54
7055	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	185	86
7056	U60269	Homo sapiens	putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	125	65
7057	AF068294	Homo sapiens	HDCMB45P	264	73
7058	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	190	95
7059	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	62
7060	AF090894	Homo sapiens	PRO0113	185	62
7061	AF107406	Homo sapiens	GW128	66	80
7062	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	86	46
7063	AF119851	Homo sapiens	PRO1722	117	74
7064	X92485	Plasmodium vivax	pva1	123	66
7065	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	79	59
7066	L23545	Homo sapiens	putative	135	44
7067	AF119851	Homo sapiens	PRO1722	301	69
7068	AF130079	Homo sapiens	PRO2852	118	71
7069	AF119851	Homo sapiens	PRO1722	150	64
7070	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	138	48
7071	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	94	39
7072	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	145	62
7073	G00397	Homo sapiens	Human secreted protein, SEQ ID NO:	155	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4478.		
7074	AF130089	Homo sapiens	PRO2550	146	60
7075	U49974	Homo sapiens	mariner transposase	198	83
7076	AF236085	Homo sapiens	CYP4F11	427	79
7077	AF130089	Homo sapiens	PRO2550	159	52
7078	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	206	85
7079	D32202	Homo sapiens	alpha 1C adrenergic receptor isoform 2	152	71
7080	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	88	62
7081	AB046048	Macaca fascicularis	unnamed portein product	135	46
7082	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	142	75
7083	X53581	Rattus norvegicus	ORF4	119	64
7084	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	111	62
7085	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	64
7086	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	71	66
7087	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	81	54
7088	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	148	50
7089	U08021	Homo sapiens	nicotinamide N-methyltransferase	116	100
7090	U93569	Homo sapiens	p40	199	82
7091	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	124	56
7092	X92485	Plasmodium vivax	pval	125	60
7093	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	109	62
7094	AF118082	Homo sapiens	PRO1902	191	50
7095	X92485	Plasmodium vivax	pval	129	67
7096	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	80	66
7097	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	162	67
7098	AF116715	Homo sapiens	PRO2829	123	63
7099	L27428	Homo sapiens	reverse transcriptase	189	50
7100	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	84	48
7101	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	65
7102	D85030	Schizosaccharomyces pombe	ribosomal protein S33 homolog	139	85
7103	G03021	Homo sapiens	Human secreted protein, SEQ ID NO: 7102.	177	77
7104	U72543	Sus scrofa	ubiquitin-like/S30 ribosomal fusion protein	129	100
7105	AC007787	AA 187-502	NFI-X3=transcription factor	190	84
7106	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	110	38
7107	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	157	56
7108	Z69381	Saccharomyces cerevisiae	N1114	450	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7109	V49572_cd1	Homo sapiens	13-NOV-1996 Human stomach cancer clone HP10122 cDNA #1.	353	70
7110	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	99	45
7111	AF068294	Homo sapiens	HDCMB45P	132	55
7112	AB033020	Homo sapiens	KIAA1194 protein	850	100
7113	AB019692	Homo sapiens	protein kinase PKNbeta	792	87
7114	M12140	Homo sapiens	envelope protein	154	79
7115	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	88	62
7116	AF124491	Homo sapiens	ARF GTPase-activating protein GIT2	1216	100
7117	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	153	54
7118	AF130089	Homo sapiens	PRO2550	184	64
7119	AF130079	Homo sapiens	PRO2852	144	68
7120	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	112	51
7121	AF032384	Xenopus laevis	metalloprotease-disintegrin	304	76
7122	K01664	Drosophila melanogaster	Bkm-like protein	99	71
7123	AJ238706	Drosophila melanogaster	monocarboxylate transporter 1 homologue	161	38
7124	X92485	Plasmodium vivax	pval	127	54
7125	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	80	65
7126	AF116712	Homo sapiens	PRO2738	118	53
7127	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	115	64
7128	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	90	62
7129	AF118090	Homo sapiens	PRO2044	280	80
7130	AF129085	Homo sapiens	carboxy terminus of Hsp70-interacting protein	593	91
7131	AF054840	Homo sapiens	tetraspan TM4SF; Tspan-3	513	83
7132	L27428	Homo sapiens	reverse transcriptase	156	51
7133	AK001647	Homo sapiens	unnamed protein product	2334	99
7134	AF130051	Homo sapiens	PRO0898	142	84
7135	X53581	Rattus norvegicus	ORF4	213	46
7136	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	101	86
7137	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	194	68
7138	U21634	Onychomys torridus	cytochrome c oxidase subunit III	111	84
7139	X60592	Homo sapiens	CDw40	201	95
7140	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	63
7141	M76979	Homo sapiens	pigment epithelial-differentiating factor	458	93
7142	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	142	54
7143	Y27677	Homo sapiens	Human secreted protein encoded by gene No. 111.	323	90
7144	AF116712	Homo sapiens	PRO2738	132	60
7145	AB024057	Homo sapiens	vascular Rab-GAP/TBC-containing protein	121	45
7146	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	144	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7147	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	141	76
7148	R06400	Homo sapiens	Lambda gt10ch2 encoded C-terminal alpha amidating enzyme.	337	85
7149	S87759	Homo sapiens	protein phosphatase 2C alpha, PP2Calpha	427	78
7150	M12140	Homo sapiens	envelope protein	541	64
7151	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	106	85
7152	X55683	Lycopersicon esculentum	extensin (class I)	70	38
7153	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	194	61
7154	AF130089	Homo sapiens	PRO2550	89	60
7155	AF100742	Homo sapiens	M-phase phosphoprotein homolog	714	94
7156	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	143	78
7157	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	174	79
7158	AL031230	Homo sapiens	dJ73M23.3 (K1AA0319)	214	45
7159	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	155	37
7160	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	46
7161	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	130	53
7162	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	107	55
7163	M13043	Mus musculus	alpha-1 (IV) collagen	80	42
7164	AB011004	Homo sapiens	UDP-N-acetylglucosamine pyrophosphorylase	257	90
7165	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	111	47
7166	AF119851	Homo sapiens	PRO1722	279	61
7167	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	136	51
7168	W73327	Homo sapiens	Bipolar affective disorder associated gene fsh16 product.	287	63
7169	Y35946	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 195.	1231	99
7170	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	132	76
7171	U83303	Homo sapiens	line-1 reverse transcriptase	184	60
7172	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	141	64
7173	AF129507	Homo sapiens	transcription factor ICBP90	245	55
7174	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	131	56
7175	AF161356	Homo sapiens	HSPC093	107	55
7176	AF218028	Homo sapiens	unknown	116	55
7177	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	117	52
7178	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	94	38
7179	AF130089	Homo sapiens	PRO2550	124	47
7180	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	66
7181	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	65
7182	Y36156	Homo sapiens	Human secreted protein #28.	127	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7183	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	121	75
7184	X92485	Plasmodium vivax	pva1	129	60
7185	AF130089	Homo sapiens	PRO2550	116	53
7186	AF130089	Homo sapiens	PRO2550	137	64
7187	X51760	Homo sapiens	zinc finger protein (583 AA)	236	56
7188	X92485	Plasmodium vivax	pva1	131	50
7189	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	152	57
7190	AF068294	Homo sapiens	HDCMB45P	163	50
7191	AF119855	Homo sapiens	PRO1847	55	50
7192	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	57
7193	M15530	Homo sapiens	B-cell growth factor	106	53
7194	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	121	41
7195	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	124	60
7196	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	94	68
7197	U60315	Molluscum contagiosum virus subtype 1	MC054L	116	36
7198	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	116	67
7199	M15530	Homo sapiens	B-cell growth factor	146	59
7200	AF090894	Homo sapiens	PRO0113	165	65
7201	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	160	57
7202	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	53
7203	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	92	65
7204	AF126163	Homo sapiens	HHLA3 protein	131	78
7205	X92485	Plasmodium vivax	pva1	116	42
7206	AF090931	Homo sapiens	PRO0483	136	83
7207	Y36156	Homo sapiens	Human secreted protein #28.	127	49
7208	Y12961	Homo sapiens	Amino acid sequence of a human secreted peptide.	158	55
7209	Y36203	Homo sapiens	Human secreted protein #75.	124	56
7210	M69008	Homo sapiens	alpha-1 type XIII collagen	90	34
7211	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	71
7212	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	60
7213	AF130089	Homo sapiens	PRO2550	163	86
7214	AF130089	Homo sapiens	PRO2550	111	52
7215	AF118082	Homo sapiens	PRO1902	150	63
7216	Y53663	Homo sapiens	A human B-cell growth factor related protein (BGFRP).	83	66
7217	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	68
7218	AF220264	Homo sapiens	MOST-1	123	66
7219	AF229067	Homo sapiens	PADI-H protein	121	52
7220	AF118086	Homo sapiens	PRO1992	130	61
7221	Y86248	Homo sapiens	Human secreted protein HCHPF68.	179	100

SEQ ID NO:	Accession No.	Species	Description	Smith - Waterman Score	% Identity
			SEQ ID NO:163.		
7222	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	78
7223	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	200	95
7224	L27428	Homo sapiens	reverse transcriptase	127	55
7225	AB008227	Adiantum capillus-veneris	Extensin	121	43
7226	D38112	Homo sapiens	cytochrome c oxidase subunit 1	113	78
7227	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	153	96
7228	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	74
7229	M15530	Homo sapiens	B-cell growth factor	137	44
7230	AF004341	Homo sapiens	cytochrome c oxidase subunit III	140	87
7231	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	162	46
7232	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	90
7233	X15769	Mus musculus	UIRNA-associated 70-kDa protein	105	29
7234	M15530	Homo sapiens	B-cell growth factor	113	61
7235	AF194537	Homo sapiens	NAG13	249	65
7236	R20313	Homo sapiens	Gly(5) beta-globin mutant.	296	80
7237	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	123	50
7238	Y36156	Homo sapiens	Human secreted protein #28.	97	80
7239	D38112	Homo sapiens	NADH dehydrogenase subunit 3	395	81
7240	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	122	70
7241	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	90
7242	AF090942	Homo sapiens	PRO0657	118	47
7243	AF119851	Homo sapiens	PRO1722	112	62
7244	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	100	53
7245	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	144	66
7246	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	129	78
7248	X92485	Plasmodium vivax	pva1	108	58
7249	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	74
7250	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	153	70
7251	U01849	Trypanosoma brucei	ORF2	93	39
7252	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	113	54
7253	G03473	Homo sapiens	Human secreted protein, SEQ ID NO: 7554.	110	83
7254	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	167	66
7255	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	179	83
7256	AF130079	Homo sapiens	PRO2852	147	70
7257	AF118082	Homo sapiens	PRO1902	80	45
7258	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	137	55
7259	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	90	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7260	X92485	Plasmodium vivax	pva1	105	85
7261	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	162	76
7262	AF130089	Homo sapiens	PRO2550	98	43
7263	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	114	60
7264	AF116661	Homo sapiens	PRO1438	139	67
7265	AF104021	Bovine viral diarrhea virus-2	polyprotein	161	40
7266	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	116	43
7267	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	112	62
7268	M15530	Homo sapiens	B-cell growth factor	154	60
7269	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	95	54
7270	AF118082	Homo sapiens	PRO1902	139	62
7271	S52010	Mus sp.	orf1 5' of EpoR	93	33
7272	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	114	50
7273	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	166	61
7274	AF130089	Homo sapiens	PRO2550	124	43
7275	X92485	Plasmodium vivax	pva1	147	44
7276	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	81	59
7277	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	146	67
7278	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	89	67
7279	AF130087	Homo sapiens	PRO2411	72	65
7280	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	130	69
7281	J03507	Homo sapiens	complement protein C7 precursor	357	81
7282	AF116661	Homo sapiens	PRO1438	117	48
7284	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	137	61
7285	AF116715	Homo sapiens	PRO2829	128	75
7286	AF130079	Homo sapiens	PRO2852	122	52
7287	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	120	50
7288	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	338	75
7289	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	114	72
7290	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	146	59
7291	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	156	58
7292	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	167	61
7293	X92485	Plasmodium vivax	pva1	122	71
7294	AF130089	Homo sapiens	PRO2550	87	62
7295	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	140	50
7296	X92485	Plasmodium	pva1	152	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
7297	AF090894	Homo sapiens	PRO0113	172	65
7298	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	121	61
7299	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	114	66
7300	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	228	80
7301	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	111	73
7302	U43360	Peromyscus maniculatus	reverse transcriptase	119	46
7303	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	76
7304	U58658	Homo sapiens	unknown	102	48
7305	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	118	53
7306	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	116	63
7307	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	149	58
7308	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	112	52
7309	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	115	54
7310	M15530	Homo sapiens	B-cell growth factor	131	54
7311	AF118082	Homo sapiens	PRO1902	168	46
7312	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	412	92
7313	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	326	74
7314	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	149	59
7315	AF289099	Maackia amurensis	ENOD2f	107	32
7316	U17009	Phytophthora infestans	SecY-independent transporter protein	135	41
7317	AF220264	Homo sapiens	MOST-1	133	72
7318	U49973	Homo sapiens	ORF2: function unknown	111	53
7319	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	274	80
7320	AB047600	Macaca fascicularis	hypothetical protein	79	56
7321	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	205	95
7322	AC005175	Homo sapiens	TA2R_HUMAN, BETA ISOFORM; TXA2-R; PROSTANOID TP RECEPTOR	127	57
7323	R48296	Homo sapiens	Human PGF-2/NT-3.	89	93
7324	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	157	60
7325	AF119855	Homo sapiens	PRO1847	172	66
7326	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	141	50
7327	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	56
7328	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	98	56
7329	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	161	64
7330	G02552	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	111	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7331	AF126163	Homo sapiens	HHLA3 protein	98	47
7332	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	122	61
7333	AF130079	Homo sapiens	PRO2852	136	54
7334	AK023563	Homo sapiens	unnamed protein product	265	73
7335	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	113	61
7336	M15530	Homo sapiens	B-cell growth factor	136	75
7337	D38112	Homo sapiens	cytochrome c oxidase subunit 1	168	81
7338	D38112	Homo sapiens	cytochrome c oxidase subunit 3	339	80
7339	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	170	74
7340	D38112	Homo sapiens	NADH dehydrogenase subunit 3	400	82
7341	L00016	Homo sapiens	urt4	295	72
7342	D38112	Homo sapiens	NADH dehydrogenase subunit 3	350	86
7343	M36647	Homo sapiens	mitochondrial hinge protein precursor	286	82
7344	X15917	Paramecium aurelia	ND2 protein (AA 1-193) (unusual start codon)	132	34
7345	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	136	82
7346	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	89	69
7347	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	133	69
7348	D38112	Homo sapiens	NADH dehydrogenase subunit 3	169	71
7349	D38112	Homo sapiens	cytochrome c oxidase subunit 1	347	83
7350	V00662	Homo sapiens	cytochrome oxidase I	325	85
7351	D38112	Homo sapiens	NADH dehydrogenase subunit 3	406	80
7352	D38112	Homo sapiens	NADH dehydrogenase subunit 3	224	79
7353	D38112	Homo sapiens	NADH dehydrogenase subunit 1	270	86
7354	D38112	Homo sapiens	NADH dehydrogenase subunit 3	167	90
7355	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	120	87
7356	D38112	Homo sapiens	NADH dehydrogenase subunit 3	362	84
7357	D38112	Homo sapiens	NADH dehydrogenase subunit 3	188	72
7358	D38112	Homo sapiens	NADH dehydrogenase subunit 3	335	72
7359	U09500	Homo sapiens	cytochrome b	275	80
7360	D38112	Homo sapiens	NADH dehydrogenase subunit 3	209	73
7361	AF118078	Homo sapiens	PRO1848	95	58
7362	AB017116	Homo sapiens	AD 1	148	89
7363	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	146	42
7364	D38112	Homo sapiens	NADH dehydrogenase subunit 1	203	82
7365	D38112	Homo sapiens	NADH dehydrogenase subunit 1	206	84
7366	D38112	Homo sapiens	NADH dehydrogenase subunit 3	408	82
7367	D38112	Homo sapiens	NADH dehydrogenase subunit 3	456	86
7368	D38112	Homo sapiens	cytochrome c oxidase subunit 3	481	85
7369	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	150	53
7370	AB017116	Homo sapiens	AD 1	145	91
7371	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	173	85
7372	AF118082	Homo sapiens	PRO1902	122	54
7373	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	163	62
7374	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	53
7375	AF090894	Homo sapiens	PRO0113	128	64
7376	AK000241	Homo sapiens	unnamed protein product	131	67

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7377	AF119855	Homo sapiens	PRO1847	164	62
7379	AF016099	Mus musculus	endonuclease/reverse transcriptase	114	37
7380	U57362	Rattus norvegicus	collagen XII alpha 1	148	47
7381	D38112	Homo sapiens	ATPase subunit 6	423	76
7382	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	135	58
7383	AB040938	Homo sapiens	KIAA1505 protein	983	76
7384	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	48
7385	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	122	75
7386	U63295	Homo sapiens	seven in absentia homolog	260	85
7387	AE003499	Drosophila melanogaster	CG12706 gene product	103	32
7388	X03342	Homo sapiens	rpL32 (aa 1-135)	123	51
7389	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	129	58
7390	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	100
7391	AK026800	Homo sapiens	unnamed protein product	137	52
7392	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	117	73
7393	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	89	70
7394	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	80
7395	M15530	Homo sapiens	B-cell growth factor	98	57
7396	L10908	Mus musculus	Gcap1 gene product	105	51
7397	AF119851	Homo sapiens	PRO1722	127	55
7398	X99256	Hyalobates lar	cytochrome oxidase subunit III	319	73
7399	D38112	Homo sapiens	cytochrome c oxidase subunit 3	497	77
7400	D38112	Homo sapiens	cytochrome c oxidase subunit 3	399	80
7401	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	170	83
7402	D38112	Homo sapiens	NADH dehydrogenase subunit 3	183	91
7403	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	88
7404	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	115	40
7405	D83006	Saccharomyces cerevisiae	gene required for phosphorylation of oligosaccharides/ has high homology with YJR061w	171	38
7406	AF144636	Gallus gallus	osteoblast regulatory factor 3A	108	44
7407	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	70
7408	D38112	Homo sapiens	cytochrome c oxidase subunit 3	407	93
7409	AF004341	Homo sapiens	cytochrome c oxidase subunit III	140	87
7410	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	111	59
7411	AF004341	Homo sapiens	cytochrome c oxidase subunit III	138	82
7412	D38112	Homo sapiens	NADH dehydrogenase subunit 3	431	82
7413	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	127	56
7414	AB036396	Rana nigromaculata	cytochrome b	109	87
7415	AF090930	Homo sapiens	PRO0478	121	76
7416	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	171	96
7417	D38112	Homo sapiens	NADH dehydrogenase subunit 3	446	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7418	AB018440	Echinococcus multilocularis	NADH dehydrogenase subunit 2	112	33
7419	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	123	66
7420	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	50
7421	AF155232	Pisum sativum	extensin	128	37
7422	AF161356	Homo sapiens	HSPC093	89	48
7423	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	162	81
7424	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	171	79
7425	AF275953	synthetic construct	Cox8ND6gfp fusion protein	214	93
7426	D38112	Homo sapiens	cytochrome c oxidase subunit 1.	156	73
7427	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	130	59
7428	AK024455	Homo sapiens	FLJ00047 protein	82	66
7429	D38112	Homo sapiens	NADH dehydrogenase subunit 1	212	82
7430	S79410	Mus musculus	nuclear localization signal binding protein	124	48
7431	D38112	Homo sapiens	cytochrome c oxidase subunit 1	195	90
7432	D38112	Homo sapiens	cytochrome c oxidase subunit 1	217	84
7433	U87145	Toxoplasma gondii	ORF D	89	36
7434	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	213	72
7435	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	135	57
7436	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	151	82
7437	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	190	88
7438	D38112	Homo sapiens	NADH dehydrogenase subunit 1	141	78
7439	AF250284	Amsacta moorei entomopoxvirus	AMV012	88	31
7440	AF004341	Homo sapiens	cytochrome c oxidase subunit III	149	85
7441	U43360	Peromyscus maniculatus	reverse transcriptase	114	52
7442	AF275807	Homo sapiens	PNAS-110	157	48
7443	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	56
7444	D38112	Homo sapiens	NADH dehydrogenase subunit 4	475	95
7445	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	146	71
7446	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	130	60
7447	X92485	Plasmodium vivax	pval	153	45
7448	AF119851	Homo sapiens	PRO1722	96	55
7449	AF130079	Homo sapiens	PRO2852	153	73
7450	AF119851	Homo sapiens	PRO1722	238	52
7451	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	113	38
7452	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	147	57
7453	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	136	63
7454	R14163	Homo sapiens	Cellular DNA-binding protein RS1.	270	42
7455	X63526	Homo sapiens	homologue to elongation factor 1-	387	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gamma from A. salina		
7456	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	140	80
7457	AF119851	Homo sapiens	PRO1722	102	55
7458	G02756	Homo sapiens	Human secreted protein, SEQ ID NO: 6837.	83	55
7459	AF119851	Homo sapiens	PRO1722	132	64
7460	L10908	Mus musculus	Gcap1 gene product	106	64
7461	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	124	54
7462	X77816	Rattus norvegicus	PR-Vbeta1	142	51
7463	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	96	35
7464	AB046048	Macaca fascicularis	unnamed poirtein product	302	62
7465	X92485	Plasmodium vivax	pva1	115	47
7466	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	116	65
7467	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	91	35
7468	AF161361	Homo sapiens	HSPC098	92	57
7469	AF216389	Homo sapiens	semaphorin Rs	288	88
7470	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	153	73
7471	AF130089	Homo sapiens	PRO2550	108	48
7472	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	159	58
7473	AF217536	Homo sapiens	truncated mevalonate kinase	115	71
7474	X61296	Rattus norvegicus	open reading frame 2	134	49
7475	U22376	Homo sapiens	alternatively spliced product using exon 13A	165	46
7476	AF119851	Homo sapiens	PRO1722	133	46
7477	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	127	69
7478	D38112	Homo sapiens	NADH dehydrogenase subunit 4	533	87
7479	S79410	Mus musculus	nuclear localization signal binding protein	122	59
7480	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	168	84
7481	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	181	80
7482	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	122	56
7483	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	132	37
7484	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	166	100
7485	D38112	Homo sapiens	cytochrome c oxidase subunit I	277	72
7486	M29294	Rattus norvegicus	small nuclear ribonucleoparticle-associated protein	132	42
7487	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	50
7488	AF090901	Homo sapiens	PRO0195	101	62
7489	X97249	Homo sapiens	leucine-rich primary response protein	304	93
7490	D38112	Homo sapiens	NADH dehydrogenase subunit 3	447	84
7491	AK024455	Homo sapiens	FLJ00047 protein	122	63
7492	U87269	Homo sapiens	p120E4F transcription factor	244	66
7493	A31036	Nicotiana glauca	PRP2	87	31

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7494	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	206	97
7495	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	166	91
7496	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	66
7497	AK024455	Homo sapiens	FLJ00047 protein	67	61
7498	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	84
7499	X75438	Sus scrofa	homologue of proline/arginine rich antibacterial peptides	116	44
7500	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	166	89
7501	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	137	61
7502	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	213	60
7503	AB042770	Pteropus dasymallus	cytochrome c oxidase subunit 3	169	89
7504	AF126163	Homo sapiens	HLA3 protein	110	62
7505	D38112	Homo sapiens	cytochrome c oxidase subunit 3	299	90
7506	D38112	Homo sapiens	cytochrome c oxidase subunit 3	194	88
7507	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	128	72
7508	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	86
7509	D38112	Homo sapiens	cytochrome c oxidase subunit 1	116	65
7510	L38908	Nicotiana tabacum	extensin	114	36
7512	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	273	73
7513	Y36156	Homo sapiens	Human secreted protein #28.	168	44
7514	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	171	96
7515	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	46
7516	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	170	84
7517	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	105	43
7518	D38112	Homo sapiens	NADH dehydrogenase subunit 3	350	82
7519	D38114	Gorilla gorilla	NADH dehydrogenase subunit 3 (ND3)	141	84
7520	U12690	Homo sapiens	cytochrome oxidase subunit II	410	85
7521	D38112	Homo sapiens	cytochrome c oxidase subunit I	112	71
7522	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	96	46
7523	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	142	57
7524	AF220264	Homo sapiens	MOST-1	86	62
7525	AF130089	Homo sapiens	PRO2550	109	35
7526	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	106	79
7527	U49973	Homo sapiens	ORF2: function unknown	105	68
7528	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	122	62
7529	X05831	Rattus norvegicus	fibronectin precursor	100	64
7530	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	60
7531	X92485	Plasmodium	pva1	120	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
7532	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	383	75
7533	D38112	Homo sapiens	NADH dehydrogenase subunit 3	321	67
7534	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	126	72
7535	AF119851	Homo sapiens	PRO1722	110	67
7536	D38112	Homo sapiens	cytochrome c oxidase subunit 3	531	81
7537	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	75
7538	X92485	Plasmodium vivax	pva1	141	48
7539	AF119900	Homo sapiens	PRO2822	86	42
7540	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	126	50
7541	M15530	Homo sapiens	B-cell growth factor	136	53
7542	X53581	Rattus norvegicus	ORF4	174	46
7543	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	138	74
7544	D38112	Homo sapiens	cytochrome c oxidase subunit 1	116	86
7545	M15530	Homo sapiens	B-cell growth factor	96	47
7546	X92485	Plasmodium vivax	pva1	149	58
7547	AF113685	Homo sapiens	PRO0974	110	48
7548	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	226	73
7549	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	316	73
7550	S79410	Mus musculus	nuclear localization signal binding protein	107	70
7551	AF130089	Homo sapiens	PRO2550	130	45
7552	R95913	Homo sapiens	Neural thread protein.	99	56
7553	U93569	Homo sapiens	putative p150	171	47
7554	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	111	75
7555	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	207	56
7556	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	59
7557	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	125	43
7558	Y86445	Homo sapiens	Human gene 42-encoded protein fragment, SEQ ID NO:360.	95	71
7559	X83413	Human herpesvirus 6	U88	108	32
7560	A18812	Brassica napus	extensin	125	38
7561	D38112	Homo sapiens	ATPase subunit 6	495	87
7562	AF130089	Homo sapiens	PRO2550	141	46
7563	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	106	61
7564	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	128	62
7565	U50191	Caenorhabditis elegans	C. elegans collagen dpy-10 gene (Levy, A.D., Yang, J. and Kramer, J.M. Mol. Biol Cell 4, 803-17, 1993)	101	37
7566	V00672	Pan troglodytes	reading frame protein 4	294	73
7567	A18812	Brassica napus	extensin	145	48
7568	D38112	Homo sapiens	cytochrome c oxidase subunit 3	241	69
7569	L00016	Homo sapiens	urf4	284	71
7570	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	115	50
7571	G00673	Homo sapiens	Human secreted protein, SEQ ID NO:	124	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4754.		
7572	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	126	65
7573	X92485	Plasmodium vivax	pva1	157	49
7574	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	151	54
7575	AF130089	Homo sapiens	PRO2550	348	70
7576	R95913	Homo sapiens	Neural thread protein.	113	45
7577	L26953	Homo sapiens	chromosomal protein	148	38
7578	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	116	46
7579	AB047948	Macaca fascicularis	hypothetical protein	173	67
7580	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	149	57
7581	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	95	51
7582	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	125	85
7583	AC004079	Homo sapiens	human HOXA3; 95% similarity to e307530 (PID:g1888441)	127	100
7584	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	171	71
7585	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	80
7586	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	100
7587	D38112	Homo sapiens	cytochrome c oxidase subunit 1	194	71
7588	D38112	Homo sapiens	NADH dehydrogenase subunit 1	115	80
7589	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	77
7590	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	112	60
7591	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	72
7592	A49807	Neisseria meningitidis	IGA-LPHA3	93	33
7593	Z67990	Caenorhabditis elegans	contains similarity to Pfam domain: PF01484 (Nematode cuticle collagen N-terminal domain), Score=27.5, E-value=0.0001, N=1	102	42
7594	U43627	Arabidopsis thaliana	extensin	99	44
7595	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	74
7596	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	49
7597	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	190	92
7598	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	96
7599	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	95
7600	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	192	85
7601	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	91
7602	D38112	Homo sapiens	NADH dehydrogenase subunit 3	333	71

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7603	D38112	Homo sapiens	cytochrome c oxidase subunit 3	190	86
7604	U09500	Homo sapiens	cytochrome b	279	93
7605	Z14016	Nicotiana tabacum	pistil extensin like protein, partial CDS	84	40
7606	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	108	71
7607	G03636	Homo sapiens	Human secreted protein, SEQ ID NO: 7717.	55	52
7608	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	54
7609	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	97	62
7610	D38112	Homo sapiens	NADH dehydrogenase subunit 3	434	87
7611	Y21418	Homo sapiens	Human high mobility group protein HMGI-C mutant fragment 2.	97	46
7613	X92485	Plasmodium vivax	pval	106	58
7614	AC003058	Arabidopsis thaliana	unknown protein	191	88
7615	S74221	Homo sapiens	IK factor=cytokine down-regulating HLA class II	133	65
7616	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	148	74
7617	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	169	56
7618	L35013	Homo sapiens	spliceosomal protein	95	55
7619	V00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	441	85
7620	AF116638	Homo sapiens	PRO1546	172	42
7621	K03202	Homo sapiens	salivary proline-rich protein precursor	146	46
7622	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	145	72
7623	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	144	67
7624	U41031	Caenorhabditis elegans	proline-rich	92	59
7625	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	130	55
7626	L19098	Choristoneura fumiferana	cytochrome oxidase I	102	66
7627	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	99	76
7628	AF126163	Homo sapiens	HHLA3 protein	117	67
7629	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	69	53
7630	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	83	55
7631	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	87	64
7632	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	120	48
7633	R95913	Homo sapiens	Neural thread protein.	126	61
7634	V00662	Homo sapiens	cytochrome oxidase I	396	85
7635	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	205	84
7636	D38112	Homo sapiens	NADH dehydrogenase subunit 3	464	85
7637	D38112	Homo sapiens	NADH dehydrogenase subunit 2	165	94
7638	AF118086	Homo sapiens	PRO1992	120	68
7639	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7640	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	95	39
7641	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	68
7642	D38112	Homo sapiens	NADH dehydrogenase subunit 3	192	91
7643	D38112	Homo sapiens	NADH dehydrogenase subunit 3	416	80
7644	AF004341	Homo sapiens	cytochrome c oxidase subunit III	133	84
7645	U93570	Homo sapiens	putative p150	206	42
7646	D38112	Homo sapiens	ATPase subunit 6	192	80
7647	AF090942	Homo sapiens	PRO0657	128	71
7648	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	134	73
7649	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	115	52
7650	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	130	61
7651	X71442	Rattus norvegicus	ORF 1; putative	105	52
7652	L07545	Leishmania tarentolae	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression	111	32
7653	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	89	53
7654	G02473	Homo sapiens	Human secreted protein, SEQ ID NO: 6554.	291	49
7655	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	165	63
7656	D38112	Homo sapiens	NADH dehydrogenase subunit 3	470	88
7657	D38112	Homo sapiens	NADH dehydrogenase subunit 3	367	80
7658	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	108	95
7659	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhla.	109	50
7660	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	112	77
7661	AP002460	Arabidopsis thaliana	gene_id:F1D9.26-unknown protein	121	40
7662	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	96
7663	AF217973	Homo sapiens	unknown	124	51
7664	X92485	Plasmodium vivax	pva1	118	59
7665	AF118082	Homo sapiens	PRO1902	123	44
7666	AB014563	Homo sapiens	KIAA0663 protein	267	90
7667	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	49
7668	AF119855	Homo sapiens	PRO1847	152	72
7669	AK025116	Homo sapiens	unnamed protein product	127	65
7670	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	140	55
7671	R14847	Homo sapiens	Protein associated with biochemical pathway involving cAMP.	164	89
7672	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	68
7673	U37426	Homo sapiens	kinesin-like spindle protein HKSP	247	81
7674	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	125	75
7675	S67633	Homo sapiens	class I major histocompatibility antigen	103	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7676	AF126163	Homo sapiens	HHLA3 protein	146	72
7677	AC005192	Homo sapiens	similar to mouse interferon-related protein PC4; 96% identical to P19182 (PID:g135861)	143	87
7678	X07882	Homo sapiens	Po protein	126	39
7679	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	148	60
7680	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	177	37
7681	AF090930	Homo sapiens	PRO0478	80	58
7682	X55654	Homo sapiens	cytochrome C oxidase II subunit	115	65
7683	AB046048	Macaca fascicularis	unnamed protein product	145	67
7684	AF130079	Homo sapiens	PRO2852	117	60
7685	M13101	Rattus norvegicus	unknown protein	114	53
7686	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	134	74
7687	AF126163	Homo sapiens	HHLA3 protein	141	84
7688	Y36156	Homo sapiens	Human secreted protein #28.	120	61
7689	M37197	Homo sapiens	CCAAT-box-binding factor	104	95
7690	AL390114	Leishmania major	probable (hvy-6) u1102, variant a DNA, complete virion genome	97	54
7691	AF220264	Homo sapiens	MOST-1	117	76
7692	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	94	31
7693	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	98	40
7694	AF118082	Homo sapiens	PRO1902	115	55
7695	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	116	56
7696	Y15163	Mus musculus	putative splice variant containing region C	133	51
7697	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	132	52
7698	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	155	77
7699	M15530	Homo sapiens	B-cell growth factor	106	79
7700	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	108	70
7701	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	166	62
7702	AF090931	Homo sapiens	PRO0483	125	68
7703	G03432	Homo sapiens	Human secreted protein, SEQ ID NO: 7513.	114	79
7704	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	63
7705	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	141	35
7706	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	58
7707	X92485	Plasmodium vivax	pva1	126	42
7708	AK023563	Homo sapiens	unnamed protein product	217	72
7709	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	58
7710	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	124	56
7711	G03714	Homo sapiens	Human secreted protein, SEQ ID NO:	131	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7795.		
7712	D38112	Homo sapiens	NADH dehydrogenase subunit 1	116	72
7713	D38112	Homo sapiens	cytochrome c oxidase subunit 1	194	58
7714	X92485	Plasmodium vivax	pva1	123	68
7715	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	137	48
7716	AF119851	Homo sapiens	PRO1722	168	60
7717	U93570	Homo sapiens	putative p150	133	35
7718	AF116712	Homo sapiens	PRO2738	94	68
7719	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	107	55
7720	U49973	Homo sapiens	ORF2: function unknown	200	85
7721	U49973	Homo sapiens	ORF1: MER37; putative transposase similar to pogo element	234	73
7722	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	155	76
7723	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	140	65
7724	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	70	73
7725	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	94	55
7726	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	130	75
7727	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	94	78
7728	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	163	65
7729	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	111	63
7730	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	119	69
7731	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	113	84
7732	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	94	38
7733	U09500	Homo sapiens	cytochrome b	463	84
7734	D38112	Homo sapiens	cytochrome c oxidase subunit 3	334	92
7735	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	399	92
7736	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	128	55
7737	AC003058	Arabidopsis thaliana	unknown protein	167	66
7738	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	86	70
7739	D86854	Catharanthus roseus	extensin	154	40
7740	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	122	57
7741	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	99	49
7742	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	117	35
7743	V00662	Homo sapiens	cytochrome oxidase 1	568	89
7744	R63235	Homo sapiens	CNS neural thread protein HB4.	145	93
7745	R63235	Homo sapiens	CNS neural thread protein HB4.	154	100
7746	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7747	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	126	71
7748	D38112	Homo sapiens	cytochrome c oxidase subunit 3	327	92
7749	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	150	71
7750	AF130079	Homo sapiens	PRO2852	147	81
7751	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	104	49
7752	U43627	Arabidopsis thaliana	extensin	116	37
7753	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	71
7754	D38112	Homo sapiens	NADH dehydrogenase subunit 1	551	83
7755	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	88	56
7756	AF119851	Homo sapiens	PRO1722	97	56
7757	U80955	Caenorhabditis elegans	similar to RE repeat region of PIR-S27806 D. melanogaster homeotic protein BarH2 protein (dual bar protein)	89	100
7758	AC002045	Homo sapiens	Unknown protein product CIT987SK-A-589H1_1 splice form 2	97	94
7759	Y02775	Homo sapiens	Human secreted protein encoded by gene 12 clone HFTCU19.	288	98
7760	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	94	80
7761	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	199	76
7762	AF090931	Homo sapiens	PRO0483	153	84
7763	X92485	Plasmodium vivax	pval	114	62
7764	AF090931	Homo sapiens	PRO0483	107	86
7765	G02752	Homo sapiens	Human secreted protein, SEQ ID NO: 6833.	103	43
7766	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	73
7767	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	148	72
7768	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	83
7769	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	68	72
7770	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	62
7771	U93569	Homo sapiens	p40	188	43
7772	AL049934	Homo sapiens	hypothetical protein	113	47
7773	AF090931	Homo sapiens	PRO0483	86	65
7774	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	92
7775	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	143	65
7776	AF126163	Homo sapiens	HHLA3 protein	141	71
7777	G00423	Homo sapiens	Human secreted protein, SEQ ID NO: 4504.	93	47
7778	AF090942	Homo sapiens	PRO0657	148	74
7779	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	194	83
7780	U14966	Homo sapiens	ribosomal protein L5	315	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7781	R59843	Homo sapiens	ApoE4Lx2 protease.	126	47
7782	AF119855	Homo sapiens	PRO1847	131	51
7783	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	79	53
7784	D38112	Homo sapiens	NADH dehydrogenase subunit 3	405	82
7785	G00331	Homo sapiens	Human secreted protein, SEQ ID NO: 4412.	64	42
7786	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	59
7787	AF118082	Homo sapiens	PRO1902	131	48
7788	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	88	64
7789	J03807	Strongylocentrotus purpuratus	histone H1-delta	111	43
7790	D38112	Homo sapiens	NADH dehydrogenase subunit 1	139	85
7791	V00662	Homo sapiens	cytochrome oxidase I	522	80
7792	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	153	72
7793	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	84	53
7794	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	82	46
7795	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	76
7796	D38112	Homo sapiens	ATPase subunit 8	166	77
7797	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	48
7798	AF090931	Homo sapiens	PRO0483	132	75
7799	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	97	57
7800	D21261	Homo sapiens	similar to human 22kDa, SM22 mRNA (HUM22SM).	99	84
7801	X64707	Homo sapiens	BBC1	232	77
7802	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	104	33
7803	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	50
7804	Y36203	Homo sapiens	Human secreted protein #75.	142	56
7805	AF119851	Homo sapiens	PRO1722	88	46
7806	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	149	57
7807	X68600	Hordeum vulgare	pZE40	90	37
7808	AK025047	Homo sapiens	unnamed protein product	138	54
7809	AF130089	Homo sapiens	PRO2550	375	71
7810	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	124	65
7811	R59842	Homo sapiens	ApoE4L1 protease.	156	58
7812	AF016446	Caenorhabditis elegans	similar to C. elegans cuticulin precursor CUT-2 (SP:P34682)	95	42
7813	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	154	65
7814	AK025047	Homo sapiens	unnamed protein product	165	71
7815	W34499	Homo sapiens	Obesity receptor C protein.	309	89
7816	AJ222673	Hepatitis C virus type 2c	core protein	95	42
7817	AB011483	Arabidopsis thaliana	contains similarity to root cap protein-gene id:MUF9.16	104	61
7818	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	154	74

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7819	X92485	Plasmodium vivax	pva1	112	61
7820	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	103	60
7821	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	174	65
7822	AF130089	Homo sapiens	PRO2550	107	67
7823	AF118086	Homo sapiens	PRO1992	143	73
7824	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	132	63
7825	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	142	59
7826	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	42
7827	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	128	65
7828	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	104	58
7829	AF132961	Homo sapiens	CGI-27 protein	154	49
7830	X70343	Nicotiana sylvestris	extensin	105	30
7831	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	100	62
7832	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	129	51
7833	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	99	46
7834	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	74	65
7835	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	163	55
7836	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	72	52
7837	AF090942	Homo sapiens	PRO0657	126	59
7838	Z33426	Human respiratory syncytial virus	glycoprotein	110	34
7839	D63480	Homo sapiens	The KIAA0146 gene product is novel.	158	89
7840	W48352	Homo sapiens	Human breast cancer related protein BCFLT1.	88	63
7841	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	156	60
7842	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	145	100
7843	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	127	66
7844	M28016	Homo sapiens	cytochrome b	214	78
7845	D38112	Homo sapiens	cytochrome c oxidase subunit 3	283	82
7846	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	94	73
7847	D38112	Homo sapiens	cytochrome b	525	83
7848	L27428	Homo sapiens	reverse transcriptase	210	67
7849	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	156	96
7850	X92485	Plasmodium vivax	pva1	121	54
7851	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	147	59
7852	D38112	Homo sapiens	NADH dehydrogenase subunit 2	191	93

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7853	W48808	Homo sapiens	Homo sapiens clone CG109_1 protein.	72	69
7854	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	76
7855	U43627	Arabidopsis thaliana	extensin	124	35
7856	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	95
7857	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	95	57
7858	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	157	91
7859	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	108	45
7860	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	159	54
7861	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	63
7862	D38112	Homo sapiens	cytochrome c oxidase subunit 3	265	77
7863	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	145	56
7864	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	100
7865	D38112	Homo sapiens	cytochrome c oxidase subunit 1	409	87
7866	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	112	50
7867	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	169	74
7868	AL031004	Arabidopsis thaliana	RSZp22 splicing factor	127	35
7869	U83771	Accipiter superciliosus	cytochrome oxidase I	168	73
7870	U83771	Accipiter superciliosus	cytochrome oxidase I	186	81
7871	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	203	36
7872	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	130	71
7873	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	44
7874	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	138	69
7875	AF119855	Homo sapiens	PRO1847	174	70
7876	AF210651	Homo sapiens	NAG18	164	76
7877	Z93244	Homo sapiens	bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	111	45
7878	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	227	79
7879	AK024455	Homo sapiens	FLJ00047 protein	120	68
7880	Y36156	Homo sapiens	Human secreted protein #28.	85	68
7881	AF116661	Homo sapiens	PRO1438	138	61
7882	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	141	55
7883	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	111	63
7884	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	106	64
7885	AK022821	Homo sapiens	unnamed protein product	175	72
7886	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7887	L27428	Homo sapiens	reverse transcriptase	165	63
7888	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	139	61
7889	M15530	Homo sapiens	B-cell growth factor	132	74
7890	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	81	64
7891	AB046048	Macaca fascicularis	unnamed portein product	150	61
7892	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	154	73
7893	AF130089	Homo sapiens	PRO2550	224	61
7894	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	127	69
7895	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	62
7896	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	50
7897	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	108	68
7898	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	144	65
7899	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	105	83
7900	AF026689	Homo sapiens	prostate-specific transglutaminase	104	57
7901	X03717	Homo sapiens	pot. unidentified reading frame	105	46
7902	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	94	67
7903	X61046	Hydra sp.	mini-collagen	107	46
7904	AF124726	Homo sapiens	acinusL	111	44
7905	U77049	Ovis aries	bactinecin 11	116	38
7906	AF118086	Homo sapiens	PRO1992	130	73
7907	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	121	48
7908	AL359782	Trypanosoma brucei	possible (hhv-6) u1 102, variant a dna, complete virion genome.	124	83
7909	AC004450	Arabidopsis thaliana	putative extensin	167	34
7910	AF130079	Homo sapiens	PRO2852	110	42
7911	AF090942	Homo sapiens	PRO0657	144	66
7912	AF090931	Homo sapiens	PRO0483	96	80
7913	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	128	46
7914	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	87	68
7915	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	105	75
7916	X92485	Plasmodium vivax	pva1	102	67
7917	AF090942	Homo sapiens	PRO0657	126	76
7918	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	108	47
7919	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	156	63
7920	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	138	61
7921	L26251	Trypanosoma brucei	CR5	95	37
7922	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	176	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7923	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	174	61
7924	L27428	Homo sapiens	reverse transcriptase	121	33
7925	Y36156	Homo sapiens	Human secreted protein #28.	137	67
7926	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	119	73
7927	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	138	65
7928	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	138	60
7929	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	166	61
7930	AF004341	Homo sapiens	cytochrome c oxidase subunit III	144	87
7931	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	176	53
7932	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	179	60
7933	V00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	279	92
7934	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	132	63
7935	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	101	64
7936	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	159	55
7937	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	320	80
7938	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	159	71
7939	AF144054	Homo sapiens	apoptosis related protein APR-4	127	65
7940	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	314	73
7941	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	121	57
7942	AB040936	Homo sapiens	KIAA1503 protein	149	71
7943	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	107	83
7944	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	74	60
7945	Y13141	Bromheadia finlaysoniana	extensin	68	35
7946	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	126	50
7947	AP000735	Arabidopsis thaliana	extensin protein-like	214	40
7948	AF161356	Homo sapiens	HSPC093	134	75
7949	AF090942	Homo sapiens	PRO0657	110	48
7950	AJ249395	Globodera pallida	cytochrome b	117	36
7951	AF116661	Homo sapiens	PRO1438	135	49
7952	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	92
7953	M15530	Homo sapiens	B-cell growth factor	143	65
7954	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	137	68
7955	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	130	62
7956	AF130089	Homo sapiens	PRO2550	153	62
7957	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	99	48
7958	AF161356	Homo sapiens	HSPC093	134	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7959	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	131	57
7960	X92485	Plasmodium vivax	pval	107	53
7961	AF210651	Homo sapiens	NAG18	113	77
7962	AF130051	Homo sapiens	PRO0898	84	71
7963	R59842	Homo sapiens	ApoE4L1 protease.	116	68
7964	AF090931	Homo sapiens	PRO0483	129	56
7965	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	151	51
7966	R95913	Homo sapiens	Neural thread protein.	110	40
7967	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	180	50
7968	AF090894	Homo sapiens	PRO0113	104	58
7969	Y21040	Homo sapiens	Human glial fibrillary acidic protein GFAP mutant fragment 49.	285	100
7970	AK001452	Homo sapiens	unnamed protein product	346	56
7971	V00672	Pan troglodytes	reading frame protein 4	134	90
7972	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	48
7973	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	104	84
7974	AF116661	Homo sapiens	PRO1438	140	62
7975	AF119882	Homo sapiens	PRO2492	112	48
7976	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	80	65
7977	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	124	89
7978	M11901	Rattus norvegicus	proline-rich salivary protein	125	36
7979	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	149	68
7980	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	289	84
7981	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	59
7982	X77816	Rattus norvegicus	PR-Vbeta1	109	69
7983	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	149	73
7984	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	128	72
7985	R59842	Homo sapiens	ApoE4L1 protease.	130	82
7986	AF090895	Homo sapiens	PRO0117	83	58
7987	X07881	Homo sapiens	proline-rich protein G1	131	41
7988	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	123	53
7989	AF090894	Homo sapiens	PRO0113	104	61
7990	Z93244	Homo sapiens	bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	100	61
7991	AK024455	Homo sapiens	FLJ00047 protein	131	56
7992	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	136	61
7993	AF210651	Homo sapiens	NAG18	133	61
7994	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	92	42
7995	D38112	Homo sapiens	cytochrome c oxidase subunit I	171	82
7996	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7997	AF090928	Homo sapiens	PRO0470	86	76
7998	AJ251579	Arabidopsis thaliana	cef protein	113	37
7999	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	119	60
8000	R95913	Homo sapiens	Neural thread protein.	105	70
8001	AF229067	Homo sapiens	PADI-H protein	118	61
8002	W88609	Homo sapiens	Secreted protein encoded by gene 76 clone HKIXL73.	83	65
8003	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	85	61
8004	S79410	Mus musculus	nuclear localization signal binding protein	123	43
8005	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	93	68
8006	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	64
8007	AF016099	Mus musculus	endonuclease/reverse transcriptase	147	38
8008	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	72
8009	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	71
8010	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	92	54
8011	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	152	59
8012	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	123	66
8013	AF161356	Homo sapiens	HSPC093	185	64
8014	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	107	54
8015	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	71	65
8016	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	139	66
8017	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	94	77
8018	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	108	46
8019	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	178	61
8020	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	85	65
8021	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	51
8022	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	202	77
8023	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	195	68
8024	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	158	53
8025	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	135	58
8026	X92485	Plasmodium vivax	pva1	128	56
8027	Y19767	Homo sapiens	SEQ ID NO 485 from W09922243.	135	61
8028	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	105	66
8029	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	126	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8030	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	117	40
8031	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	126	72
8032	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	125	41
8033	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	113	69
8034	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	102	66
8035	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	221	95
8036	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	106	36
8037	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	113	55
8038	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	108	64
8039	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	110	68
8040	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	169	86
8041	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	170	56
8042	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	95	58
8043	AK024455	Homo sapiens	FLJ00047 protein	152	68
8044	AF220264	Homo sapiens	MOST-1	83	68
8045	AK024455	Homo sapiens	FLJ00047 protein	131	55
8046	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	181	78
8047	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	147	61
8048	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	102	43
8049	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	59
8050	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	154	56
8051	D00570	Mus musculus	open reading frame (196 AA)	127	59
8052	AF040964	Homo sapiens	unknown protein IT1	143	50
8053	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	83
8054	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	108	70
8055	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	134	62
8056	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	65
8057	AF090895	Homo sapiens	PRO0117	110	77
8058	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	90
8059	AF118082	Homo sapiens	PRO1902	117	50
8060	AK022217	Homo sapiens	unnamed protein product	145	53
8061	AF130089	Homo sapiens	PRO2550	160	76
8062	AF119851	Homo sapiens	PRO1722	177	54
8063	D38112	Homo sapiens	NADH dehydrogenase subunit 3	362	73
8064	D38112	Homo sapiens	NADH dehydrogenase subunit 3	426	85
8065	D38112	Homo sapiens	NADH dehydrogenase subunit 3	344	90
8066	AF068294	Homo sapiens	HDCMB45P	146	60
8067	V00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	461	87
8068	D38112	Homo sapiens	NADH dehydrogenase subunit 4	504	90

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8069	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	97	40
8070	R59842	Homo sapiens	ApoE4L1 protease.	147	47
8071	AF119851	Homo sapiens	PRO1722	139	59
8072	X92485	Plasmodium vivax	pval	183	45
8073	AF116712	Homo sapiens	PRO2738	95	52
8074	AF213465	Homo sapiens	dual oxidase	184	80
8075	AF090895	Homo sapiens	PRO0117	153	57
8076	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	162	73
8077	T85403_cd1	Homo sapiens	19-APR-1993 Human cadherin-11 coding sequence.	284	98
8078	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	99	63
8079	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	162	73
8080	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	142	52
8081	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	37
8082	X05285	Drosophila melanogaster	fibrillarin	100	34
8083	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	142	65
8084	G02216	Homo sapiens	Human secreted protein, SEQ ID NO: 6297.	380	82
8085	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	64
8086	X92485	Plasmodium vivax	pval	138	64
8087	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	82
8088	D38112	Homo sapiens	NADH dehydrogenase subunit 5	180	79
8089	U27143	Homo sapiens	protein kinase C inhibitor-I	119	41
8090	AF119851	Homo sapiens	PRO1722	85	47
8091	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	112	73
8092	S79410	Mus musculus	nuclear localization signal binding protein	133	64
8093	AF119854	Homo sapiens	PRO1843	522	100
8094	X92485	Plasmodium vivax	pval	115	82
8095	D38112	Homo sapiens	NADH dehydrogenase subunit 1	598	86
8096	AF097473	Mus musculus	ORF1	109	46
8097	AF097473	Mus musculus	ORF1	109	46
8098	Y17833	Human endogenous retrovirus K	pol protein	281	73
8099	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	156	69
8100	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	126	42
8101	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	126	65
8102	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	145	70
8103	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	163	71

SEQ ID NO:	Accession No:	Species	Description	Smith-Waterman Score	% Identity
8104	AF130089	Homo sapiens	PRO2550	130	42
8105	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	116	57
8106	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	132	61
8107	AF090942	Homo sapiens	PRO0657	123	41
8108	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	134	38
8109	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	101	77
8110	D38112	Homo sapiens	cytochrome c oxidase subunit 1	340	90
8111	AF130089	Homo sapiens	PRO2550	123	86
8112	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	122	90
8113	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	182	47
8114	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	101	77
8115	G00452	Homo sapiens	Human secreted protein, SEQ ID NO: 4533.	72	50
8116	D38112	Homo sapiens	NADH dehydrogenase subunit 3	459	88
8117	L17318	Rattus norvegicus	proline-rich proteoglycan	110	45
8118	S79410	Mus musculus	nuclear localization signal binding protein	125	62
8119	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	106	78
8120	D38112	Homo sapiens	NADH dehydrogenase subunit 1	106	84
8121	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	110	45
8122	D86854	Catharanthus roseus	extensin	142	35
8123	X92485	Plasmodium vivax	pva1	144	53
8124	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	59
8125	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	67
8126	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	145	62
8127	X07881	Homo sapiens	proline-rich protein G1	142	37
8128	X70343	Nicotiana glauca	extensin	102	29
8129	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	113	48
8130	AF090895	Homo sapiens	PRO0117	150	71
8131	D00570	Mus musculus	open reading frame (251 AA)	130	41
8132	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	106	61
8133	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	128	61
8134	AF130079	Homo sapiens	PRO2852	181	77
8135	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	109	58
8136	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	98	64
8137	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	112	43
8138	AF119900	Homo sapiens	PRO2822	113	57
8139	D38112	Homo sapiens	NADH dehydrogenase subunit 3	427	86

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8140	AF004341	Homo sapiens	cytochrome c oxidase subunit III	155	88
8141	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	163	58
8142	D70836	Homo sapiens	Zinc-finger protein	156	47
8143	AC002291	Arabidopsis thaliana	extensin	153	37
8144	X55683	Lycopersicon esculentum	extensin (class I)	85	34
8145	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	100	76
8146	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	108	63
8147	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	110	79
8148	M22332	Homo sapiens	unknown protein	156	40
8149	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	92	76
8150	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	131	66
8151	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	441	76
8152	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	67
8153	AF130089	Homo sapiens	PRO2550	129	42
8154	AF130089	Homo sapiens	PRO2550	173	50
8155	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	64
8156	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	171	82
8157	L27428	Homo sapiens	reverse transcriptase	181	50
8158	U11271	Homo sapiens	thromboxane A2 receptor	138	73
8159	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	145	53
8160	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	139	58
8161	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	155	59
8162	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	64
8163	AF161361	Homo sapiens	HSFC098	89	66
8164	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	117	58
8165	AF130089	Homo sapiens	PRO2550	121	63
8166	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	148	85
8167	X92485	Plasmodium vivax	pval	97	56
8168	X92485	Plasmodium vivax	pval	115	57
8169	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	124	61
8170	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	60
8171	X92485	Plasmodium vivax	pval	105	44
8172	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	75	64
8173	S79410	Mus musculus	nuclear localization signal binding protein	106	65
8174	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	108	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8175	Y36203	Homo sapiens	Human secreted protein #75.	150	51
8176	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	114	41
8177	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	135	68
8178	AF090928	Homo sapiens	PRO0470	119	72
8179	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	141	75
8180	AF220264	Homo sapiens	MOST-1	94	61
8181	AF119851	Homo sapiens	PRO1722	143	73
8182	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	134	64
8183	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	143	59
8184	X92485	Plasmodium vivax	pval	127	72
8185	X92485	Plasmodium vivax	pval	130	65
8186	AF119851	Homo sapiens	PRO1722	285	64
8187	AF090942	Homo sapiens	PRO0657	137	38
8188	AF090931	Homo sapiens	PRO0483	154	66
8189	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	148	43
8190	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	268	79
8191	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	110	43
8192	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	129	78
8193	AF113685	Homo sapiens	PRO0974	86	52
8194	Y36203	Homo sapiens	Human secreted protein #75.	132	61
8195	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	225	77
8196	S80119	Rattus sp.	reverse transcriptase homolog	105	40
8197	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	124	39
8198	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	121	60
8199	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	91	68
8200	Y36203	Homo sapiens	Human secreted protein #75.	131	56
8201	Y36203	Homo sapiens	Human secreted protein #75.	136	44
8202	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	166	48
8203	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	50
8204	Y36203	Homo sapiens	Human secreted protein #75.	127	58
8205	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	139	61
8206	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	190	92
8207	AF090931	Homo sapiens	PRO0483	160	87
8208	AF126163	Homo sapiens	HHLA3 protein	107	67
8209	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	93	41
8210	Y36156	Homo sapiens	Human secreted protein #28.	100	62
8211	AF161356	Homo sapiens	HSPC093	73	60
8212	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	107	34
8213	AB046048	Macaca	unnamed protein product	146	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		fascicularis			
8214	AF130079	Homo sapiens	PRO2852	121	59
8215	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	109	50
8216	AF090930	Homo sapiens	PRO0478	153	79
8217	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	105	60
8218	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	135	56
8219	M11901	Rattus norvegicus	proline-rich salivary protein	102	42
8220	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	95	32
8221	X52235	Homo sapiens	ORF1	174	39
8222	AF130089	Homo sapiens	PRO2550	159	67
8223	AF068294	Homo sapiens	HDCMB45P	161	58
8224	M62387	Oryctolagus cuniculus	ubiquitin conjugating-protein	219	90
8225	AF113685	Homo sapiens	PRO0974	136	65
8226	D38112	Homo sapiens	NADH dehydrogenase subunit 3	430	85
8227	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	115	58
8228	Y36156	Homo sapiens	Human secreted protein #28.	117	50
8229	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	130	44
8230	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	145	50
8231	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	105	46
8232	S62928	Homo sapiens	PRB1M protein precursor	113	37
8233	AB047600	Macaca fascicularis	hypothetical protein	142	62
8234	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	104	48
8235	U12695	Pan paniscus	cytochrome oxidase subunit II	259	84
8236	K01664	Drosophila melanogaster	Bkm-like protein	116	61
8237	AF116661	Homo sapiens	PRO1438	135	56
8238	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	107	53
8239	U93572	Homo sapiens	p40	168	49
8240	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	100	72
8241	Z70292	Homo sapiens	chemokine CC-1	231	83
8242	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	119	82
8243	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	97	83
8244	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	114	78
8245	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	81	65
8246	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	74	60
8247	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	115	58
8248	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	58
8249	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	84
8250	AF118082	Homo sapiens	PRO1902	136	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8251	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	196	59
8252	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	106	81
8253	AF130089	Homo sapiens	PRO2550	143	53
8254	AK024455	Homo sapiens	FLJ00047 protein	151	68
8255	AK022821	Homo sapiens	unnamed protein product	140	68
8256	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	53
8257	M24509	Mus musculus	ferritin heavy chain	347	69
8258	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	142	57
8259	U93570	Homo sapiens	p40	254	57
8260	AF218028	Homo sapiens	unknown	129	71
8261	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	77	68
8262	D38112	Homo sapiens	cytochrome c oxidase subunit 3	604	90
8263	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	60
8264	AL139298	Streptomyces coelicolor A3(2)	putative membrane protein	92	34
8265	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	138	70
8266	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	100	64
8267	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	113	38
8268	X92485	Plasmodium vivax	pval	102	63
8269	X61048	Hydra sp.	mini-collagen	110	46
8270	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	88	82
8271	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	121	75
8272	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	48
8273	AF090944	Homo sapiens	PRO0663	122	42
8274	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	81	85
8275	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	140	54
8276	AF130089	Homo sapiens	PRO2550	275	56
8277	L27428	Homo sapiens	reverse transcriptase	105	27
8278	S79410	Mus musculus	nuclear localization signal binding protein	112	54
8279	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	159	73
8280	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	109	71
8281	AF104921	Homo sapiens	succinyl-CoA synthetase alpha subunit	188	42
8282	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	39
8283	X55683	Lycopersicon esculentum	extensin (class I)	96	36
8284	AF225910	Mus musculus	DAZ-associated protein 1	117	33
8285	AF130089	Homo sapiens	PRO2550	347	75
8286	AB046100	Macaca fascicularis	unnamed protein product	140	45
8287	X55684	Lycopersicon	extensin (class I)	67	45

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		esculentum			
8288	AF029670	Homo sapiens	Rad51C truncated protein	186	69
8289	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	149	50
8290	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	119	67
8291	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	152	50
8292	D89999	Gallus gallus	muscle derived protein	1134	66
8293	L11566	Homo sapiens	ribosomal protein L18	335	69
8294	W61170	Homo sapiens	Partial polypeptide sequence from CP140 partial cDNA.	441	95
8295	S62077	Homo sapiens	HP1hs alpha=25 kda chromosomal autoantigen	175	94
8296	AF119882	Homo sapiens	PRO2492	125	48
8297	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	54
8298	AK025116	Homo sapiens	unnamed protein product	259	82
8300	X92485	Plasmodium vivax	pva1	162	47
8301	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	157	76
8302	AF092176	Homo sapiens	MHC class II antigen	280	84
8303	AF118082	Homo sapiens	PRO1902	174	52
8304	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	105	50
8305	AK023563	Homo sapiens	unnamed protein product	244	60
8306	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	66
8307	U15647	Mus musculus	reverse transcriptase	107	38
8308	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	110	40
8309	AB005540	Rattus rattus	PCTAIRE2	166	59
8310	M37679	Mus musculus	Ig heavy chain precursor	95	64
8311	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	137	82
8312	W29643	Homo sapiens	Human secreted protein CW383.1.	312	100
8313	AF113685	Homo sapiens	PRO0974	116	39
8314	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	128	69
8315	Z28407	Homo sapiens	ribosomal protein L8	497	78
8316	AE003536	Drosophila melanogaster	CG6451 gene product	237	51
8317	M19419	Mus musculus	proline-rich salivary protein	115	39
8318	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	92	53
8319	Y29862	Homo sapiens	Human secreted protein clone du515.21.	399	81
8320	Z34278	Homo sapiens	mucin	103	25
8321	AL359782	Trypanosoma brucei	possible (bhv-6) u1102, variant a dna, complete virion genome.	142	91
8322	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	82	62
8323	Z46791	Caenorhabditis elegans	contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=67.1, E-value=1.2e-16, N=3; PF01484 (Nematode cuticle collagen N-terminal domain), Score=82.0, E-value=3.9e-21, N=1	122	37
8324	AF021232	Homo sapiens	TRAIL-R4-A	113	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8325	AB046085	Macaca fascicularis	unnamed protein product	292	75
8326	AF113944	Muntiacus muntjak	prion protein	96	39
8327	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	125	63
8328	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	123	62
8329	AJ005897	Homo sapiens	JM5	275	73
8330	AF119900	Homo sapiens	PRO2822	138	76
8331	AF163573	Homo sapiens	CARKL	359	84
8332	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	103	37
8333	AF026246	Homo sapiens	HERV-E integrase	354	78
8334	J03756	Homo sapiens	hGH-V2	362	82
8335	AB001517	Homo sapiens	KNP-1 alpha protein	126	76
8336	X97490	Mus musculus	PNG protein	469	98
8337	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	74
8338	V18354_cd1	Homo sapiens	17-NOV-1992 Human R20 seven transmembrane (7TM) receptor genomic DNA.	379	92
8339	V18354_cd1	Homo sapiens	17-NOV-1992 Human R20 seven transmembrane (7TM) receptor genomic DNA.	402	93
8340	Z11502	Homo sapiens	intestine-specific annexin	383	89
8341	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	110	54
8342	AC003113	Arabidopsis thaliana	F24O1.6	68	50
8343	X12517	Homo sapiens	C protein (AA 1-159)	321	82
8344	D86549	Homo sapiens	p97 homologous protein	279	96
8345	Y73384	Homo sapiens	HTRM clone 2284580 protein sequence.	1513	100
8346	AP001745	Homo sapiens	human cDNA DKFZp586F0422, Accession No. AL050173	118	40
8347	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	121	49
8348	AF091090	Homo sapiens	unknown	125	44
8349	AF106542	Homo sapiens	pregnancy-specific beta-1 glycoprotein 1	145	100
8350	AF090942	Homo sapiens	PRO0657	252	65
8351	L23116	Homo sapiens	galactocerebrosidase	185	85
8352	AJ243803	Streptomyces coelicolor A3(2)	hypothetical protein	97	36
8353	Y11339	Homo sapiens	GalNAc alpha-2,6-sialyltransferase 1	306	100
8354	U09477	Homo sapiens	p53-binding protein	388	100
8355	L27584	Homo sapiens	Ca channel B3 subunit	197	100
8356	AF071569	Homo sapiens	multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform	574	100
8357	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	321	81
8358	Y12916	Homo sapiens	Amino acid sequence of a human secreted peptide.	759	100
8359	AF038961	Homo sapiens	SL15 protein	166	100
8360	W75093	Homo sapiens	Human secreted protein encoded by gene 37 clone HFVGS85.	328	90
8361	R95326	Homo sapiens	Tumor necrosis factor receptor I death domain ligand (clone 2DD).	386	97

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8362	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor; PDPr	269	88
8363	X07855	Homo sapiens	G-Protein	289	98
8364	AL110247	Homo sapiens	hypothetical protein	265	97
8365	AB046774	Homo sapiens	KIAA1554 protein	3619	99
8366	M10050	Homo sapiens	fatty acid binding protein	97	100
8367	M20882	Homo sapiens	pregnancy-specific beta-glycoprotein e	1097	99
8368	AB051901	Homo sapiens	VDUP1	662	98
8369	U72678	Mus musculus	EF-9	176	65
8370	AL117237	Homo sapiens	hypothetical protein	478	60
8371	M10617	Homo sapiens	L-FABP	104	84
8372	AJ249980	Homo sapiens	hypothetical protein	1527	97
8373	AF003136	Caenorhabditis elegans	contains weak similarity to an AMP-binding motif	242	55
8374	X91638	Gallus gallus	BRM protein	225	90
8375	W75093	Homo sapiens	Human secreted protein encoded by gene 37 clone HFVGS85.	369	100
8376	Z36714	Homo sapiens	cyclin F	519	95
8377	X86401	Homo sapiens	L-arginine: glycine amidinotransferase	200	97
8378	M12413	Homo sapiens	apolipoprotein B100	1278	99
8379	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	159	66
8380	AF151860	Homo sapiens	CGI-102 protein	202	77
8381	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	255	92
8382	AF017807	Homo sapiens	Arp2/3 complex 16kDa subunit	418	87
8383	U28727	Homo sapiens	pregnancy-associated plasma protein-A preproform	196	97
8384	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	128	85
8385	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	203	69
8386	AF090931	Homo sapiens	PRO0483	145	77
8387	S63758	Mus sp.	metallothionein-I gene transcription activator	324	98
8388	W89030	Homo sapiens	Polypeptide fragment encoded by gene 165.	174	66
8389	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	93	70
8390	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	157	46
8391	V29245_cd1	Homo sapiens	15-NOV-1996 Nucleotide sequence of the human selenium-binding protein.	421	82
8392	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	184	77
8393	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	99	77
8394	AK023563	Homo sapiens	unnamed protein product	285	75
8395	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	161	75
8396	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	121	61
8397	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	108	70
8398	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	57
8399	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	63
8400	W88607	Homo sapiens	Secreted protein encoded by gene 74 clone HHSEG23.	146	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8401	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	90	69
8402	AF119851	Homo sapiens	PRO1722	133	65
8403	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	67	76
8404	L06498	Homo sapiens	ribosomal protein S20	170	94
8405	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	58
8406	AF118086	Homo sapiens	PRO1992	142	80
8407	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	153	81
8408	AF090919	Homo sapiens	PRO0327	96	74
8409	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	62
8410	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	150	100
8411	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	103	75
8412	AF116715	Homo sapiens	PRO2829	158	76
8413	AF229067	Homo sapiens	PADI-H protein	137	56
8414	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	131	77
8415	AF068294	Homo sapiens	HDCMB45P	132	54
8416	W34499	Homo sapiens	Obesity receptor C protein.	251	77
8417	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	272	57
8418	S79410	Mus musculus	nuclear localization signal binding protein	113	54
8419	AK025047	Homo sapiens	unnamed protein product	128	58
8420	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	130	46
8421	AL132841	Caenorhabditis elegans	Y15E3A.3	135	56
8422	AF130051	Homo sapiens	PRO0898	164	72
8423	G00092	Homo sapiens	Human secreted protein, SEQ ID NO: 4173.	161	96
8424	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	100
8425	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	134	75
8426	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	91	48
8427	AF194641	Homo sapiens	immunoglobulin lambda light chain variable region	174	69
8428	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	146	68
8429	M64322	Homo sapiens	protein tyrosine phosphatase	201	100
8430	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	135	55
8431	AF090931	Homo sapiens	PRO0483	158	87
8432	J04495	Macaca mulatta	alpha-globin	150	100
8433	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	150	78
8434	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	137	48
8435	AJ272324	Homo sapiens	adaptor molecule-1	333	100
8436	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	91	48
8437	M18085	Homo sapiens	glycoprotein Iib	154	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8438	X92485	Plasmodium vivax	pva1	138	64
8439	G03136	Homo sapiens	Human secreted protein, SEQ ID NO: 7217.	126	56
8440	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	105	72
8441	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	122	55
8442	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	139	69
8443	Y36203	Homo sapiens	Human secreted protein #75.	103	70
8444	AB034633	Mus musculus	deubiquitinating enzyme	129	100
8445	U01849	Trypanosoma brucei	ORF2	95	41
8446	J05497	Rattus norvegicus	snRNP-associated polypeptide N	115	37
8447	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	137	50
8448	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	100
8449	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	94
8450	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	63
8451	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	91
8452	W78226	Homo sapiens	Fragment of human secreted protein encoded by gene 1.	804	97
8453	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	109	100
8454	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	138	88
8455	AF099505	Homo sapiens	colon carcinoma related protein	100	63
8456	AF217511	Homo sapiens	uncharacterized bone marrow protein BM034	130	96
8457	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	70
8458	L17007	Didelphis marsupialis	protamine 1	101	80
8459	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	145	62
8460	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	121	75
8461	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	110	81
8462	AF016371	Homo sapiens	U-snRNP-associated cyclophilin	108	70
8463	Y19767	Homo sapiens	SEQ ID NO 485 from W09922243.	80	93
8464	AF130089	Homo sapiens	PRO2550	190	65
8465	AF197913	Helicoverpa armigera nuclear polyhedrosis virus	basic DNA-binding protein BDBP	159	55
8466	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	183	70
8467	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	97	60
8468	AF118082	Homo sapiens	PRO1902	72	42
8469	AF217449	Schistosoma mekongi	NADH dehydrogenase subunit 6	107	40
8470	G03258	Homo sapiens	Human secreted protein, SEQ ID NO:	88	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7339.		
8471	AF090931	Homo sapiens	PRO0483	161	79
8472	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	127	56
8473	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	50
8474	AF022789	Homo sapiens	ubiquitin hydrolyzing enzyme 1	140	100
8475	X03145	Homo sapiens	pot. ORF VI	349	81
8476	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	65
8477	R59842	Homo sapiens	ApoE4L1 protease.	115	69
8478	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	112	56
8479	K01664	Drosophila melanogaster	Bkm-like protein	140	44
8480	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	95	70
8481	AF090931	Homo sapiens	PRO0483	111	67
8482	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	122	92
8483	M69297	Homo sapiens	ORF 3	102	39
8484	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	148	72
8485	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	136	65
8486	AF032906	Homo sapiens	cathepsin Z precursor; CTSZ	299	100
8487	X15917	Paramecium aurelia	ND2 protein (AA 1-193) (unusual start codon)	94	35
8488	U93574	Homo sapiens	putative p150	109	35
8489	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	142	72
8490	X92485	Plasmodium vivax	pva1	120	85
8491	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	109	42
8492	M15530	Homo sapiens	B-cell growth factor	126	64
8493	AF090895	Homo sapiens	PRO0117	123	60
8494	G02403	Homo sapiens	Human secreted protein, SEQ ID NO: 6484.	166	100
8495	AF116661	Homo sapiens	PRO1438	126	63
8496	AF130089	Homo sapiens	PRO2550	298	70
8497	AF090895	Homo sapiens	PRO0117	113	75
8498	AF090930	Homo sapiens	PRO0478	142	68
8499	AF126163	Homo sapiens	HHLA3 protein	139	72
8500	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	109	75
8501	S79410	Mus musculus	nuclear localization signal binding protein	98	48
8502	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	132	63
8503	AF119851	Homo sapiens	PRO1722	107	53
8504	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	158	67
8505	AF090931	Homo sapiens	PRO0483	128	50
8506	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	126	56
8507	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	154	82
8508	X92485	Plasmodium	pva1	83	70

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
8509	AL390114	Leishmania major	extremely cysteine/valine rich protein	144	50
8510	AL160493	Leishmania major	probable (hliv-6) u1102, variant a DNA, complete virion genome	124	86
8511	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	141	51
8512	AF229067	Homo sapiens	PADI-H protein	155	76
8513	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	170	68
8514	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	157	66
8515	AF090930	Homo sapiens	PRO0478	88	80
8516	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	134	59
8517	K01664	Drosophila melanogaster	Bkm-like protein	102	92
8518	M31145	Homo sapiens	insulin-like growth factor binding protein precursor	460	96
8519	M18193	Homo sapiens	inter-alpha-trypsin inhibitor heavy chain old gene name 'ITI'	118	41
8520	AF116689	Homo sapiens	PRO2168	127	92
8521	AF130051	Homo sapiens	PRO0898	133	85
8522	L27428	Homo sapiens	reverse transcriptase	201	72
8523	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	108	74
8524	AF161356	Homo sapiens	HSPC093	127	60
8525	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	95	83
8526	AF118086	Homo sapiens	PRO1992	95	64
8527	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	50
8528	AB046048	Macaca fascicularis	unnamed poeitin product	154	62
8529	AF130089	Homo sapiens	PRO2550	150	70
8530	Y03000	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	111	55
8531	AP000516	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	65
8532	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	172	59
8533	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	395	91
8534	S79410	Mus musculus	nuclear localization signal binding protein	100	45
8535	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	107	95
8536	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	128	89
8537	Z28407	Homo sapiens	ribosomal protein L8	242	79
8538	AF130089	Homo sapiens	PRO2550	139	71
8539	Q55625_cd1	Homo sapiens	22-JUN-1992 Human beta globin 5'-UTR-CDS-3'-UTR.	274	76
8540	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	154	61
8541	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	69
8542	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	64
8543	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	240	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6953.		
8544	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	117	85
8545	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	110	95
8546	AF119851	Homo sapiens	PRO1722	146	80
8547	U49973	Homo sapiens	ORF2: function unknown	105	86
8548	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	71
8549	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	152	53
8550	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	80	40
8551	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	140	74
8552	V00672	Pan troglodytes	reading frame protein 4	142	92
8553	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	164	63
8554	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	148	71
8555	AB046100	Macaca fascicularis	unnamed protein product	144	58
8556	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	322	73
8557	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	140	62
8558	U30888	Homo sapiens	tRNA-Guanine Transglycosylase	276	86
8559	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	114	71
8560	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	108	72
8561	G03136	Homo sapiens	Human secreted protein, SEQ ID NO: 7217.	110	57
8562	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	140	83
8563	W34499	Homo sapiens	Obesity receptor C protein.	188	92
8564	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	124	56
8565	L07946	Volvox carteri	histone H1-I	108	38
8566	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	132	77
8567	M13941	Human herpesvirus 4	nuclear antigen 1	100	43
8568	Y36156	Homo sapiens	Human secreted protein #28.	136	67
8569	X70343	Nicotiana glauca	extensin	92	34
8570	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	381	87
8571	V00672	Pan troglodytes	reading frame protein 4	146	93
8572	D38116	Pan paniscus	ATPase subunit 6	116	96
8573	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	132	52
8574	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	217	100
8575	M58009	Pan troglodytes	cytochrome c oxidase subunit II	271	84
8576	D38112	Homo sapiens	ATPase subunit 6	117	96
8577	D38112	Homo sapiens	ATPase subunit 6	180	93
8578	D38112	Homo sapiens	NADH dehydrogenase subunit I	179	91
8579	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	88

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8580	M15530	Homo sapiens	B-cell growth factor	109	71
8581	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	77
8582	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	109	47
8583	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	71
8584	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	241	97
8585	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	185	80
8586	M28016	Homo sapiens	cytochrome b	129	92
8587	M58009	Pan troglodytes	cytochrome c oxidase subunit II	153	96
8588	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	90
8589	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	109	51
8590	L00016	Homo sapiens	urf4	176	94
8591	AF150105	Homo sapiens	small zinc finger-like protein	523	100
8592	U15306	Homo sapiens	NFX1	123	95
8594	R44519	Homo sapiens	Adult human alpha-globin V107S.	222	78
8595	Y03000	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	128	70
8596	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	151	90
8597	X67688	Homo sapiens	transketolase	123	84
8598	L00016	Homo sapiens	urf4	130	85
8599	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	109	54
8600	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	89
8601	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	151	54
8602	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	115	43
8603	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	95
8604	S79980	Bos taurus	ribosomal protein L37	109	84
8605	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	127	48
8606	D38112	Homo sapiens	ATPase subunit 6	202	100
8607	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	42
8608	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	127	58
8609	AF229067	Homo sapiens	PADI-H protein	112	78
8610	AF130089	Homo sapiens	PRO2550	125	86
8611	J03071	Homo sapiens	chorionic somatomammotropin CS-5	710	97
8612	AL390114	Leishmania major	extremely cysteine/valine rich protein	104	41
8613	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	84
8614	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	70
8615	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	91
8616	M28016	Homo sapiens	cytochrome b	148	93
8617	AF118082	Homo sapiens	PRO1902	94	66
8618	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	182	82
8619	X02585	Xenopus laevis	unidentified open reading frame 1 (166	170	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			aa)		
8620	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	125	57
8621	AC004450	Arabidopsis thaliana	putative extensin	140	48
8622	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	79
8623	AF130089	Homo sapiens	PRO2550	150	78
8624	L00016	Homo sapiens	urf4	280	92
8625	AF130051	Homo sapiens	PRO0898	161	76
8626	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	123	49
8627	L00016	Homo sapiens	urf4	201	95
8628	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	169	82
8629	AF119851	Homo sapiens	PRO1722	171	65
8630	X55654	Homo sapiens	cytochrome C oxidase II subunit	120	92
8631	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	56
8632	X55654	Homo sapiens	cytochrome C oxidase II subunit	107	95
8633	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	132	86
8634	AJ224997	Rattus norvegicus	huntingtin	73	59
8635	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	80
8636	M19061	Ateles Geoffroyi	delta-globin	100	40
8637	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	102	65
8638	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	104	50
8639	AF116715	Homo sapiens	PRO2829	158	76
8640	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	142	62
8641	Y09010	Mus musculus	Ser/Thr kinase	193	95
8642	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	227	79
8643	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	116	95
8644	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	88
8645	V46311_cdl	Homo sapiens	12-JAN-1998 Human secreted protein cDNA from clone D157.	197	100
8646	Y17379	Homo sapiens	NADH:ubiquinone oxidoreductase 51-kD subunit	240	97
8647	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	142	68
8648	AJ388520	Canis familiaris	Ribosomal protein	134	100
8649	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	136	56
8650	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	116	80
8651	S79410	Mus musculus	nuclear localization signal binding protein	99	36
8652	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	136	64
8653	AF229067	Homo sapiens	PADI-H protein	134	69
8654	AF090942	Homo sapiens	PRO0657	103	42
8655	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8656	U37359	Homo sapiens	MRE11 homologue hMre11	238	97
8657	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	113	60
8658	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	124	83
8659	AF161356	Homo sapiens	HSPC093	149	64
8660	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	121	44
8661	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	107	37
8662	U19098	Lycopersicon chilense	proline-rich protein	72	48
8663	AF118082	Homo sapiens	PRO1902	95	75
8664	AF130089	Homo sapiens	PRO2550	307	79
8665	AL390114	Leishmania major	extremely cysteine/valine rich protein	115	40
8666	X55683	Lycopersicon esculentum	extensin (class I)	102	32
8667	AK026841	Homo sapiens	unnamed protein product	276	100
8668	AL109963	Homo sapiens	dJ1188J21.1 (FSH primary response (LRPR1, rat) homolog 1)	597	100
8669	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	123	58
8670	W48352	Homo sapiens	Human breast cancer related protein BCLT1.	103	65
8671	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	121	61
8672	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	82
8673	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	211	93
8674	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	126	61
8675	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	114	66
8676	X55691	Lycopersicon esculentum	glycine-rich protein	85	38
8677	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	188	80
8678	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	183	75
8679	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	71
8680	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	96	82
8681	U80761	Homo sapiens	CTG26 alternate open reading frame	136	88
8682	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	137	93
8683	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	107	45
8684	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	90
8685	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	127	55
8686	W64486	Homo sapiens	Human DR3 protein.	139	100
8687	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	134	33
8688	K03202	Homo sapiens	salivary proline-rich protein precursor	119	35
8689	U36448	Homo sapiens	Ca2+-dependent activator protein for	107	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			secretion		
8690	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	80	43
8691	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	147	74
8692	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	95
8693	AF130089	Homo sapiens	PRO2550	126	35
8694	M58009	Pan troglodytes	cytochrome c oxidase subunit II	233	97
8695	M11902	Mus musculus	proline-rich salivary protein	98	35
8696	W34499	Homo sapiens	Obesity receptor C protein.	263	83
8697	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	181	73
8698	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	48
8699	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	88
8700	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	51
8701	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	73
8702	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	133	62
8703	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	92
8704	D38112	Homo sapiens	ATPase subunit 6	117	96
8705	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	97	58
8706	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	115	79
8707	AF118086	Homo sapiens	PRO1992	167	81
8708	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	114	51
8709	L10908	Mus musculus	Gcap1 gene product	179	38
8710	S79410	Mus musculus	nuclear localization signal binding protein	135	69
8711	AF130089	Homo sapiens	PRO2550	399	78
8712	X55654	Homo sapiens	cytochrome C oxidase II subunit	107	95
8713	AF118082	Homo sapiens	PRO1902	123	58
8714	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	173	81
8715	V35554_cdl	Homo sapiens	21-NOV-1996 Human tumour antigen protein (clone 3) encoding cDNA.	258	83
8716	AF130089	Homo sapiens	PRO2550	143	51
8717	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	92	52
8718	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	147	71
8719	AF153208	Homo sapiens	GC-rich sequence DNA-binding factor candidate	115	70
8720	AF090931	Homo sapiens	PRO0483	145	87
8721	X92485	Plasmodium vivax	pva1	125	79
8722	U72543	Sus scrofa	ubiquitin-like/S30 ribosomal fusion protein	201	97
8723	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	223	85
8724	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	121	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8725	AF130051	Homo sapiens	PRO0898	102	72
8726	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	185	78
8727	R24750	Homo sapiens	hGH variant #38 - 174S 176Y 10F 14S 18F 21L 167S 171D 175T 179T.	116	82
8728	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	92	72
8729	X53375	Helianthus annuus	anther-specific protein SF18	114	39
8730	S74221	Homo sapiens	IK factor=cytokine down-regulating HLA class II	159	42
8731	AC003058	Arabidopsis thaliana	unknown protein	166	89
8732	AB027508	Homo sapiens	hVPS11	194	50
8733	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	144	93
8734	AF266479	Homo sapiens	rectachrome 1	116	74
8735	AL132841	Caenorhabditis elegans	Y15E3A.3	125	60
8736	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	152	65
8737	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	79	56
8738	U93565	Homo sapiens	putative p150	190	52
8739	AF026689	Homo sapiens	prostate-specific transglutaminase	117	57
8740	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	109	70
8741	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	165	61
8742	M58009	Pan troglodytes	cytochrome c oxidase subunit II	213	97
8743	M17887	Homo sapiens	acidic ribosomal phosphoprotein (P2)	106	74
8744	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	116	49
8745	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	134	68
8746	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	135	71
8747	M76546	Helianthus annuus	hydroxyproline-rich protein	94	40
8748	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	173	76
8749	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	67
8750	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	272	57
8751	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	131	71
8752	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	123	37
8753	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	180	55
8754	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	105	44
8755	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	78
8756	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	284	87
8757	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	190	89

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8758	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	103	40
8759	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	120	61
8760	AF132984	Homo sapiens	nuclear pore complex interacting protein NP1P	196	94
8761	AF130079	Homo sapiens	PRO2852	125	65
8762	AF155232	Pisum sativum	extensin	177	42
8763	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	95
8764	X75438	Sus scrofa	homologue of proline/arginine rich antibacterial peptides	96	38
8765	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	157	96
8766	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	137	75
8767	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	207	95
8768	AL161543	Arabidopsis thaliana	extensin like protein	100	38
8769	K03202	Homo sapiens	salivary proline-rich protein precursor	110	47
8770	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	178	78
8771	D83407	Homo sapiens	a thyroid hormone responsive gene in human skin fibroblasts	133	100
8772	V00662	Homo sapiens	URF A6L (NADH dehydrogenase subunit)	172	73
8773	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	107	66
8774	AL390114	Leishmania major	extremely cysteine/valine rich protein	117	100
8775	AF090931	Homo sapiens	PRO0483	175	88
8776	S79410	Mus musculus	nuclear localization signal binding protein	125	58
8777	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	126	73
8778	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	154	70
8779	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	149	50
8780	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	170	91
8781	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	103	65
8782	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	184	70
8783	AC003058	Arabidopsis thaliana	unknown protein	169	97
8784	U55376	Caenorhabditis elegans	F16H11.2 gene product	141	90
8785	U55376	Caenorhabditis elegans	F16H11.2 gene product	150	100
8786	AL132841	Caenorhabditis elegans	Y15E3A.3	127	96
8787	AF266479	Homo sapiens	rectachrome 1	148	61
8788	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	106	95
8789	AL132841	Caenorhabditis elegans	Y15E3A.3	162	96
8790	AC006693	Caenorhabditis	Hypothetical protein W02H5.e	180	94

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		<i>elegans</i>			
8791	U28971	<i>Caenorhabditis elegans</i>	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	159	80
8792	AF150105	<i>Homo sapiens</i>	small zinc finger-like protein	505	98
8793	AL390935	<i>Leishmania major</i>	probable pro0195	85	31
8794	Y19767	<i>Homo sapiens</i>	SEQ ID NO 485 from WO9922243.	115	55
8795	AF118082	<i>Homo sapiens</i>	PRO1902	123	75
8796	D38112	<i>Homo sapiens</i>	ATPase subunit 6	438	82
8797	AF118086	<i>Homo sapiens</i>	PRO1992	156	81
8798	Y53037	<i>Homo sapiens</i>	Human secreted protein clone dx219_13 protein sequence SEQ ID NO:80.	196	100
8799	X92485	<i>Plasmodium vivax</i>	pva1	132	63
8800	G02532	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 6613.	170	65
8801	G00397	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4478.	123	58
8802	AF116909	<i>Homo sapiens</i>	unknown	116	63
8803	X92485	<i>Plasmodium vivax</i>	pva1	127	82
8804	G03438	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7519.	140	67
8805	Z95114	<i>Homo sapiens</i>	bK212A2.2 (apolipoprotein L, 2)	294	100
8806	AF143369	<i>Mus musculus</i>	msg1-related protein 2	348	83
8807	G00500	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4581.	110	76
8808	AP000616	<i>Oryza sativa</i>	similar to RING-H2 finger protein RHA1a (AF078683)	129	91
8809	AF230279	<i>Caenorhabditis elegans</i>	SWI3-like protein; PSA-1	126	37
8810	D38112	<i>Homo sapiens</i>	NADH dehydrogenase subunit 4L	168	82
8811	Y86248	<i>Homo sapiens</i>	Human secreted protein HCHPF68, SEQ ID NO:163.	122	54
8812	D38112	<i>Homo sapiens</i>	ATPase subunit 6	207	100
8813	W99376	<i>Homo sapiens</i>	Human fibroblast growth factor 2 24 kD isoform N-terminus.	93	41
8814	G03043	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7124.	157	57
8815	X54978	<i>Bos taurus</i>	17,000 dalton myosin light chain	133	96
8816	M58459	<i>Homo sapiens</i>	ribosomal protein S4Y isoform	260	100
8817	D38112	<i>Homo sapiens</i>	NADH dehydrogenase subunit 1	256	90
8818	U23947	<i>Mycoplasma pulmonis</i>	VsaD1	132	31
8819	G03172	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7253.	140	69
8820	L00016	<i>Homo sapiens</i>	urf4	205	90
8821	X55683	<i>Lycopersicon esculentum</i>	extensin (class I)	111	43
8822	AL160493	<i>Leishmania major</i>	probable (hhv-6) u1102, variant a DNA, complete virion genome	94	43
8823	X66285	<i>Mus musculus</i>	HCl ORF	94	53
8824	AF061340	<i>Artibeus jamaicensis</i>	F1 ATPase subunit 6	97	90
8825	M18093	<i>Phaseolus vulgaris</i>	hydroxyproline-rich glycoprotein	123	36
8826	AF119855	<i>Homo sapiens</i>	PRO1847	113	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8827	M28016	Homo sapiens	cytochrome b	140	93
8828	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	56
8829	AK024455	Homo sapiens	FLJ00047 protein	145	59
8830	D38112	Homo sapiens	ATPase subunit 6	194	95
8831	D38112	Homo sapiens	ATPase subunit 6	184	90
8832	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	60
8833	AF130079	Homo sapiens	PRO2852	115	88
8834	AB003784	Drosophila simulans	Histone H3	135	100
8835	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	173	82
8836	X70343	Nicotiana glauca	extensin	112	37
8837	L17318	Rattus norvegicus	proline-rich proteoglycan	142	38
8838	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	148	74
8839	W34625	Homo sapiens	Human C3 protein mutant FT-3.	277	100
8840	AF116638	Homo sapiens	PRO1546	78	41
8841	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	138	61
8842	AF130087	Homo sapiens	PRO2411	131	67
8843	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	150	72
8844	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	155	60
8845	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	66
8846	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	68
8847	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	146	70
8848	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	68
8849	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	273	79
8850	K02120	Bovine leukemia virus	gag	201	54
8851	AF229067	Homo sapiens	PADI-H protein	162	57
8852	AF090931	Homo sapiens	PRO0483	125	82
8853	R14584	Homo sapiens	TGF beta 1 binding protein encoded by clone BPA 13.	189	100
8854	U52197	Mus musculus	poly(A) polymerase III	183	85
8855	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	193	72
8856	G00549	Homo sapiens	Human secreted protein, SEQ ID NO: 4630.	104	66
8857	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	93	64
8858	Q55625_cd1	Homo sapiens	22-JUN-1992 Human beta globin 5'-UTR-CDS-3'-UTR.	412	98
8859	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	152	67
8860	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	112	72
8861	AF130079	Homo sapiens	PRO2852	160	64
8862	G00407	Homo sapiens	Human secreted protein, SEQ ID NO:	101	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4488.		
8863	X64707	Homo sapiens	BBC1	216	100
8864	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	127	65
8865	G00092	Homo sapiens	Human secreted protein, SEQ ID NO: 4173.	210	100
8866	AL137351	Homo sapiens	hypothetical protein	327	100
8867	AF090942	Homo sapiens	PRO0657	105	38
8868	AK023050	Homo sapiens	unnamed protein product	137	60
8869	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	101	65
8870	AF216751	Homo sapiens	CDA14	282	96
8871	AL133262	Homo sapiens	dJ319D22.1 (CDC5-like protein)	158	90
8872	V32779_cd1	Homo sapiens	11-MAR-1997 Novel human F0 ATP synthase subunit encoding DNA sequence.	267	81
8873	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	118	58
8874	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	89	43
8875	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	154	63
8876	AK001873	Homo sapiens	unnamed protein product	373	100
8877	X52138	Homo sapiens	L7a protein	259	82
8878	X52138	Homo sapiens	L7a protein	273	87
8879	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	57
8880	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	128	57
8881	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	159	71
8882	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	153	67
8883	AF130089	Homo sapiens	PRO2550	134	79
8884	U36898	Rattus norvegicus	pheromone receptor VN6	143	53
8885	S79410	Mus musculus	nuclear localization signal binding protein	143	64
8886	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	138	92
8887	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	124	72
8888	R48296	Homo sapiens	Human PGF-2/NT-3.	118	66
8889	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	81	77
8890	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	120	50
8891	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	121	77
8892	X53375	Helianthus annuus	anther-specific protein SF18	109	64
8893	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	119	54
8894	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	136	68
8895	AF090894	Homo sapiens	PRO0113	114	60
8896	AF161356	Homo sapiens	HSPC093	148	51
8897	AF116638	Homo sapiens	PRO1546	91	45
8898	U22231	Felis catus	ribosomal protein S3a	201	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8899	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	114	75
8900	AF090894	Homo sapiens	PRO0113	114	61
8901	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	63
8902	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	95
8903	R90288	Homo sapiens	Modified pigment epithelium-derived factor (rPEDF).	258	88
8904	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	86
8905	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	66
8906	X70343	Nicotiana glauca	extensin	122	37
8907	G02386	Homo sapiens	Human secreted protein, SEQ ID NO: 6467.	162	70
8908	AF130089	Homo sapiens	PRO2550	125	85
8909	AF220264	Homo sapiens	MOST-1	113	47
8910	Y25769	Homo sapiens	Human secreted protein encoded from gene 59.	119	77
8911	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	77	52
8912	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	162	83
8913	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	104	77
8914	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	138	64
8915	AF090944	Homo sapiens	PRO0663	73	58
8916	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	151	76
8917	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	84	47
8918	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	64
8919	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	254	82
8920	AJ245416	Homo sapiens	G7b protein	360	86
8921	D90228	Homo sapiens	mitochondrial acetoacetyl-CoA thiolase precursor	190	100
8922	AF229067	Homo sapiens	PADI-H protein	157	65
8923	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	65
8924	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	62	68
8925	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	116	63
8926	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	65
8927	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	59
8928	AF287892	Homo sapiens	sialic acid binding immunoglobulin-like lectin 8 long splice variant	994	76
8929	AF030131	Mus musculus	Plenty of SH3s; POSH	181	77
8930	J02459	bacteriophage lambda	E (capsid component;341)	814	98
8931	U13866	unidentified cloning vector	non-functional lacZ alpha peptide	112	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8932	U67540	Methanococcus jannaschii	conserved hypothetical protein	98	56
8933	Z74472	Caenorhabditis elegans	<p>predicted using Genefinder—contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=84.3, E-value=8.1e-22, N=2; PF01484 (Nematode cuticle collagen N-terminal domain), Score=34.2, E-value=9.9e-07, N=1—cDNA EST yk100d10.3 comes from this gene; cDNA EST EMBL:D65979 comes from this gene—cDNA EST yk100d4.3 comes from this gene; cDNA EST yk123g7.3 comes from this gene—cDNA EST yk58e6.3 comes from this gene; cDNA EST yk67a5.3 comes from this gene—cDNA EST EMBL:T01590 comes from this gene; cDNA EST yk60c11.3 comes from this gene—cDNA EST yk89c10.3 comes from this gene; cDNA EST yk85g9.3 comes from this gene—cDNA EST yk83e2.5 comes from this gene; cDNA EST yk75f2.3 comes from this gene—cDNA EST CEESK90F comes from this gene; cDNA EST yk79f5.5 comes from this gene—cDNA EST yk64b12.3 comes from this gene; cDNA EST yk64h9.3 comes from this gene—cDNA EST yk74d1.3 comes from this gene; cDNA EST yk75e4.3 comes from this gene—cDNA EST yk83c2.3 comes from this gene; cDNA EST yk91c12.3 comes from this gene—cDNA EST yk98f2.3 comes from this gene; cDNA EST yk60h4.5 comes from this gene—cDNA EST yk60c11.5 comes from this gene; cDNA EST yk64h9.5 comes from this gene—cDNA EST yk64a9.5 comes from this gene; cDNA EST yk64b12.5 comes from this gene—cDNA EST yk67a5.5 comes from this gene; cDNA EST yk74d1.5 comes from this gene—cDNA EST yk75e4.5 comes from this gene; cDNA EST yk75f2.5 comes from this gene—cDNA EST yk79e6.5 comes from this gene; cDNA EST yk80d2.5 comes from this gene—cDNA EST yk85g9.5 comes from this gene; cDNA EST yk89c10.5 comes from this gene—cDNA EST yk89c4.5 comes from this gene; cDNA EST yk90c11.5 comes from this gene—cDNA EST yk91c12.5 comes from this gene; cDNA EST yk96e2.5 comes from this gene—cDNA EST yk98c2.5 comes from this gene; cDNA EST yk98f2.5 comes from this gene—cDNA EST yk98h11.5 comes</p>	101	38

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			from this gene; cDNA EST yk107e7.5 comes from this gene-cDNA EST yk313g9.3 comes from this gene; cDNA EST yk313g9.5 comes from this gene-cDNA EST yk312g1.3 comes from this gene; cDNA EST yk312g1.5 comes from this gene-cDNA EST yk293c4.3 comes from this gene; cDNA EST yk293c4.5 comes from this gene		
8934	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	63
8935	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	48
8936	X03741	Homo sapiens	myosin heavy chain (635 AA)	1343	99
8937	M29295	Rattus norvegicus	small nuclear ribonucleoparticle-associated protein	106	52
8938	D00097	Homo sapiens	serum amyloid P component	188	100
8939	W34499	Homo sapiens	Obesity receptor C protein.	255	83
8940	L00016	Homo sapiens	urf4	293	83
8941	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	164	94
8942	AB007148	Homo sapiens	ribosomal protein S3a	153	73
8943	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	213	95
8944	M10119	Homo sapiens	ferritin light subunit	129	100
8945	M74718	Homo sapiens	SEF2-1A protein	118	84
8946	AL355178	Homo sapiens	dJ947L8.1.6 (novel CUB and Sushi (SCR repeat) domain protein)	366	51
8947	Y56033	Homo sapiens	Polypyrrolone-rich domain from dynamin.	70	51
8948	X06547	Homo sapiens	glutathione S-transferase (GST-Pi) (AA 1 - 210)	172	97
8949	AF119851	Homo sapiens	PRO1722	154	78
8950	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	123	88
8951	X54802	Homo sapiens	cytochrome-c oxidase subunit IV	116	95
8952	AJ011580	bacteriophage PS34	gp23	338	98
8953	Y59441	Homo sapiens	Human delta3 fragment #5.	271	96
8954	J02459	bacteriophage lambda	B (capsid component;533)	807	99
8955	AL132841	Caenorhabditis elegans	Y15E3A.3	172	94
8956	W34499	Homo sapiens	Obesity receptor C protein.	166	89
8957	X92485	Plasmodium vivax	pva1	135	71
8958	AB010340	Mus musculus	mszf81	122	60
8959	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	103	51
8960	X14898	Cricetulus sp.	ORF (AA 1-286) (1 is 2nd base in codon)	108	54
8961	AF090931	Homo sapiens	PRO0483	119	82
8962	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	130	72
8963	AF170724	Homo sapiens	cell cycle checkpoint protein CHFR	1364	99
8964	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	151	43
8965	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	250	74

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8966	Y87233	Homo sapiens	Human signal peptide containing protein HSPP-10 SEQ ID NO:10.	445	100
8967	AF127085	Mus musculus	semaphorin cytoplasmic domain-associated protein 3B	112	80
8968	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	109	46
8969	AF090894	Homo sapiens	PRO0113	153	61
8970	Y19730	Homo sapiens	SEQ ID NO 448 from WO9922243.	158	49
8971	U38544	Mus musculus	alpha-1 type I collagen	102	52
8972	X92485	Plasmodium vivax	pval	113	50
8973	AF241228	Xenopus laevis	Friend of GATA	143	100
8974	AF090930	Homo sapiens	PRO0478	79	41
8975	AF238374	Homo sapiens	mutant fibroblast growth factor receptor 3; FGFR3	115	50
8976	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	43
8977	AB001838	Homo sapiens	recoverin	179	80
8978	AF118082	Homo sapiens	PRO1902	73	70
8979	AF116715	Homo sapiens	PRO2829	102	76
8980	AF090942	Homo sapiens	PRO0657	132	61
8981	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	158	65
8982	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	108	84
8983	A00127	Homo sapiens	melanoma associated antigen P97	366	94
8984	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	158	88
8985	Y59778	Homo sapiens	Human normal ovarian tissue derived protein 55.	71	61
8986	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	42
8987	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	98	50
8988	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	80	51
8989	Y24025	Homo sapiens	Amino acid sequence of the human MMSC1 protein.	160	100
8990	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	130	67
8991	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	165	82
8992	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	111	62
8993	M28016	Homo sapiens	cytochrome b	130	100
8994	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	133	90
8995	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	298	89
8996	Y16430	Mus musculus	ribosomal protein L35a	101	65
8997	Y45318	Homo sapiens	Human secreted protein fragment encoded from gene 18.	96	76
8998	AL049659	Arabidopsis thaliana	putative protein	126	42
8999	AE003500	Drosophila melanogaster	CG12379 gene product	285	67
9000	R37991	Homo sapiens	Sequence of a new cytokine which inhibits induction by gamma interferon of expression of Class II histocompatibility antigens.	124	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9001	AF090930	Homo sapiens	PRO0478	193	89
9002	AP000381	Arabidopsis thaliana	gb AAF57656.1~gene_id:K17E12.13~s similar to unknown protein	193	29
9003	M17885	Homo sapiens	acidic ribosomal phosphoprotein (P0)	364	66
9004	D63424	Homo sapiens	glycogen synthase kinase 3alpha	126	81
9005	AP000616	Oryza sativa	similar to RJNG-H2 finger protein RHA1a (AF078683)	113	75
9006	AL117637	Homo sapiens	hypothetical protein	257	92
9007	AE001381	Plasmodium falciparum	hypothetical protein	141	26
9008	W34499	Homo sapiens	Obesity receptor C protein.	152	86
9009	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	199	80
9010	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	202	94
9011	AF090931	Homo sapiens	PRO0483	135	68
9012	M11717	Homo sapiens	heat shock protein	696	100
9013	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	123	75
9014	R59842	Homo sapiens	ApoE4L1 protease.	86	85
9015	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	96	65
9016	AF229067	Homo sapiens	PADI-H protein	119	54
9017	AF090944	Homo sapiens	PRO0663	138	54
9018	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	103	50
9019	X92485	Plasmodium vivax	pval	101	73
9020	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	82	72
9021	AF073519	Homo sapiens	small EDRK-rich factor I, long isoform	116	66
9022	AF229067	Homo sapiens	PADI-H protein	127	45
9023	M33112	Homo sapiens	amyloid-beta protein	105	67
9024	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	79	68
9025	AF161361	Homo sapiens	HSPC098	130	55
9026	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	169	72
9027	AF130051	Homo sapiens	PRO0898	138	77
9028	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	132	49
9029	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	117	58
9030	AC002310	Homo sapiens	Unknown gene product	155	85
9031	X92485	Plasmodium vivax	pval	112	42
9032	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	130	52
9033	G00487	Homo sapiens	Human secreted protein, SEQ ID NO: 4568.	123	69
9034	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	138	61
9035	AL390114	Leishmania major	extremely cysteine/valine rich protein	111	66
9036	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	173	59
9037	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	100	54
9038	AF220264	Homo sapiens	MOST-1	96	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9039	AF130051	Homo sapiens	PRO0898	119	68
9040	AF116715	Homo sapiens	PRO2829	121	63
9041	L76200	Homo sapiens	guanylate kinase	193	83
9042	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	125	55
9043	AF152513	Homo sapiens	protocadherin gamma A6 short form protein	334	100
9044	AF130079	Homo sapiens	PRO2852	125	33
9045	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	128	64
9046	AF090942	Homo sapiens	PRO0657	126	65
9047	AF284223	Homo sapiens	terra-like protein	228	100
9048	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	68
9049	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	132	92
9050	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	123	75
9051	AL034344	Homo sapiens	dJ118B18.1 (forkhead box C1)	323	100
9052	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	106	62
9053	AF225910	Mus musculus	DAZ-associated protein 1	100	45
9054	AF130087	Homo sapiens	PRO2411	147	70
9055	W80400	Homo sapiens	A. secreted protein encoded by clone dd71.2.	858	97
9056	X70343	Nicotiana glauca	extensin	113	33
9057	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	57
9058	R95913	Homo sapiens	Neural thread protein.	142	38
9059	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	131	56
9060	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	131	50
9061	X70343	Nicotiana glauca	extensin	103	42
9062	AJ271872	Nicotiana glauca	extensin	129	33
9063	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	151	73
9064	AF266164	Rattus norvegicus	densin-180 variant D	144	96
9065	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	135	68
9066	M28016	Homo sapiens	cytochrome b	178	87
9067	M28016	Homo sapiens	cytochrome b	193	95
9068	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	148	60
9069	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	111	100
9070	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	141	72
9071	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	147	64
9072	AL390114	Leishmania major	extremely cysteine/valine rich protein	109	69
9073	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	171	85
9074	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	88	88
9075	Y14482	Homo sapiens	Fragment of human secreted protein	137	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded by gene 17.		
9076	L38941	Homo sapiens	ribosomal protein L34	139	88
9077	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	164	86
9078	X55684	Lycopersicon esculentum	extensin (class I)	72	35
9079	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	82
9080	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	229	59
9081	AF130089	Homo sapiens	PRO2550	118	71
9082	X92485	Plasmodium vivax	pva1	125	71
9083	AF216650	Homo sapiens	MTAP	154	73
9084	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	124	78
9085	J02459	bacteriophage lambda	E (capsid component;341)	191	73
9086	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	138	61
9087	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	130	75
9088	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	144	61
9089	AK024455	Homo sapiens	FLJ00047 protein	145	82
9090	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	181	60
9091	AF090895	Homo sapiens	PRO0117	87	66
9092	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	211	86
9093	AF130079	Homo sapiens	PRO2852	157	74
9094	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	180	82
9095	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	97	42
9096	X65551	Homo sapiens	antigen of the monoclonal antibody Ki-67	106	65
9097	W34499	Homo sapiens	Obesity receptor C protein.	231	80
9098	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	127	63
9099	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	129	78
9100	AF229067	Homo sapiens	PADI-H protein	162	59
9101	G00673	Homo sapiens	Human secreted protein, SEQ ID NO: 4754.	157	65
9102	Y60010	Homo sapiens	Human endometrium tumour EST encoded protein 70.	69	63
9103	R95913	Homo sapiens	Neural thread protein.	124	72
9104	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	104	68
9105	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	156	88
9106	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	170	57
9107	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	163	89
9108	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	123	41
9109	L41944	Homo sapiens	interferon receptor	162	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9110	AK000496	Homo sapiens	unnamed protein product	138	78
9111	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	81	62
9112	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	52
9113	M26361	Mus musculus	LINE/fg H-chain fusion protein	105	50
9114	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	119	56
9115	AF119900	Homo sapiens	PRO2822	140	58
9116	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	158	60
9117	L00016	Homo sapiens	urf5	171	97
9118	AC006276	Homo sapiens	R28379_3	138	100
9119	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	72
9120	AF119855	Homo sapiens	PRO1847	155	81
9121	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	105	84
9122	Y87103	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	115	78
9123	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	134	53
9124	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	103	40
9125	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	96	63
9126	AF130089	Homo sapiens	PRO2550	125	78
9127	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	98	56
9128	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	107	75
9129	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	131	49
9130	AK024455	Homo sapiens	FLJ00047 protein	130	78
9131	W88435	Homo sapiens	Disease associated protein kinase DAPK-4.	336	100
9132	U63332	Homo sapiens	super cysteine rich protein, SCRP	144	59
9133	Y94922	Homo sapiens	Human secreted protein clone pv6_1 protein sequence SEQ ID NO:50.	154	90
9134	AF317425	Homo sapiens	GAC-1	182	70
9135	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	174	54
9136	AF116715	Homo sapiens	PRO2829	116	71
9137	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	122	65
9138	AF130089	Homo sapiens	PRO2550	140	62
9139	AF161221	Homo sapiens	kallikrein-like protein 6	204	90
9140	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	110	48
9141	U27486	Pseudorabies virus	EP0	84	44
9142	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	150	96
9143	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	220	80
9144	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	84
9145	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	180	77
9146	U52077	Homo sapiens	mariner transposase	365	78
9147	W88627	Homo sapiens	Secreted protein encoded by gene 94	143	67

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HPMBQ32.		
9148	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	100	81
9149	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	118	66
9150	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	54
9151	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	101	70
9152	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	66
9153	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	160	72
9154	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	106	63
9155	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	95	80
9156	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	133	67
9157	G03924	Homo sapiens	Human secreted protein, SEQ ID NO: 8005.	265	80
9158	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	131	72
9159	AF130089	Homo sapiens	PRO2550	180	61
9160	AF116715	Homo sapiens	PRO2829	184	82
9161	K01664	Drosophila melanogaster	Bkm-like protein	200	69
9162	D88146	Homo sapiens	UDP-galactose transporter 2	101	100
9163	AF107406	Homo sapiens	GW128	155	60
9164	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	97	51
9165	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	60
9166	AF210651	Homo sapiens	NAG18	83	65
9167	V00672	Pan troglodytes	reading frame protein 4	119	95
9168	Y01155	Homo sapiens	Secreted protein encoded by gene 4 clone HIBCW32.	225	74
9169	AF161356	Homo sapiens	HSPC093	100	75
9170	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	174	66
9171	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	86
9172	AF119855	Homo sapiens	PRO1847	178	59
9173	AF130087	Homo sapiens	PRO2411	129	48
9174	AF130079	Homo sapiens	PRO2852	149	59
9175	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	101	90
9176	AF090894	Homo sapiens	PRO0113	118	65
9177	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	105	46
9178	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	100	52
9179	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	70
9180	AF116715	Homo sapiens	PRO2829	127	64
9181	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	144	71
9182	AF229067	Homo sapiens	PADI-H protein	164	64
9183	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	134	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6613.		
9184	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	106	64
9185	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	132	57
9186	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	113	65
9187	AF090931	Homo sapiens	PRO0483	117	68
9188	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	67
9189	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	130	47
9190	D38112	Homo sapiens	cytochrome c oxidase subunit 1	269	85
9191	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	150	40
9192	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	153	73
9193	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	62
9194	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	103	31
9195	X77816	Rattus norvegicus	PR-Vbeta1	98	47
9196	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	107	48
9197	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	111	68
9198	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	164	83
9199	J02459	bacteriophage lambda	E (capsid component;341)	235	85
9200	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	117	65
9201	X67640	Homo sapiens	HS24/P52	222	75
9202	X67640	Homo sapiens	HS24/P52	231	81
9203	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	128	66
9204	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	107	74
9206	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	186	66
9207	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	136	56
9208	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	160	67
9209	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	68
9210	AF116715	Homo sapiens	PRO2829	123	81
9211	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	70
9212	AF118086	Homo sapiens	PRO1992	84	57
9213	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	115	62
9214	J02459	bacteriophage lambda	E (capsid component;341)	247	92
9215	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	74	76
9216	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	134	74

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9217	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	137	53
9218	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	130	44
9219	AP000616	Oryza sativa	similar to RfNG-H2 finger protein RHA1a (AF078683)	110	68
9220	L41944	Homo sapiens	interferon receptor	141	50
9221	AF130079	Homo sapiens	PRO2852	170	70
9222	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	100	85
9223	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	142	56
9224	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	104	63
9225	U80761	Homo sapiens	CTG26 alternate open reading frame	92	84
9226	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	157	65
9227	AK027208	Homo sapiens	unnamed protein product	138	68
9228	B25722	Homo sapiens	Human secreted protein sequence encoded by gene 9 SEQ ID NO:111.	125	87
9229	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	127	88
9230	AK025047	Homo sapiens	unnamed protein product	179	64
9231	AF090894	Homo sapiens	PRO0113	195	57
9232	AB046048	Macaca fascicularis	unnamed protein product	176	54
9233	AB008227	Adiantum capillus-veneris	Extensin	93	34
9234	AF130089	Homo sapiens	PRO2550	98	73
9235	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	135	52
9236	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	162	62
9237	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	59
9238	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	126	52
9239	AE003499	Drosophila melanogaster	CG12706 gene product	166	37
9240	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	161	64
9241	X92485	Plasmodium vivax	pva1	112	61
9242	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	69	42
9243	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	140	80
9244	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	92
9245	M22332	Homo sapiens	unknown protein	117	40
9246	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	109	66
9247	AL136173	Homo sapiens	dJ914B9.1 (novel protein (HSPIC162) similar to Rattus norvegicus bithoraxoid-like protein)	305	76
9248	AF116661	Homo sapiens	PRO1438	141	53
9249	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	144	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9250	J02459	bacteriophage lambda	E (capsid component;341)	245	89
9251	J02459	bacteriophage lambda	E (capsid component;341)	245	92
9252	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	128	63
9253	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	124	72
9254	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	90
9255	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	132	65
9256	X52164	Mus musculus	Q300 protein (AA 1-77)	106	62
9257	AF217374	Acanthaster planci	cytochrome oxidase subunit I	259	98
9258	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	64
9259	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	107	54
9260	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	66
9261	M28016	Homo sapiens	cytochrome b	148	93
9262	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	68
9263	R55749	Homo sapiens	Extracellular domain of human high affinity IFN-gamma receptor.	116	83
9264	K02403	Homo sapiens	complement component C4A	9025	99
9265	X92485	Plasmodium vivax	pval	161	55
9266	AK024455	Homo sapiens	FLJ00047 protein	98	83
9267	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	103	51
9268	AF130089	Homo sapiens	PRO2550	124	77
9269	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	94	54
9270	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	96	81
9271	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO.163.	132	53
9272	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	72
9273	AF229067	Homo sapiens	PADI-H protein	127	54
9274	Y36203	Homo sapiens	Human secreted protein #75.	154	77
9275	X92485	Plasmodium vivax	pval	157	72
9276	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	132	60
9277	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	156	84
9278	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	138	84
9279	Y20772	Homo sapiens	Human neurofilament-M mutant protein fragment 54.	112	70
9280	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	146	59
9281	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	103	63
9282	K01664	Drosophila melanogaster	Bkm-like protein	89	60
9283	X92485	Plasmodium	pval	124	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
9284	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	95	75
9285	AF130087	Homo sapiens	PRO2411	138	78
9286	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	140	54
9287	AF004340	Homo sapiens	ATPase 6/8	98	100
9288	S79410	Mus musculus	nuclear localization signal binding protein	102	68
9289	J02459	bacteriophage lambda	1 (tail component;223)	457	97
9290	AC003058	Arabidopsis thaliana	unknown protein	177	84
9291	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	107	87
9292	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	311	91
9293	S79410	Mus musculus	nuclear localization signal binding protein	139	61
9294	R28916	Homo sapiens	Type III procollagen (prior art).	117	33
9295	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	126	77
9296	AF130089	Homo sapiens	PRO2550	137	52
9297	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	93	79
9298	U22376	Homo sapiens	alternatively spliced product using exon 13A	239	77
9299	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	134	69
9300	AL390114	Leishmania major	extremely cysteine/valine rich protein	105	24
9301	D90282	Homo sapiens	carbamyl phosphate synthetase I (EC 6.3.4.16)	276	96
9302	J02459	bacteriophage lambda	E (capsid component;341)	231	93
9303	M15077	Photinus pyralis	Luciferase	557	100
9304	L00016	Homo sapiens	urf4	303	93
9305	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	69
9306	L46721	Homo sapiens	mucin	204	80
9307	S79410	Mus musculus	nuclear localization signal binding protein	110	84
9308	J02459	bacteriophage lambda	E (capsid component;341)	218	93
9309	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	78	66
9310	AF130075	Homo sapiens	PRO2532	92	69
9311	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	97	51
9312	J02459	bacteriophage lambda	E (capsid component;341)	201	79
9313	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	133	95
9314	AK024455	Homo sapiens	FLJ00047 protein	128	68
9315	D38112	Homo sapiens	ATPase subunit 6	223	81
9316	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	113	85
9317	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	117	88
9318	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	257	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9319	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	101	61
9320	AK001116	Homo sapiens	unnamed protein product	96	40
9321	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	174	60
9322	AF037081	Pan troglodytes	ribonuclease k6 precursor	109	100
9323	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	149	63
9324	AF153056	Fasciola hepatica	tegumental antigen	60	44
9325	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	200	69
9326	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	80	57
9327	AF118086	Homo sapiens	PRO1992	139	60
9328	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	110	73
9329	AF107406	Homo sapiens	GW128	142	56
9330	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	75
9331	X92485	Plasmodium vivax	pva1	121	56
9332	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	179	52
9333	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	67
9334	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	46
9335	M22332	Homo sapiens	unknown protein	158	60
9336	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	95	46
9337	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	160	76
9338	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	150	68
9339	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	169	59
9340	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSIW18.	154	64
9341	AK024455	Homo sapiens	FLJ00047 protein	117	79
9342	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	191	76
9343	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	133	82
9344	AF032457	Homo sapiens	BimEL	123	100
9345	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	117	46
9346	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	153	75
9347	X53020	Plasmodium falciparum	erythrocyte membrane-associated antigen	68	75
9348	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	120	70
9349	AF130089	Homo sapiens	PRO2550	116	69
9350	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	165	72
9351	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	94	82
9352	AL080242	Homo sapiens	bA554C12.1 (RBX1 or ROC1 (ring-box or ring finger protein 1))	184	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9353	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	125	64
9354	X71442	Rattus norvegicus	ORF 1; putative	96	40
9355	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	98	46
9356	AF090931	Homo sapiens	PRO0483	148	76
9357	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	144	56
9358	AC005175	Homo sapiens	TA2R_HUMAN, BETA ISOFORM; TXA2-R; PROSTANOID TP RECEPTOR	153	63
9359	AF116715	Homo sapiens	PRO2829	125	66
9360	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	143	72
9361	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	178	75
9362	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	90	57
9363	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	86	76
9364	AF229067	Homo sapiens	PADI-H protein	116	51
9365	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	248	64
9366	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	104	76
9367	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	95	76
9368	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	105	74
9369	R86406	Homo sapiens	Human matrix metalloprotease MMPm1a.	108	83
9370	AF181977	Hepatitis GB virus C	E2 protein	95	38
9371	AF090931	Homo sapiens	PRO0483	151	62
9372	AF090894	Homo sapiens	PRO0113	133	57
9373	AK002154	Homo sapiens	unnamed protein product	226	55
9374	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	71
9375	U77494	Homo sapiens	RANBP8	166	100
9376	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	155	52
9377	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	126	63
9378	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	151	78
9379	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	97	68
9380	AL160493	Leishmania major	probable (hvh-6) u1102, variant a DNA, complete virion genome	117	62
9381	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	104	47
9382	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	57
9384	AB047936	Macaca fascicularis	hypothetical protein	95	41
9385	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	57	64
9386	U04810	Homo sapiens	tastin	151	100
9387	U79260	Homo sapiens	unknown	97	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9388	U18339	Variola virus	D4L	103	65
9389	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	134	75
9390	AL390935	Leishmania major	possible dopap	99	88
9391	AB015633	Homo sapiens	type II membrane protein	108	100
9392	AF113685	Homo sapiens	PRO0974	98	62
9393	AF064819	Homo sapiens	serine protease DESC1	227	69
9394	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	219	68
9395	G01400	Homo sapiens	Human secreted protein, SEQ ID NO: 5481.	104	100
9396	AK024455	Homo sapiens	FLJ00047 protein	153	68
9397	AF033260	porcine endogenous type C retrovirus	reverse transcriptase	155	53
9398	X12517	Homo sapiens	C protein (AA 1-159)	147	55
9399	AB029948	Homo sapiens	mitochondrial seryl-tRNA synthetase	1203	100
9400	Y87075	Homo sapiens	Human secreted protein sequence SEQ ID NO:114.	234	93
9401	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	150	58
9402	M15530	Homo sapiens	B-cell growth factor	113	74
9403	X56932	Homo sapiens	23 kD highly basic protein	114	85
9404	AC018748	Arabidopsis thaliana	Contains similarity to P11 protein from Drosophila melanogaster gb X59691.	75	65
9405	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	114	88
9406	AF220264	Homo sapiens	MOST-1	124	70
9407	AF119851	Homo sapiens	PRO1722	157	65
9408	X92485	Plasmodium vivax	pva1	163	78
9409	X92485	Plasmodium vivax	pva1	165	77
9410	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	97	55
9411	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	104	64
9412	AF130089	Homo sapiens	PRO2550	147	55
9413	AF130089	Homo sapiens	PRO2550	175	65
9414	L14848	Homo sapiens	MHC class I-related protein	225	97
9415	R95913	Homo sapiens	Neural thread protein.	107	74
9416	AB001684	Chlorella vulgaris	ORF49b	68	53
9417	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	111	50
9418	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	107	73
9419	AL050285	Homo sapiens	hypothetical protein	194	100
9420	AF090944	Homo sapiens	PRO0663	132	59
9421	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	153	61
9422	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	140	70
9423	M20030	Homo sapiens	small proline rich protein	62	41
9424	AF116718	Homo sapiens	PRO2900	396	100
9425	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	102	35
9426	X61047	Hydra sp.	mini-collagen	92	45

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9427	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	105	71
9428	L10908	Mus musculus	Gcap1 gene product	107	44
9429	Y19767	Homo sapiens	SEQ ID NO 485 from WO922243.	79	87
9430	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	123	61
9431	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	111	80
9432	X12580	Medicago sativa	put. nodulin (soybean N-75 homolog.)	87	33
9433	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	106	48
9434	AC003028	Arabidopsis thaliana	30S ribosomal protein S31	79	42
9435	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	106	75
9436	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	207	75
9437	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	163	85
9438	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	84	57
9439	AF118086	Homo sapiens	PRO1992	145	75
9440	AF229067	Homo sapiens	PADI-H protein	140	64
9441	M36913	Zea mays	cell wall protein (put.); putative	107	38
9442	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	161	59
9443	AF229067	Homo sapiens	PADI-H protein	147	85
9444	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	171	79
9445	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	155	57
9446	X92485	Plasmodium vivax	pval	97	55
9447	AF119851	Homo sapiens	PRO1722	123	55
9448	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	88
9449	AL391688	Homo sapiens	bA524D16A.2.1 (novel protein similar to mouse granuphilin-a)	258	97
9450	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	91
9451	X92485	Plasmodium vivax	pval	123	88
9452	X83000	Myocastor coypus	lipase related protein 2	168	43
9453	M35603	Mus musculus	Hox-3.1 protein	447	78
9454	M35520	Canis familiaris	GTP-binding protein (rab5)	271	98
9455	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	362	86
9456	A13595	synthetic construct	immunosuppressive protein PP15	111	100
9457	X67788	Rattus norvegicus	ezrin, p81	185	97
9458	U28068	Mus musculus	neurogenic differentiation factor	132	89
9459	AF155140	Homo sapiens	gonadotropin-regulated testicular RNA helicase; GRTH	556	88
9460	AF155140	Homo sapiens	gonadotropin-regulated testicular RNA helicase; GRTH	379	94
9461	AF169689	Homo sapiens	protocadherin alpha 10 alternate isoform	208	95
9462	U73193	Homo sapiens	inward rectifier potassium channel	236	96

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			Kir1.2		
9463	U83278	Bos taurus	neural specific protein CRMP-2	157	61
9464	W48352	Homo sapiens	Human breast cancer related protein BCLTL1	74	57
9465	AL031673	Homo sapiens	dj694B14.3 (PUTATIVE novel haloacid dehalogenase-like hydrolase family protein similar to (archaea) bacterial proteins)	444	100
9466	X67247	Homo sapiens	ribosomal protein S8	519	90
9467	S79410	Mus musculus	nuclear localization signal binding protein	115	51
9468	U80761	Homo sapiens	CTG26 alternate open reading frame	95	84
9469	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	145	71
9470	AF130056	Homo sapiens	PRO1367	98	76
9471	X71354	Homo sapiens	vesicular monoamine transporter	102	95
9472	U66372	Bos taurus	ribosomal protein S29	120	95
9473	D32002	Homo sapiens	nuclear cap binding protein	583	96
9474	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	469	91
9475	V49572_cd1	Homo sapiens	13-NOV-1996 Human stomach cancer clone HP10122 cDNA #1.	562	100
9476	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	247	88
9477	AB043820	Homo sapiens	platelet glycoprotein VI-2	95	47
9478	AB020236	Homo sapiens	ribosomal protein L27A	437	86
9479	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	149	52
9480	AF205633	Homo sapiens	ninjurin2	364	100
9481	D14886	Homo sapiens	TFIIA-37	196	100
9482	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	166	76
9483	AF178842	Homo sapiens	Rhesus blood group-associated glycoprotein	128	75
9484	AF134895	Homo sapiens	glyoxylate reductase	838	95
9485	AC004832	Homo sapiens	similar to 45 kDa secretory protein ; similar to CAA10644.1 (PID:g4164418)	562	98
9486	Z35761	Homo sapiens	TEL/ABL	230	71
9487	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	149	72
9488	AL032631	Caenorhabditis elegans	predicted using Genefinder	159	31
9489	AJ271079	Oenothera elata subsp. hookeri	Ycf2 protein	113	36
9490	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	135	40
9491	Y53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	124	61
9492	Y21091	Homo sapiens	Human p53 cellular tumour antigen mutant protein fragment 28.	85	41
9493	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	153	76
9494	AF119851	Homo sapiens	PRO1722	94	54
9495	R04932	Homo sapiens	Interferon-gamma receptor segment from clone 39 responsible for binding the target.	142	100
9496	U40952	Caenorhabditis elegans	C03B1.10 gene product	103	75
9497	M63838	Homo sapiens	interferon-gamma induced protein	128	92

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9498	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	147	44
9499	AF108831	Homo sapiens	K/Cl cotransporter 3	244	77
9500	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	154	68
9501	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	139	63
9502	AE003499	Drosophila melanogaster	CG12706 gene product	180	36
9503	X02344	Homo sapiens	beta-tubulin	363	94
9504	D78014	Homo sapiens	dihydropyrimidinase related protein-3	189	84
9505	U59446	Brassica napus	myrosinase-binding protein related protein	116	40
9506	AB010437	Rattus rattus	cadherin-8	239	50
9507	AF229067	Homo sapiens	PADI-H protein	178	74
9508	AJ224819	Homo sapiens	tumor suppressor	291	85
9509	AF017275	Mus musculus	growth factor independence-1B	242	40
9510	AF177203	Homo sapiens	cerebral cell adhesion molecule	388	52
9511	AY007160	Homo sapiens	similar to Homo sapiens CGI-57 protein mRNA with GenBank Accession Number AF151815.1	1333	99
9512	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete viron genome	104	66
9513	X52164	Mus musculus	Q300 protein (AA 1-77)	92	59
9514	X80035	Oryctolagus cuniculus	cysteine rich hair keratin associated protein	96	40
9515	D86491	Xenopus laevis	Nf1	1777	76
9516	Y70761	Homo sapiens	Human beta-amyloid peptide (BAP) binding protein, BBP3.	168	80
9517	AK024500	Homo sapiens	FLJ00109 protein	1714	100
9518	AF008220	Bacillus subtilis	YtaG	104	41
9519	AF099977	Mus musculus	schlafen4	163	35
9520	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	162	72
9521	AL035068	Homo sapiens	dJ116G19.1 (novel protein)	102	76
9522	B24527	Homo sapiens	Human secreted protein sequence encoded by gene 15 SEQ ID NO: 153.	729	90
9523	AF129756	Homo sapiens	MSH5	182	100
9524	AJ238706	Drosophila melanogaster	monocarboxylate transporter 1 homologue	126	32
9525	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	250	97
9526	D86604	Mus musculus	Bach2	200	92
9527	AB032918	Hylabates moloch	dopamine receptor D4	91	36
9528	AB007830	Homo sapiens	CSR2	995	99
9529	AC004472	Homo sapiens	P1.11659.4	449	98
9530	AF273047	Homo sapiens	CTCL tumor antigen se20-7	104	29
9531	AF130079	Homo sapiens	PRO2852	153	67
9532	X07881	Homo sapiens	proline-rich protein G1	105	43
9533	AK001845	Homo sapiens	unnamed protein product	1368	63
9534	S79410	Mus musculus	nuclear localization signal binding protein	94	41
9535	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	185	86
9536	X99583	Homo sapiens	CHL1 protein	635	98
9537	AL022170	Homo sapiens	dJ501N12.1	111	37
9538	X66179	Xenopus laevis	p70 S6 kinase	120	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9539	U68380	Gallus gallus	csdp	289	98
9540	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	97	90
9541	AB013918	Homo sapiens	CAD	369	78
9542	U29380	Caenorhabditis elegans	similar to adenylate cyclase	501	42
9543	AF020312	Mus musculus	proline-rich protein 9-1	95	51
9544	G03435	Homo sapiens	Human secreted protein, SEQ ID NO: 7516.	142	96
9545	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	142	66
9546	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	110	47
9547	AB044546	Homo sapiens	mitogen-activated protein kinase kinase	407	60
9548	U52111	Homo sapiens	Ca2+/Calmodulin-dependent protein kinase I	660	100
9549	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	129	68
9550	Y87852	Homo sapiens	Human FGF-5 protein fragment.	146	100
9551	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	109	50
9552	D45131	Homo sapiens	basigin	311	66
9553	A14656	synthetic construct	protein antigen	450	89
9554	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	133	52
9555	X73458	Homo sapiens	protein kinase	568	85
9556	AJ131890	Homo sapiens	DNA polymerase lambda	1549	100
9557	S56555	Homo sapiens	paraoxonase/arylesterase	224	85
9558	M22332	Homo sapiens	unknown protein	90	38
9559	B24598	Homo sapiens	Human secreted protein sequence encoded by gene 47 SEQ ID NO:224.	66	44
9560	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	95	51
9561	Y08061	Homo sapiens	Human c-myc protein fragment.	77	76
9562	X55687	Lycopersicon esculentum	extensin (class II)	69	60
9563	AC002333	Arabidopsis thaliana	putative SF16 protein {Helianthus annuus}	111	31
9564	AF118082	Homo sapiens	PRO1902	106	61
9565	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	85	52
9566	U10323	Homo sapiens	NF45 protein	480	82
9567	AF100757	Homo sapiens	COP9 complex subunit 4	686	90
9568	AL035608	Homo sapiens	dJ479J7.2 (transmembrane 4 superfamily member 6)	293	90
9569	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	118	63
9570	U47856	Araneus diadematus	fibroin-4	98	44
9571	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	83	54
9572	AJ006239	Homo sapiens	dihydropteridine reductase	461	84
9573	G00821	Homo sapiens	Human secreted protein, SEQ ID NO: 4902.	248	75
9574	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	90	36
9575	V00488	Homo sapiens	alpha globin	508	84
9576	AF116719	Homo sapiens	PRO2987	483	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9577	L77967	Ovis aries	small proline-rich protein with paired repeat	62	38
9578	D38112	Homo sapiens	NADH dehydrogenase subunit 4	474	92
9579	P90387	Homo sapiens (Human)	N-terminal of human serum albumin polypeptide.	274	67
9580	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	271	88
9581	U15779	Homo sapiens	p70	101	57
9582	M19419	Mus musculus	proline-rich salivary protein	102	36
9583	L22030	Glycine max	hydroxyproline-rich glycoprotein	114	40
9584	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	105	32
9585	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	61
9586	U93569	Homo sapiens	putative p150	232	51
9587	AF144054	Homo sapiens	apoptosis related protein APR-4	120	52
9588	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	128	58
9589	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	90	61
9590	L27428	Homo sapiens	reverse transcriptase	120	46
9591	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	85	62
9592	AJ133489	Canis familiaris	albumin	204	60
9593	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	294	68
9594	M15386	Homo sapiens	gamma-globin	316	77
9595	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	134	68
9596	AF116719	Homo sapiens	PRO2987	309	89
9597	AF116719	Homo sapiens	PRO2987	485	94
9598	AF068294	Homo sapiens	HDCMB45P	131	34
9599	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	152	70
9600	AF118082	Homo sapiens	PRO1902	151	59
9601	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	186	68
9602	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	176	65
9603	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	261	80
9604	AF194537	Homo sapiens	NAG13	154	61
9605	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	96	67
9606	K02576	Homo sapiens	salivary proline-rich protein 1	100	33
9607	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	134	48
9608	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	129	67
9609	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	101	32
9610	AF118080	Homo sapiens	PRO1880	237	100
9611	AF119851	Homo sapiens	PRO1722	138	81
9612	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	178	55
9613	AF090930	Homo sapiens	PRO0478	88	71
9614	AF068294	Homo sapiens	HDCMB45P	121	49
9615	G01657	Homo sapiens	Human secreted protein, SEQ ID NO:	118	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			5738.		
9616	AF090931	Homo sapiens	PRO0483	143	63
9617	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	92	44
9618	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	121	56
9619	AB046061	Macaca fascicularis	unnamed protein product	93	44
9620	Y87116	Homo sapiens	Human secreted protein sequence SEQ ID NO:155.	122	71
9621	AF113685	Homo sapiens	PRO0974	156	65
9622	AF097178	Equus caballus	glyceraldehyde-3-phosphate dehydrogenase	119	75
9623	U83303	Homo sapiens	line-1 reverse transcriptase	134	62
9624	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	112	53
9625	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	123	77
9626	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	164	73
9627	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	236	71
9628	AF130079	Homo sapiens	PRO0252	138	50
9629	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	130	60
9630	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	167	61
9631	G03102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	87	50
9632	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	128	41
9633	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	134	81
9634	AF118082	Homo sapiens	PRO1902	114	57
9635	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	133	54
9636	L07543	Leishmania tarentolae	MURF4	85	42
9637	U49973	Homo sapiens	ORF2: function unknown	163	44
9638	AF090895	Homo sapiens	PRO0117	77	41
9639	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	108	71
9640	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	90	46
9641	AF118078	Homo sapiens	PRO1848	114	66
9642	AK024455	Homo sapiens	FLJ00047 protein	131	79
9643	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	130	62
9644	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	141	42
9645	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	69	62
9646	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	69	35
9647	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	478	90
9648	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	155	50
9649	G02538	Homo sapiens	Human secreted protein, SEQ ID NO:	104	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6619.		
9650	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	173	38
9651	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	118	36
9652	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	162	64
9653	D00570	Mus musculus	open reading frame (196 AA)	182	51
9654	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	54
9655	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	105	74
9656	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	82	70
9657	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	79	39
9658	M24732	Homo sapiens	lamin-like protein	76	31
9659	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	161	73
9660	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preduct.	149	48
9661	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	135	62
9662	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	126	71
9663	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	141	63
9664	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	153	66
9665	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	142	93
9666	AF113685	Homo sapiens	PRO0974	112	73
9667	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	133	62
9668	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	102	47
9669	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPPG94.	80	41
9670	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	106	58
9671	AF090942	Homo sapiens	PRO0657	118	66
9672	AF161356	Homo sapiens	HSPC093	94	63
9673	AF090930	Homo sapiens	PRO0478	167	64
9674	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	98	50
9675	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	87	70
9676	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	119	60
9677	X13412	Rattus rattus	flk protein	614	69
9678	AJ006770	Cicer arietinum	extensin	163	48
9679	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	120	67
9680	G00494	Homo sapiens	Human secreted protein, SEQ ID NO: 4575.	106	58
9681	U63542	Homo sapiens	FAP protein	120	68
9682	M15530	Homo sapiens	B-cell growth factor	146	76
9683	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	180	62
9684	AF321379	Callicebus moloch	gamma2-globin	108	86

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9685	L27428	Homo sapiens	reverse transcriptase	122	39
9686	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	77	51
9687	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	104	58
9688	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	123	58
9689	X81713	Homo sapiens	smallest subunit of TFIIA	210	91
9690	AF193330	Human respiratory syncytial virus	G protein	100	25
9691	AF150100	Homo sapiens	small zinc finger-like protein	205	83
9692	AF068294	Homo sapiens	HDCMB45P	122	54
9693	AF189307	Homo sapiens	unknown	96	50
9694	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	165	50
9695	AF130089	Homo sapiens	PRO2550	198	68
9696	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	170	80
9697	AK024455	Homo sapiens	FLJ00047 protein	137	63
9698	M24732	Homo sapiens	lamin-like protein	92	42
9699	AF116715	Homo sapiens	PRO2829	119	75
9700	AF130089	Homo sapiens	PRO2550	234	57
9701	V00662	Homo sapiens	ATPase 6	255	77
9702	L10908	Mus musculus	Gcap1 gene product	93	35
9703	AF130089	Homo sapiens	PRO2550	208	78
9704	AF194537	Homo sapiens	NAG13	89	51
9705	U79260	Homo sapiens	unknown	98	77
9706	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	78	43
9707	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	70	92
9708	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	136	60
9709	AF194537	Homo sapiens	NAG13	99	48
9710	AF130089	Homo sapiens	PRO2550	87	58
9711	X03145	Homo sapiens	pot. ORF III	135	41
9712	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	97	35
9713	AF116695	Homo sapiens	PRO2221	185	50
9714	AF130051	Homo sapiens	PRO0898	108	68
9715	AF130089	Homo sapiens	PRO2550	143	50
9716	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	124	49
9717	L27428	Homo sapiens	reverse transcriptase	133	50
9718	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	88	43
9719	L27428	Homo sapiens	reverse transcriptase	127	56
9720	M74009	Theropithecus gelada	cytochrome c oxidase subunit II	283	67
9721	M10546	Homo sapiens	cytochrome oxidase I	292	84
9722	AF130051	Homo sapiens	PRO0898	96	57
9723	U93564	Homo sapiens	putative p150	144	49
9724	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	373	76
9725	AK000496	Homo sapiens	unnamed protein product	155	55
9726	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	94	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9727	AF130086	Homo sapiens	PRO2550	154	40
9728	AF130089	Homo sapiens	PRO2550	127	61
9729	M19419	Mus musculus	proline-rich salivary protein	98	39
9730	D90053	Sus scrofa	destrin	119	43
9731	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	138	50
9732	AF090942	Homo sapiens	PRO0657	72	45
9733	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	110	44
9734	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	94
9735	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	150	85
9736	L27428	Homo sapiens	reverse transcriptase	217	33
9737	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	89	65
9738	AF007064	Saccharomyces cerevisiae	basic protein	108	31
9739	B01372	Homo sapiens	Neuron-associated protein.	128	60
9740	G03140	Homo sapiens	Human secreted protein, SEQ ID NO: 7221.	109	50
9741	AF194537	Homo sapiens	NAG13	123	54
9742	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	101	77
9743	X92485	Plasmodium vivax	pval	106	41
9744	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	122	76
9745	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	128	50
9746	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	87	64
9747	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	163	69
9748	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	124	74
9749	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	97	66
9750	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	156	71
9751	G03925	Homo sapiens	Human secreted protein, SEQ ID NO: 8006.	157	71
9752	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	97	51
9753	X92485	Plasmodium vivax	pval	91	39
9754	Y07786	Vibrio cholerae	Rfc-like protein	92	32
9755	AF068294	Homo sapiens	HDCMB45P	125	63
9756	L27428	Homo sapiens	reverse transcriptase	91	34
9757	AK024455	Homo sapiens	FLJ00047 protein	143	59
9758	S79410	Mus musculus	nuclear localization signal binding protein	103	41
9759	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	96	67
9760	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	179	58
9761	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	154	65
9762	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	91	78

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7888.		
9763	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	119	60
9764	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	111	85
9765	R13556	Homo sapiens	Protein encoded downstream of lhc_M oncoprotein.	116	36
9766	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	165	74
9767	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	162	74
9768	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	117	52
9769	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	92	50
9770	AF130089	Homo sapiens	PRO2550	104	31
9771	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	154	62
9772	U52077	Homo sapiens	mariner transposase	194	56
9773	Y87297	Homo sapiens	Human signal peptide containing protein HSP74 SEQ ID NO:74.	345	100
9774	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	73	36
9775	M11901	Rattus norvegicus	proline-rich salivary protein	96	32
9776	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	124	53
9777	L27428	Homo sapiens	reverse transcriptase	251	53
9778	K02576	Homo sapiens	salivary proline-rich protein 1	141	40
9779	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	111	58
9780	AJ224997	Rattus norvegicus	huntingtin	64	64
9781	AF283769	Homo sapiens	similar to GenBank Accession Number AC021163	119	53
9782	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	81	50
9783	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	68
9784	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	85	65
9785	AF144054	Homo sapiens	apoptosis related protein APR-4	83	53
9786	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	75	41
9787	M64792	Rattus norvegicus	salivary proline-rich protein	122	45
9788	D90053	Sus scrofa	destrin	146	43
9789	A18812	Brassica napus	extensin	104	34
9790	AF130089	Homo sapiens	PRO2550	102	66
9791	AF130089	Homo sapiens	PRO2550	326	70
9792	D38112	Homo sapiens	cytochrome c oxidase subunit I	495	79
9793	M10546	Homo sapiens	cytochrome oxidase I	343	75
9794	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	106	58
9795	X92485	Plasmodium vivax	pva1	108	48
9796	M15530	Homo sapiens	B-cell growth factor	119	70
9797	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	148	65
9798	X61046	Hydra sp.	mini-collagen	101	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9799	U93571	Homo sapiens	p40	82	36
9800	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	170	52
9801	X92485	Plasmodium vivax	pval	113	45
9802	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	63	44
9803	D38112	Homo sapiens	cytochrome c oxidase subunit 3	583	89
9804	G01736	Homo sapiens	Human secreted protein, SEQ ID NO: 5817.	150	47
9805	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	132	71
9806	X92485	Plasmodium vivax	pval	106	53
9807	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	163	67
9808	AF119851	Homo sapiens	PRO1722	341	68
9809	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	77	57
9810	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	72
9811	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	65
9812	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	118	37
9813	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	121	72
9814	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	72	92
9815	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	71	71
9816	AF118082	Homo sapiens	PRO1902	93	45
9817	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	207	59
9818	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	99	46
9819	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	130	69
9820	L10908	Mus musculus	Gcap1 gene product	99	37
9821	A00469	Homo sapiens	growth hormone	254	81
9822	U79260	Homo sapiens	unknown	85	39
9823	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	125	62
9824	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	103	74
9825	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	126	51
9826	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	148	44
9827	Y24789	Homo sapiens	Human secreted protein bf377. 1.	265	100
9828	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	72	60
9829	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	118	45
9830	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	104	51
9831	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	118	74
9832	AF151866	Homo sapiens	CGI-108 protein	115	31
9833	U93563	Homo sapiens	putative p150	127	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9834	AE003859	Xylella fastidiosa	hypothetical protein	97	30
9835	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	138	65
9836	B01372	Homo sapiens	Neuron-associated protein	150	88
9837	G03115	Homo sapiens	Human secreted protein, SEQ ID NO: 7196.	115	57
9838	AF068294	Homo sapiens	HDCMB45P	90	65
9839	S77772	Homo sapiens	aspartylglucosaminidase, AGA [C-terminal, alternatively spliced] (EC 3.5.1.26)	71	66
9840	AF090942	Homo sapiens	PRO0657	115	76
9841	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	75	54
9842	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	156	67
9843	AF130089	Homo sapiens	PRO2550	216	75
9844	M15530	Homo sapiens	B-cell growth factor	113	67
9845	U93567	Homo sapiens	p40	248	75
9846	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	151	55
9847	AK024455	Homo sapiens	FLJ00047 protein	151	64
9848	AF118082	Homo sapiens	PRO1902	58	81
9849	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	129	65
9850	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	329	77
9851	AF090944	Homo sapiens	PRO0663	122	80
9852	X71442	Rattus norvegicus	ORF 1; putative	109	48
9853	AF130089	Homo sapiens	PRO2550	126	60
9854	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	98	62
9855	U93563	Homo sapiens	putative p150	136	48
9856	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	276	74
9857	AF017777	Drosophila melanogaster	la costa	99	43
9858	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	99	37
9859	K02576	Homo sapiens	salivary proline-rich protein 1	106	37
9860	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	138	71
9861	AF116909	Homo sapiens	unknown	103	43
9862	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	113	38
9863	Y21811	Homo sapiens	CPF polypeptide 36PRO.	131	58
9864	U93567	Homo sapiens	p40	252	70
9865	AF090895	Homo sapiens	PRO0117	164	60
9866	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	109	47
9867	AF090930	Homo sapiens	PRO0478	106	84
9868	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	167	84
9869	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	83	60
9870	AF119900	Homo sapiens	PRO2822	134	48
9871	AF116715	Homo sapiens	PRO2829	111	81
9872	U52077	Homo sapiens	mariner transposase	332	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9873	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	95	85
9874	U93570	Homo sapiens	putative p150	243	44
9875	L27428	Homo sapiens	reverse transcriptase	127	54
9876	S80119	Rattus sp.	reverse transcriptase homolog	163	43
9877	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	64
9878	AF187823	Zea mays	transposase DOPA	132	38
9879	W40353	Homo sapiens	Human unspecified protein from US5702907.	101	41
9880	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	133	43
9881	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	101	59
9882	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	148	52
9883	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	57	65
9884	X92485	Plasmodium vivax	pva1	129	43
9885	M64792	Rattus norvegicus	salivary proline-rich protein	98	37
9886	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	89	59
9887	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	155	54
9888	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	121	40
9889	D38112	Homo sapiens	NADH dehydrogenase subunit 2	346	68
9890	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	133	38
9891	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	143	66
9892	X53581	Rattus norvegicus	ORF7	81	56
9893	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	109	53
9894	AE003859	Xylella fastidiosa	hypothetical protein	99	27
9895	U83303	Homo sapiens	line-1 reverse transcriptase	157	58
9896	L26953	Homo sapiens	chromosomal protein	107	68
9897	AL390114	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	95	51
9898	U93569	Homo sapiens	putative p150	106	52
9899	U15647	Mus musculus	reverse transcriptase	118	47
9900	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	118	70
9901	U93563	Homo sapiens	putative p150	116	39
9902	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	153	81
9903	X03145	Homo sapiens	pot. ORF V	148	54
9904	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	84	65
9905	AF066073	Dictyostelium discoideum	SP85; PsB	113	52
9906	AF090895	Homo sapiens	PRO0117	125	58
9907	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	102	57
9908	M24732	Homo sapiens	lamin-like protein	95	35

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9909	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	96	55
9910	AF118080	Homo sapiens	PRO1880	120	66
9911	AF116719	Homo sapiens	PRO2987	216	72
9912	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	150	75
9913	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	129	76
9914	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	72	58
9915	G00233	Homo sapiens	Human secreted protein, SEQ ID NO: 4314.	103	71
9916	S79410	Mus musculus	nuclear localization signal binding protein	114	75
9917	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	75	83
9918	AF116712	Homo sapiens	PRO2738	106	69
9919	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	90	77
9920	AF068294	Homo sapiens	HDCMB45P	296	59
9921	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	58	54
9922	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	143	69
9923	U38979	Homo sapiens	hPMSR3	135	46
9924	AB002317	Homo sapiens	KIAA0319	294	75
9925	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	169	42
9926	U49973	Homo sapiens	ORF1; MER37; putative transposase, similar to pogo element	153	59
9927	G00214	Homo sapiens	Human secreted protein, SEQ ID NO: 4295.	261	97
9928	Y14483	Homo sapiens	Fragment of human secreted protein encoded by gene 18.	863	76
9929	AF130051	Homo sapiens	PRO0898	128	60
9930	AF130089	Homo sapiens	PRO2550	123	41
9931	AF064597	Homo sapiens	LINE-1 like protein	101	48
9932	AF027144	Homo sapiens	zinc finger protein	76	42
9933	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	120	44
9934	U93569	Homo sapiens	putative p150	105	68
9935	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	133	51
9936	Y73344	Homo sapiens	HTRM clone 0258181 protein sequence.	145	46
9937	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	123	77
9938	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	40
9939	D63643	Homo sapiens	clathrin coat assembly protein-like	232	69
9940	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	75	65
9941	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	176	71
9942	X04588	Homo sapiens	cytoskeletal tropomyosin (AA 1-248)	379	81
9943	G03683	Homo sapiens	Human secreted protein, SEQ ID NO: 7764.	58	52
9944	AF130114	Homo sapiens	PRO2459	117	67
9945	U49973	Homo sapiens	ORF1; MER37; putative transposase	297	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			similar to pogo element		
9946	D00570	Mus musculus	open reading frame (251 AA)	214	63
9947	X03717	Homo sapiens	pot. unidentified reading frame	76	35
9948	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	127	64
9949	J02621	Homo sapiens	high mobility group protein 14	90	50
9950	AF090931	Homo sapiens	PRO0483	114	75
9951	AF164612	Homo sapiens	Gag protein	132	63
9952	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	112	65
9953	Y08061	Homo sapiens	Human c-myc protein fragment.	118	59
9954	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	138	74
9955	G00974	Homo sapiens	Human secreted protein, SEQ ID NO: 5055.	94	38
9956	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	124	61
9957	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	177	51
9958	X92485	Plasmodium vivax	pva1	137	44
9959	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	142	53
9960	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	174	68
9961	S79410	Mus musculus	nuclear localization signal binding protein	123	38
9962	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	124	56
9963	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	80	57
9964	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	136	82
9965	Y27908	Homo sapiens	Human secreted protein encoded by gene No. 119.	92	53
9966	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	76	40
9967	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	136	38
9968	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	101	67
9969	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	90	83
9970	Y36156	Homo sapiens	Human secreted protein #28.	170	68
9971	U79260	Homo sapiens	unknown	142	67
9972	L27428	Homo sapiens	reverse transcriptase	108	63
9973	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	119	60
9974	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	78	85
9975	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	79	39
9976	AF090944	Homo sapiens	PRO0663	109	73
9977	AF116715	Homo sapiens	PRO2829	120	56
9978	U93563	Homo sapiens	putative p150	132	57
9979	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	97	80
9980	U42580	Paramecium bursaria	A658R	70	40

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		Chlorella virus 1			
9981	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	87	61
9982	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	135	70
9983	X61047	Hydra sp.	mini-collagen	90	36
9984	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	98	40
9985	Y41552	Homo sapiens	Fragment of human secreted protein encoded by gene 80.	90	42
9986	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	132	52
9987	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	115	41
9988	AF042832	Homo sapiens	forkhead-related transcription factor FREAC-9	89	36
9989	X03717	Homo sapiens	pot. unidentified reading frame	105	67
9990	AL390935	Leishmania major	possible dopap	118	74
9991	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	109	58
9992	AF130114	Homo sapiens	PRO2459	115	68
9993	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	83
9994	AF068294	Homo sapiens	HDCMB45P	196	43
9995	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	117	54
9996	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	74	53
9997	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	132	55
9998	AF102771	Homo sapiens	cardiac-specific ras association (RalGDS/AF-6) domain family 1 protein isoform 1D	148	100
9999	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	213	88
10000	D38112	Homo sapiens	ATPase subunit 6	279	69
10001	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	97	39
10002	AK000496	Homo sapiens	unnamed protein product	154	74
10003	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	125	74
10004	B07702	Homo sapiens	Protein encoded by the endogenous fragment of HERV-W.	143	56
10005	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	97	65
10006	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	154	72
10007	AF021231	Mus musculus	acetylcholinesterase-associated collagen	109	41
10008	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	69	78
10009	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	170	78
10010	AF130051	Homo sapiens	PRO0898	134	67
10011	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	100	44
10012	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	95	78
10013	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	90	52
10014	AF130052	Homo sapiens	PRO0956	104	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10015	X92485	Plasmodium vivax	pva1	119	46
10016	AF130089	Homo sapiens	PRO2550	171	56
10017	AF130089	Homo sapiens	PRO2550	172	58
10018	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	146	38
10019	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	109	54
10020	G02584	Homo sapiens	Human secreted protein, SEQ ID NO: 6665.	109	43
10021	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	70	51
10022	AF090942	Homo sapiens	PRO0657	113	67
10023	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	77	33
10024	X55681	Lycopersicon esculentum	extensin (class I)	95	35
10025	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	93	61
10026	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	153	42
10027	Y73377	Homo sapiens	HTRM clone 1645941 protein sequence.	1180	84
10028	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	108	59
10029	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	112	65
10030	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	163	82
10031	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	131	66
10032	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	74	48
10033	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	104	85
10034	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	192	60
10035	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	153	55
10036	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	128	76
10037	AF118086	Homo sapiens	PRO1992	148	68
10038	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	125	47
10039	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	137	65
10040	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	139	45
10041	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	128	75
10042	U83303	Homo sapiens	line-1 reverse transcriptase	100	33
10043	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	102	64
10044	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	135	71
10045	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	148	46
10046	X92485	Plasmodium vivax	pva1	98	58

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10047	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	102	87
10048	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	63	84
10049	U09202	Homo sapiens	ornithine decarboxylase antizyme	202	67
10050	X92485	Plasmodium vivax	pva1	77	34
10051	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	87	40
10052	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	114	57
10053	AC005396	Arabidopsis thaliana	putative proline-rich protein	100	33
10054	G03600	Homo sapiens	Human secreted protein, SEQ ID NO: 7681.	91	94
10055	X73434	Ovis aries	KAP5.4 keratin protein	76	45
10056	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	82	62
10057	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	66
10058	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	116	55
10059	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	130	73
10060	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	100	42
10061	L27428	Homo sapiens	reverse transcriptase	107	43
10062	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	92	47
10063	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	95	46
10064	AF220264	Homo sapiens	MOST-1	135	48
10065	AF130114	Homo sapiens	PRO2459	87	68
10066	D86853	Catharanthus roseus	extensin	115	35
10067	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	79	71
10068	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	102	54
10069	U16359	Rattus norvegicus	nitric oxide synthase	93	77
10070	AJ233597	Mus famulus	reverse transcriptase	65	36
10071	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	94	67
10072	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	51
10073	AK024455	Homo sapiens	FLJ00047 protein	146	66
10074	X92485	Plasmodium vivax	pva1	121	36
10075	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	64
10076	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	73	43
10077	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	165	75
10078	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	106	72
10079	AF130050	Homo sapiens	PRO0872	102	63
10080	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	130	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			8153.		
10081	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	285	78
10082	AF068294	Homo sapiens	HDCMB45P	144	68
10083	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	98	48
10084	X92485	Plasmodium vivax	pval	108	53
10085	AF118082	Homo sapiens	PRO1902	117	57
10086	AF090942	Homo sapiens	PRO0657	88	53
10087	AF118086	Homo sapiens	PRO1992	172	71
10088	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	119	68
10089	K02576	Homo sapiens	salivary proline-rich protein I	117	34
10090	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	154	77
10091	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	138	56
10092	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	90	56
10093	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	134	66
10094	M15530	Homo sapiens	B-cell growth factor	116	64
10095	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	124	65
10096	M15530	Homo sapiens	B-cell growth factor	87	68
10097	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	84	79
10098	G00369	Homo sapiens	Human secreted protein, SEQ ID NO: 4450.	150	66
10099	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	157	70
10100	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	103	60
10101	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	114	70
10102	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	130	53
10103	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	156	52
10104	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	87	60
10105	L27428	Homo sapiens	reverse transcriptase	220	38
10106	W90834	Homo sapiens	Human lymphocyte targeted peptide #2.	91	43
10107	AF161356	Homo sapiens	HSPC093	227	61
10108	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	123	64
10109	AF130089	Homo sapiens	PRO2550	126	77
10110	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	118	60
10111	M63274	Plasmodium falciparum	malaria antigen	81	54
10112	AF090944	Homo sapiens	PRO0663	133	70
10113	L27428	Homo sapiens	reverse transcriptase	91	32
10114	Y17221	Homo sapiens	Human secreted protein (clone fk317-3).	112	64
10115	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	85	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10116	L27428	Homo sapiens	reverse transcriptase	112	44
10117	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	115	61
10118	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	79	34
10119	AF194537	Homo sapiens	NAG13	295	51
10120	D00570	Mus musculus	open reading frame (196 AA)	97	40
10121	X77816	Rattus norvegicus	PR-Vbeta1	122	47
10122	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	55
10123	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	92	66
10124	AF090942	Homo sapiens	PRO0657	127	78
10125	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	145	68
10126	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	113	49
10127	U93563	Homo sapiens	putative p150	94	35
10128	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	146	79
10129	AF130089	Homo sapiens	PRO2550	208	75
10130	M15530	Homo sapiens	B-cell growth factor	102	73
10131	X55685	Lycopersicon esculentum	extensin (class I)	122	30
10132	L27428	Homo sapiens	reverse transcriptase	197	40
10133	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	99	73
10134	AF194537	Homo sapiens	NAG13	220	48
10135	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	116	75
10136	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	117	61
10137	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	223	59
10138	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	178	75
10139	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	170	52
10140	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	133	64
10141	AF072164	Homo sapiens	HFSE-1	80	60
10142	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	103	74
10143	M15530	Homo sapiens	B-cell growth factor	91	40
10144	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	103	61
10145	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	162	65
10146	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	128	53
10147	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	112	61
10148	X71975	Drosophila melanogaster	put. homologue to S.cerevisiae GARI gene	118	39
10149	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH 8c)	123	49
10150	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	163	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10151	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	106	83
10152	AL390114	Leishmania major	extremely cysteine/valine rich protein	117	52
10153	AF113685	Homo sapiens	PRO0974	133	62
10154	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	129	67
10155	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	89	50
10156	K02576	Homo sapiens	salivary proline-rich protein 1	131	41
10157	AB011099	Homo sapiens	KIAA0527 protein	94	35
10158	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	78	72
10159	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	139	71
10160	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	161	68
10161	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	162	88
10162	M15530	Homo sapiens	B-cell growth factor	137	63
10163	AF090895	Homo sapiens	PRO0117	93	67
10164	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	60
10165	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	126	52
10166	AF118082	Homo sapiens	PRO1902	111	55
10167	AF090895	Homo sapiens	PRO0117	112	75
10168	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	135	69
10169	AF090942	Homo sapiens	PRO0657	149	67
10170	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	145	68
10171	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	85	51
10172	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	136	62
10173	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	158	63
10174	AF090942	Homo sapiens	PRO0657	75	44
10175	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	97	47
10176	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WO9901020.	108	75
10177	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	168	80
10178	M22332	Homo sapiens	unknown protein	131	62
10179	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	160	60
10180	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	65	68
10181	AF119900	Homo sapiens	PRO2822	132	72
10182	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	114	56
10183	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	124	59
10184	AF210651	Homo sapiens	NAG18	150	65
10185	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	109	46
10186	X71442	Rattus	ORF 1; putative	91	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		norvegicus			
10187	AK024455	Homo sapiens	FLJ00047 protein	122	54
10188	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	82	72
10189	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	78	61
10190	AF220264	Homo sapiens	MOST-1	165	81
10191	Y91617	Homo sapiens	Human secreted protein sequence encoded by gene 19 SEQ ID NO:290.	54	44
10192	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	119	80
10193	X92485	Plasmodium vivax	pva1	128	57
10194	X61296	Rattus norvegicus	open reading frame 2	79	72
10195	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	116	62
10196	AF130089	Homo sapiens	PRO2550	144	62
10197	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	124	56
10198	AF090942	Homo sapiens	PRO0657	133	76
10199	S79304	Rattus sp.	cytochrome oxidase subunit I; COX I	280	66
10200	S61070	Homo sapiens	reverse transcriptase homolog-pol (retroviral element)	188	49
10201	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	51
10202	AF068294	Homo sapiens	HDCMB45P	174	65
10203	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	174	50
10204	U93572	Homo sapiens	putative p150	77	40
10205	L27428	Homo sapiens	reverse transcriptase	133	50
10206	J02621	Homo sapiens	high mobility group protein 14	94	57
10207	AF130079	Homo sapiens	PRO2852	144	73
10208	R95913	Homo sapiens	Neural thread protein.	134	51
10209	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	154	76
10210	AB046048	Macaca fascicularis	unnamed protein product	162	60
10211	AF090931	Homo sapiens	PRO0483	128	79
10212	AF130051	Homo sapiens	PRO0898	144	76
10213	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	95	54
10214	AF130089	Homo sapiens	PRO2550	158	70
10215	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	96	55
10216	M15894	Homo sapiens	chorionic somatomammotropin precursor	116	63
10217	AK024372	Homo sapiens	unnamed protein product	85	56
10218	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	118	69
10219	M37679	Mus musculus	Ig heavy chain precursor	64	83
10220	G03806	Homo sapiens	Human secreted protein, SEQ ID NO: 7887.	91	69
10221	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	127	47
10222	Y36505	Homo sapiens	Fragment of human secreted protein encoded by gene 29.	102	48
10223	AF090940	Homo sapiens	PRO0644	105	76
10224	U49974	Homo sapiens	mariner transposase	155	76
10225	K02576	Homo sapiens	salivary proline-rich protein I	154	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10226	AF293639	Homo sapiens	dioxin receptor repressor	819	98
10227	L27428	Homo sapiens	reverse transcriptase	137	44
10228	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	106	70
10229	U93566	Homo sapiens	p40	206	80
10230	Y08061	Homo sapiens	Human c-myc protein fragment.	114	66
10231	AF118082	Homo sapiens	PRO1902	76	52
10232	AF118086	Homo sapiens	PRO1992	99	75
10233	X53375	Helianthus annuus	anther-specific protein SF18	95	64
10234	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	156	72
10235	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	100	35
10236	L27428	Homo sapiens	reverse transcriptase	244	50
10237	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	93	70
10238	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	142	72
10239	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	149	80
10240	S52010	Mus sp.	1st Met is at position 21	98	42
10241	AL110147	Homo sapiens	hypothetical protein	125	35
10242	X98485	Plasmodium vivax	putative	85	51
10243	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	70	65
10244	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO: 103.	125	49
10245	U49973	Homo sapiens	ORF2: function unknown	150	81
10246	K02576	Homo sapiens	salivary proline-rich protein 1	113	56
10247	AF130089	Homo sapiens	PRO2550	139	73
10248	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	160	59
10249	U93565	Homo sapiens	putative p150	109	43
10250	AF130089	Homo sapiens	PRO2550	104	54
10251	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	78	36
10252	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	110	58
10253	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	123	54
10254	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	95	57
10255	X03145	Homo sapiens	pot. ORF V	76	63
10256	Y01405	Homo sapiens	Secreted protein encoded by gene 23 clone HDPBA48.	116	65
10257	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	113	68
10258	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	138	68
10259	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	135	60
10260	G02528	Homo sapiens	Human secreted protein, SEQ ID NO: 6609.	95	59
10261	M86246	Homo sapiens	EHS-2	96	62
10262	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	180	66
10263	G03790	Homo sapiens	Human secreted protein, SEQ ID NO:	102	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7871.		
10264	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	313	84
10265	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	144	56
10266	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	150	61
10267	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	408	89
10268	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	74	26
10269	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	133	52
10270	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	105	61
10271	X61048	Hydra sp.	mini-collagen	121	40
10272	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	150	66
10273	L24521	Homo sapiens	transformation-related protein	134	51
10274	G03806	Homo sapiens	Human secreted protein, SEQ ID NO: 7887.	96	47
10275	U59446	Brassica napus	myrosinase-binding protein related protein	115	39
10276	G01480	Homo sapiens	Human secreted protein, SEQ ID NO: 5561.	482	98
10277	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	143	81
10278	U93564	Homo sapiens	putative p150	130	46
10279	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	123	44
10280	AF090944	Homo sapiens	PRO0663	156	73
10281	AF130079	Homo sapiens	PRO2852	146	75
10282	X89401	Homo sapiens	ribosomal protein L21	108	48
10283	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	65	66
10284	Y25821	Homo sapiens	Human secreted protein fragment encoded from gene 41.	1602	98
10285	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	308	43
10286	AF090931	Homo sapiens	PRO0483	131	74
10287	Y48480	Homo sapiens	Human breast tumour-associated protein 25.	203	90
10288	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	116	44
10289	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	160	64
10290	X67863	Mus musculus	T2	147	37
10291	AF229067	Homo sapiens	PADI-H protein	123	43
10292	AF078844	Homo sapiens	hqp0376 protein	125	59
10293	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	123	37
10294	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	103	64
10295	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	162	70
10296	V00662	Homo sapiens	ATPase 6	268	88
10297	AB007861	Homo sapiens	KLAA0401	424	92
10298	M24732	Homo sapiens	lamin-like protein	183	40
10299	D90053	Sus scrofa	destrin	123	48
10300	X61047	Hydra sp.	mini-collagen	86	43

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10301	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	180	50
10302	AF118078	Homo sapiens	PRO1848	157	63
10303	X55681	Lycopersicon esculentum	extensin (class I)	87	36
10304	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	105	62
10305	X70944	Homo sapiens	PTB-associated splicing factor	84	32
10306	AF068294	Homo sapiens	HDCMB45P	220	42
10307	S79410	Mus musculus	nuclear localization signal binding protein	96	41
10308	AJ005559	Mus musculus	SPR2A protein	64	42
10309	AL353995	Arabidopsis thaliana	AtAGP4	98	38
10310	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	213	92
10311	M15386	Homo sapiens	gamma-globin	614	88
10312	V00488	Homo sapiens	alpha globin	574	90
10313	AL049730	Arabidopsis thaliana	pEARL1 1-like protein	117	38
10314	AL356299	Homo sapiens	bK3216D2.1.1 (S-adenosylhomocysteine hydrolase (SAHH), isoform 1)	256	70
10315	AF194537	Homo sapiens	NAG13	113	63
10316	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	99	62
10317	AF090931	Homo sapiens	PRO0483	86	68
10318	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	102	77
10319	L29219	Homo sapiens	clk1; putative	341	100
10320	V00488	Homo sapiens	alpha globin	314	89
10321	AJ223953	Homo sapiens	hPTTG	354	89
10322	X79389	Homo sapiens	glutathione transferase T1	78	75
10323	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	101	66
10324	AF116715	Homo sapiens	PRO2829	128	73
10325	AF116619	Homo sapiens	PRO1051	125	77
10326	Y14318	Homo sapiens	peroxisomal ABC-transporter	249	100
10327	U73844	Homo sapiens	ESE-1a	185	90
10328	AB051901	Homo sapiens	VDUP1	132	83
10329	AL163300	Homo sapiens	human ubiquitin conjugating enzyme G2 EC 6.3.2.19.	720	100
10330	AF117237	Homo sapiens	prefoldin subunit 2	729	100
10331	D42054	Homo sapiens	KIAA0092 gene product is distantly related to smooth muscle myosin.	352	84
10332	AF038965	Homo sapiens	26S proteasome ATPase subunit	431	100
10333	Y94960	Homo sapiens	Human secreted protein clone m1117_1 protein sequence SEQ ID NO: 126.	399	96
10334	X60376	Brassica napus	proline-rich protein	114	31
10335	M34427	Homo sapiens	T-plastin	343	91
10336	V00488	Homo sapiens	alpha globin	445	88
10337	M15386	Homo sapiens	gamma-globin	402	85
10338	X61123	Homo sapiens	BTG1	367	90
10339	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	278	87
10340	A03992	synthetic construct	growth hormone	145	61
10341	G00437	Homo sapiens	Human secreted protein, SEQ ID NO:	126	57

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4518.		
10342	U02680	Homo sapiens	protein tyrosine kinase	140	92
10343	AF180681	Homo sapiens	guanine nucleotide exchange factor	1425	88
10344	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	123	69
10345	V00488	Homo sapiens	alpha globin	318	93
10346	M17885	Homo sapiens	acidic ribosomal phosphoprotein (P0)	329	98
10347	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	100	66
10348	U29953	Homo sapiens	pigment epithelium-derived factor	359	74
10349	G01790	Homo sapiens	Human secreted protein, SEQ ID NO: 5871.	85	66
10350	V00488	Homo sapiens	alpha globin	361	90
10351	U93567	Homo sapiens	p40	203	84
10352	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	253	85
10353	AF194537	Homo sapiens	NAG13	196	41
10354	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	297	81
10355	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	144	65
10356	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	94	54
10357	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	153	68
10358	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	136	53
10359	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	95	77
10360	X61296	Rattus norvegicus	open reading frame 2	87	40
10361	L24521	Homo sapiens	transformation-related protein	103	32
10362	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	101	55
10363	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	89	80
10364	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	101	58
10365	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	322	85
10366	S58722	Homo sapiens	X-linked retinopathy protein [C-terminal, clone XEH.8c]	101	59
10367	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	125	53
10368	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	120	59
10369	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	60	83
10370	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	169	81
10371	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	80	75
10372	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	60	83
10373	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	89	77
10375	AF130089	Homo sapiens	PRO2550	139	78
10376	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 146	146	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7874.		
10377	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	96	51
10378	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	132	58
10379	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	117	71
10380	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	125	54
10381	U93569	Homo sapiens	putative p150	160	60
10382	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	140	77
10383	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	83	71
10384	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	137	63
10385	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	67	50
10386	X62691	Homo sapiens	ribosomal protein homologous to yeast S24	117	58
10387	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	141	45
10388	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	153	70
10389	U93570	Homo sapiens	putative p150	112	58
10390	AF090942	Homo sapiens	PRO0657	126	68
10391	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	123	64
10392	AF130089	Homo sapiens	PRO2550	144	71
10393	U40739	Homo sapiens	cyclin C	464	86
10394	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	151	75
10395	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	137	35
10396	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	165	66
10397	AF090930	Homo sapiens	PRO0478	133	80
10398	AK024455	Homo sapiens	FLJ00047 protein	153	62
10399	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	142	69
10400	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	73	51
10401	AB030033	Dictyostelium discoideum	AmiB	82	33
10402	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	113	63
10403	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	148	77
10404	AK024455	Homo sapiens	FLJ00047 protein	138	71
10405	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	128	59
10406	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	143	76
10407	AF090942	Homo sapiens	PRO0657	105	64
10408	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH 8c}	93	54
10409	J02621	Homo sapiens	high mobility group protein 14	140	64
10410	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	87	46
10411	G03798	Homo sapiens	Human secreted protein, SEQ ID NO:	79	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7879.		
10412	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	79	66
10413	AF130079	Homo sapiens	PRO2852	184	90
10414	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	237	77
10415	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	122	64
10416	AF016099	Mus musculus	endonuclease/reverse transcriptase	89	78
10417	S80864	Homo sapiens	cytochrome c-like polypeptide	184	52
10418	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	131	75
10419	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	160	90
10420	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	131	59
10421	AF090942	Homo sapiens	PRO0657	134	57
10423	L78669	Homo sapiens	CoxII/D-loop DNA fusion protein	106	90
10424	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	105	75
10425	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	130	64
10426	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	122	64
10427	AF068294	Homo sapiens	HDCMB45P	256	56
10428	AF194537	Homo sapiens	NAG13	182	54
10429	AF090931	Homo sapiens	PRO0483	108	79
10430	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	68
10431	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10432	X67920	Homo sapiens	tryptophanyl-tRNA synthetase	138	84
10433	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	294	78
10434	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10435	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	125	75
10436	S79410	Mus musculus	nuclear localization signal binding protein	117	72
10437	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	120	67
10438	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	140	69
10439	AF130089	Homo sapiens	PRO2550	106	80
10440	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	331	83
10441	W94294	Homo sapiens	Human phosphatidylinositol transfer protein gamma.	143	96
10442	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	121	87
10443	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10444	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	141	67
10445	U93567	Homo sapiens	p40	262	69
10446	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	112	92
10447	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1	120	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			protein		
10448	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	104	68
10449	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	115	80
10450	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	117	80
10451	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	104	80
10452	AF130089	Homo sapiens	PRO2550	315	68
10453	G02530	Homo sapiens	Human secreted protein, SEQ ID NO: 6611.	110	71
10454	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	86	34
10455	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	113	83
10456	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	180	83
10457	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	119	96
10458	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	133	58
10459	Y41710	Homo sapiens	Human PRO618 protein sequence.	894	71
10460	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	84	71
10461	K02401	Homo sapiens	chorionic somatomammotropin	471	88
10462	G02113	Homo sapiens	Human secreted protein, SEQ ID NO: 6194.	241	73
10463	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	93	68
10464	U15647	Mus musculus	reverse transcriptase	110	47
10465	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	97	57
10466	G02754	Homo sapiens	Human secreted protein, SEQ ID NO: 6835.	145	93
10467	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	137	57
10468	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	62	55
10469	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	93	86
10470	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	119	63
10471	AF068294	Homo sapiens	HDCMB45P	117	43
10472	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	335	72
10473	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	121	62
10474	X79238	Homo sapiens	ribosomal protein L30	126	58
10475	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10476	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	106	61
10477	AC006693	Caenorhabditis elegans	Hypothetical protein W02H5.e	119	41
10478	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	87	66
10479	AF130079	Homo sapiens	PRO2852	97	54
10480	AK024455	Homo sapiens	FLJ00047 protein	135	69

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10481	K02401	Homo sapiens	chorionic somatomammotropin	463	80
10482	G00398	Homo sapiens	Human secreted protein, SEQ ID NO: 4479.	69	83
10483	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	132	61
10484	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	119	80
10485	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	90	54
10486	U79260	Homo sapiens	unknown	105	90
10487	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	243	53
10488	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	90	78
10489	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	120	64
10490	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	123	60
10491	Y48576	Homo sapiens	Human breast tumour-associated protein 37.	471	84
10492	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	176	77
10493	S79410	Mus musculus	nuclear localization signal binding protein	135	64
10494	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	123	44
10495	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	86	46
10496	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	145	40
10497	AL3359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhala.	111	50
10498	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	96	73
10499	AL132841	Caenorhabditis elegans	Y15E3A.3	142	96
10500	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	120	49
10501	AF220264	Homo sapiens	MOST-1	93	83
10502	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	116	57
10503	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	100	70
10504	AF090931	Homo sapiens	PRO0483	88	80
10505	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	89	72
10506	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	121	81
10507	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	188	82
10508	AF130050	Homo sapiens	PRO0872	101	74
10509	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	176	68
10510	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	120	96
10511	AK026249	Homo sapiens	unnamed protein product	97	68
10512	X95276	Plasmodium falciparum	ORF91	75	29
10513	X17093	Homo sapiens	leukocyte antigen F	397	91
10514	W48351	Homo sapiens	Human breast cancer related protein	115	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
10515	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	154	68
10516	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	86	47
10517	AF090944	Homo sapiens	PRO0663	118	48
10518	S58722	Homo sapiens	X-linked retinopathy protein [C-terminal, clone XEH.8c]	131	77
10519	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	230	58
10520	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10521	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	130	40
10522	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10523	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	139	69
10524	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	125	100
10525	J04495	Macaca mulatta	alpha-globin	144	90
10526	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	105	61
10527	AF130089	Homo sapiens	PRO2550	132	67
10528	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	90	53
10529	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	112	75
10530	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	157	79
10531	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	59
10532	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	121	63
10533	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	112	43
10534	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	131	65
10535	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	95	60
10536	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	157	79
10537	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	199	90
10538	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	113	75
10539	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	120	65
10540	AF130089	Homo sapiens	PRO2550	195	67
10541	Y60522	Homo sapiens	Human normal bladder tissue EST encoded protein 194.	73	72
10542	G01175	Homo sapiens	Human secreted protein, SEQ ID NO: 5256.	83	100
10543	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	81	54
10544	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	147	75
10545	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	109	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10546	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	123	46
10547	AF130089	Homo sapiens	PRO2550	133	63
10548	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	246	80
10549	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	122	51
10550	J02459	bacteriophage lambda	J (tail: host specificity; 1132)	772	97
10551	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	158	80
10552	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	50
10553	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	184	71
10554	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	107	60
10555	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	140	69
10556	U49973	Homo sapiens	ORF2: function unknown	91	70
10557	AF151850	Homo sapiens	CGI-92 protein	459	63
10558	X66285	Mus musculus	HC1 ORF	92	30
10559	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	127	67
10560	AF130050	Homo sapiens	PRO0872	100	71
10561	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	335	80
10562	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	126	58
10563	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	127	76
10564	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	158	62
10565	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	77
10566	V00488	Homo sapiens	alpha globin	464	89
10567	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	162	81
10568	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	113	72
10569	G03040	Homo sapiens	Human secreted protein, SEQ ID NO: 7121.	127	47
10570	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	125	65
10571	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	79	88
10572	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	158	80
10573	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	138	56
10574	AF119900	Homo sapiens	PRO2822	154	55
10575	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	87	72
10576	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	131	66
10577	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	80	47
10578	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	121	53
10579	Y91577	Homo sapiens	Human secreted protein sequence	335	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded by gene 2 SEQ ID NO:250.		
10580	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	104	47
10581	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	324	68
10582	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	129	66
10583	AF090895	Homo sapiens	PRO0117	137	63
10584	L27428	Homo sapiens	reverse transcriptase	98	50
10585	G00418	Homo sapiens	Human secreted protein, SEQ ID NO: 4499.	101	68
10586	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	108	82
10587	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	166	76
10588	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	100	70
10589	X03145	Homo sapiens	pot. ORF I	120	43
10590	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	139	70
10591	AF144054	Homo sapiens	apoptosis related protein APR-4	92	50
10592	AK024455	Homo sapiens	FLJ00047 protein	111	75
10593	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	143	58
10594	G03636	Homo sapiens	Human secreted protein, SEQ ID NO: 7717.	116	54
10595	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	196	57
10596	AF130089	Homo sapiens	PRO2550	140	66
10597	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	115	52
10598	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	79	71
10599	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	79
10600	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	119	67
10601	AF090895	Homo sapiens	PRO0117	106	68
10602	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	83	72
10603	AF090930	Homo sapiens	PRO0478	119	70
10604	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	120	83
10605	AF132949	Homo sapiens	CGI-15 protein	114	96
10606	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	176	77
10607	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	155	74
10608	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	127	63
10609	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	88	60
10610	AF130089	Homo sapiens	PRO2550	86	90
10611	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	149	72
10612	L27428	Homo sapiens	reverse transcriptase	311	52
10613	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	83	84
10614	D00570	Mus musculus	open reading frame (196 AA)	116	69

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10615	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	290	62
10616	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	125	51
10617	AF116695	Homo sapiens	PRO2221	131	56
10618	M64793	Rattus norvegicus	salivary proline-rich protein	101	48
10619	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	104	65
10620	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	112	58
10621	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	336	85
10622	AF118082	Homo sapiens	PRO1902	80	73
10623	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	136	50
10624	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	109	67
10625	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	92	75
10626	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	121	62
10627	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	104	52
10628	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	137	66
10629	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	67
10630	U93569	Homo sapiens	putative p150	104	52
10631	AF090895	Homo sapiens	PRO0117	136	70
10632	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	89	57
10633	AF113685	Homo sapiens	PRO0974	130	64
10634	AK024455	Homo sapiens	FLJ00047 protein	103	63
10635	M24732	Homo sapiens	lamin-like protein	80	65
10636	U49974	Homo sapiens	mariner transposase	116	72
10637	AK024455	Homo sapiens	FLJ00047 protein	158	67
10638	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	121	64
10639	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	137	57
10640	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	123	72
10641	L27428	Homo sapiens	reverse transcriptase	150	54
10642	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	68	81
10643	U93565	Homo sapiens	putative p150	282	57
10644	AF090942	Homo sapiens	PRO0657	153	74
10645	Y48333	Homo sapiens	Human prostate cancer-associated protein 30.	196	90
10646	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	242	73
10647	U79260	Homo sapiens	unknown	95	77
10648	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	149	64
10649	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	158	87
10650	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	339	89

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10651	U15183	Mycobacterium leprae	proline-rich antigen	102	37
10652	AF217536	Homo sapiens	truncated mevalonate kinase	138	70
10653	AF119855	Homo sapiens	PRO1847	74	100
10654	M15530	Homo sapiens	B-cell growth factor	94	52
10655	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	144	54
10656	M15317	Plasmodium falciparum	histidine-rich protein	124	51
10657	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	143	66
10658	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	114	77
10659	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	172	55
10660	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	150	78
10661	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10662	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	151	71
10663	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10664	AK000496	Homo sapiens	unnamed protein product	140	77
10665	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	147	75
10666	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10667	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	149	78
10668	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	303	78
10669	D00526	Rattus norvegicus	L-gulono-gamma-lactone oxidase	108	73
10670	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	143	65
10671	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	409	84
10672	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	110	65
10673	G00423	Homo sapiens	Human secreted protein, SEQ ID NO: 4504.	123	43
10674	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	85	36
10675	U93565	Homo sapiens	putative p150	115	45
10676	AF109907	Homo sapiens	S164	205	65
10677	G02620	Homo sapiens	Human secreted protein, SEQ ID NO: 6701.	118	73
10678	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	106	62
10679	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10680	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	248	54
10681	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	88	52
10682	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	126	77
10683	S58722	Homo sapiens	X-linked retinopathy protein {C-	123	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			terminal, clone XEH.8c}		
10684	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	123	72
10685	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	99	40
10686	AF068294	Homo sapiens	HDCMB45P	182	54
10687	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	104	53
10688	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	277	76
10689	G00233	Homo sapiens	Human secreted protein, SEQ ID NO: 4314.	118	65
10690	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	143	71
10691	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	97	81
10692	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	160	68
10693	AF130089	Homo sapiens	PRO2550	133	56
10694	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	129	71
10695	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	123	71
10696	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	161	45
10697	G00648	Homo sapiens	Human secreted protein, SEQ ID NO: 4729.	88	56
10698	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	75	71
10699	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	92	38
10700	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	132	55
10701	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	54
10702	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	66	73
10703	S79410	Mus musculus	nuclear localization signal binding protein	124	44
10704	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	113	78
10705	S79410	Mus musculus	nuclear localization signal binding protein	119	50
10706	AK025116	Homo sapiens	unnamed protein product	160	84
10707	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10708	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10709	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	230	76
10710	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	96	45
10711	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	174	70
10712	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	127	50
10713	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	148	45
10714	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	151	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10715	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	157	67
10716	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	109	68
10717	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	151	52
10718	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	84	80
10719	M19973	Rattus norvegicus	cytochrome PB24	104	45
10720	AL390114	Leishmania major	probable (hhv-6) uI 102, variant a DNA, complete virion genome	103	72
10721	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	161	52
10722	L27428	Homo sapiens	reverse transcriptase	159	42
10723	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	127	75
10724	Y00311	Homo sapiens	Human secreted protein encoded by gene 54.	84	50
10725	AF090895	Homo sapiens	PRO0117	170	71
10726	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	105	42
10727	K03205	Homo sapiens	salivary proline-rich protein precursor	123	38
10728	U93563	Homo sapiens	putative p150	162	64
10729	X14576	Murine leukemia virus	gag fusion protein	172	41
10730	AF090895	Homo sapiens	PRO0117	151	60
10731	AF119851	Homo sapiens	PRO1722	127	54
10732	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	152	61
10733	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	156	76
10734	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	135	73
10735	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	151	65
10736	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	141	75
10737	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	74
10738	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	124	69
10739	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	91	60
10740	AF130051	Homo sapiens	PRO0898	90	63
10741	AF090895	Homo sapiens	PRO0117	129	55
10742	AF119900	Homo sapiens	PRO2822	164	85
10743	AJ005560	Mus musculus	SPR2B protein	88	35
10744	Z79996	Homo sapiens	cB33F2.1 (PUTATIVE novel protein similar to C-terminal parts of APOL (apolipoprotein L) and TNF-inducible protein CG12-1)	185	100
10745	G03140	Homo sapiens	Human secreted protein, SEQ ID NO: 7221.	94	88
10746	X82208	Homo sapiens	beta-centractin	134	96
10747	D49744	Mus musculus	farnesyltransferase alpha subunit	228	60
10748	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	127	50
10749	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	153	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4523.		
10750	AF130089	Homo sapiens	PRO2550	147	62
10751	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	108	71
10752	D17652	Homo sapiens	HBp15/L22	416	72
10753	AB002389	Homo sapiens	KIAA0391	486	86
10754	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	238	73
10755	S79410	Mus musculus	nuclear localization signal binding protein	103	57
10756	AF130089	Homo sapiens	PRO2550	104	72
10757	X75421	Hypocrea jecorina	actin	197	66
10758	AF298594	Nicotiana glauca	arabinogalactan protein	107	30
10759	U94832	Homo sapiens	KSRP	95	40
10760	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	179	82
10761	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	271	80
10762	Z81528	Caenorhabditis elegans	predicted using GeneFinder—contains similarity to Pfam domain: PF00939 (Sodium:sulfate symporter transmembrane region), Score=2.8, E-value=1.2, N=1; PF01757 (Domain of unknown function), Score=556.0, E-value=8.1e-164, N=1	103	27
10763	V00662	Homo sapiens	ATPase 6	593	83
10764	A06977	Homo sapiens	albumin	610	81
10765	X67863	Mus musculus	T2	109	46
10766	AF137030	Homo sapiens	transmembrane protein 2	620	96
10767	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	101	66
10768	X15324	Homo sapiens	angiotensinogen	529	89
10769	M64983	Homo sapiens	fibrinogen beta chain	604	87
10770	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	381	83
10771	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	133	73
10772	M64110	Homo sapiens	caldesmon	346	94
10773	AB014566	Homo sapiens	KIAA0666 protein	145	78
10774	AL138810	Homo sapiens	dJ179L10.2 (Similar to CGI-29 protein)	216	90
10775	AJ223953	Homo sapiens	hPITG	353	82
10776	U92288	Human herpesvirus 6	HN1	113	39
10777	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	143	78
10778	X12796	Bos taurus	HMG1 protein (AA 1 - 215)	435	96
10779	U86782	Homo sapiens	26S proteasome-associated pad1 homolog	477	89
10780	M60047	Homo sapiens	heparin binding protein	514	81
10781	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	99	48
10782	AF130079	Homo sapiens	PRO2852	175	48
10783	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	115	64
10784	M11147	Homo sapiens	ferritin light chain	439	83
10785	AF090931	Homo sapiens	PRO0483	145	55
10786	AF072441	Homo sapiens	calcineurin binding protein cabin 1	498	90
10787	AF116715	Homo sapiens	PRO2829	127	88

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10788	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	631	91
10789	AC005253	Homo sapiens	R26445_1	403	84
10790	M15386	Homo sapiens	gamma-globin	617	82
10791	Y95005	Homo sapiens	Human secreted protein vc57_1, SEQ ID NO:50.	716	95
10792	G01285	Homo sapiens	Human secreted protein, SEQ ID NO: 5366.	165	52
10793	X67863	Mus musculus	T2	128	50
10794	Y82326	Homo sapiens	Human arginase 1 SEQ ID NO:17.	507	80
10795	Y00755	Homo sapiens	extracellular matrix protein BM-40 (AA 1 - 303)	559	87
10796	AF119851	Homo sapiens	PRO1722	117	71
10797	AF090930	Homo sapiens	PRO0478	146	63
10798	V00488	Homo sapiens	alpha globin	509	84
10799	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	131	42
10800	X83618	Homo sapiens	hydroxymethylglutaryl-CoA synthase	422	78
10801	AF132952	Homo sapiens	CGI-18 protein	341	88
10802	M17375	Gallus gallus	type XII collagen	88	42
10803	K02401	Homo sapiens	chorionic somatomammotropin	436	85
10804	K02401	Homo sapiens	chorionic somatomammotropin	410	86
10805	U61232	Homo sapiens	cofactor E	359	77
10806	D86438	Homo sapiens	Iba1 (ionized calcium binding adapter molecule 1)	406	77
10807	AF118082	Homo sapiens	PRO1902	105	38
10808	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	148	60
10809	AF090942	Homo sapiens	PRO0657	163	52
10810	U63332	Homo sapiens	super cysteine rich protein; SCRP	116	86
10811	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	104	45
10812	X61296	Rattus norvegicus	open reading frame 2	156	41
10813	U82303	Homo sapiens	unknown	103	64
10814	G01478	Homo sapiens	Human secreted protein, SEQ ID NO: 5559.	75	77
10815	U52077	Homo sapiens	mariner transposase	131	85
10816	D38112	Homo sapiens	ATPase subunit 6	251	74
10817	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	103	80
10818	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	102	52
10819	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	94	66
10820	Y21811	Homo sapiens	CPF polypeptide 36PRO.	200	62
10821	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	161	60
10822	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	70
10823	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	337	63
10824	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	122	61
10825	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	122	68
10826	J03634	Homo sapiens	erythroid differentiation protein precursor	222	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10827	D38112	Homo sapiens	NADH dehydrogenase subunit 5	452	78
10828	V00488	Homo sapiens	alpha globin	132	86
10829	Y01138	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	131	70
10830	AF090942	Homo sapiens	PRO0657	122	43
10831	AF090931	Homo sapiens	PRO0483	141	72
10832	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	138	63
10833	G03806	Homo sapiens	Human secreted protein, SEQ ID NO: 7887.	88	57
10834	AF118082	Homo sapiens	PRO1902	109	62
10835	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	135	44
10836	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	152	86
10837	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	143	47
10838	U52077	Homo sapiens	mariner transposase	259	67
10839	M10546	Homo sapiens	cytochrome oxidase I	341	83
10840	Y44361	Homo sapiens	Human cell cycle regulation protein-2.	144	60
10841	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	96	56
10842	D38112	Homo sapiens	cytochrome c oxidase subunit 3	565	80
10843	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	100
10844	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	157	81
10845	AF014889	Homo sapiens	NADH dehydrogenase subunit 2	416	85
10846	AF194537	Homo sapiens	NAG13	177	70
10847	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	108	40
10848	M15530	Homo sapiens	B-cell growth factor	92	67
10849	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	98	52
10850	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	121	76
10851	AF116712	Homo sapiens	PRO2738	84	57
10852	V00662	Homo sapiens	ATPase 6	278	84
10853	U01849	Trypanosoma brucei	ORF1	93	37
10854	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	93	61
10855	AF130089	Homo sapiens	PRO2550	126	72
10856	AF130079	Homo sapiens	PRO2852	154	75
10857	AK025116	Homo sapiens	unnamed protein product	113	70
10858	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	114	71
10859	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	97	56
10860	M36647	Homo sapiens	mitochondrial hinge protein precursor	207	78
10861	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	83	50
10862	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	126	46
10863	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	148	63
10864	B01372	Homo sapiens	Neuron-associated protein.	106	38
10865	U38964	Homo sapiens	hPMSR2	152	68
10866	AF119855	Homo sapiens	PRO1847	142	67

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10867	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	99	75
10868	U79260	Homo sapiens	unknown	94	47
10869	R07037	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	151	52
10870	AJ010025	Homo sapiens	unr-interacting protein	100	64
10871	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	110	44
10872	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	136	71
10873	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	126	61
10874	AF130089	Homo sapiens	PRO2550	115	88
10875	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	114	59
10876	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	83	48
10877	AF118086	Homo sapiens	PRO1992	145	82
10878	AF116712	Homo sapiens	PRO2738	110	55
10879	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	123	77
10880	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	111	61
10881	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	106	51
10882	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	107	67
10883	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	101	65
10884	U79260	Homo sapiens	unknown	111	56
10885	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	153	60
10886	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	107	57
10887	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	148	80
10888	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	142	58
10889	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	156	67
10890	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	105	52
10891	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	187	65
10892	A67510	Mus musculus	MUS MUSCULUS GENOMIC DNA CONTAINING N ALLELE OF FV1 GENE.	120	37
10893	AJ223410	Homo sapiens	EBI1-ligand chemokine	174	77
10894	D38112	Homo sapiens	cytochrome c oxidase subunit I	475	83
10895	V00662	Homo sapiens	ATPase 6	316	95
10896	V00662	Homo sapiens	ATPase 6	427	82
10897	U09500	Homo sapiens	cytochrome b	403	92
10898	U93564	Homo sapiens	p40	215	91
10899	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	69	77
10900	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	159	60
10901	AC003058	Arabidopsis thaliana	unknown protein	93	43

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10902	M10546	Homo sapiens	cytochrome oxidase I	302	66
10903	G00447	Homo sapiens	Human secreted protein, SEQ ID NO: 4528.	102	58
10904	AK024455	Homo sapiens	FLJ00047 protein	118	74
10905	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	108	64
10906	AF090942	Homo sapiens	PRO0657	149	74
10907	J01415	Homo sapiens	cytochrome oxidase subunit 3	167	91
10908	D38112	Homo sapiens	ATPase subunit 6	355	68
10909	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	145	72
10910	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	72
10911	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	144	53
10912	V00662	Homo sapiens	ATPase 6	289	69
10913	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	93	51
10914	V00662	Homo sapiens	cytochrome oxidase III	509	86
10915	J03071	Homo sapiens	chorionic somatomammotropin CS-2	459	80
10916	Z28029	Saccharomyces cerevisiae	ORF YKL030w	96	32
10917	G03102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	94	56
10918	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	114	36
10919	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	117	88
10920	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	103	39
10921	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	99	95
10922	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	75	63
10923	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	125	85
10924	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	140	73
10925	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	77	38
10926	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	111	58
10927	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	139	75
10928	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	78
10929	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	77	57
10930	K02576	Homo sapiens	salivary proline-rich protein 1	95	53
10931	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	83	54
10932	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	262	84
10933	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	113	72
10934	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	120	62
10935	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	69

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10936	J02963	Homo sapiens	platelet glycoprotein IIb precursor	120	56
10937	AB028893	Homo sapiens	ribosomal protein S11	279	53
10939	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	127	55
10940	AF119900	Homo sapiens	PRO2822	154	53
10941	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	127	62
10942	K02576	Homo sapiens	salivary proline-rich protein I	109	41
10943	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	61
10944	AF116715	Homo sapiens	PRO2829	119	69
10945	M10546	Homo sapiens	cytochrome oxidase I	303	95
10946	L27428	Homo sapiens	reverse transcriptase	112	51
10947	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	90
10948	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	121	83
10949	AF116715	Homo sapiens	PRO2829	134	67
10950	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	139	83
10952	AF130079	Homo sapiens	PRO2852	119	79
10953	Z38128	Mus musculus	histone H1	126	35
10954	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	135	53
10955	L22029	Glycine max	hydroxyproline-rich glycoprotein	126	37
10956	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	81	69
10957	AF118082	Homo sapiens	PRO1902	90	51
10958	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	116	53
10959	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	82	51
10960	U79260	Homo sapiens	unknown	97	52
10961	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	194	66
10962	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	124	48
10963	G03084	Homo sapiens	Human secreted protein, SEQ ID NO: 7165.	66	73
10964	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	87
10965	Z28029	Saccharomyces cerevisiae	ORF YKL030w	99	70
10966	V00672	Pan troglodytes	reading frame protein 5	107	70
10967	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	138	58
10968	K02401	Homo sapiens	chorionic somatomammotropin	478	77
10969	D38112	Homo sapiens	cytochrome c oxidase subunit 3	642	86
10970	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	156	57
10971	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	126	56
10972	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	103	51
10973	K02401	Homo sapiens	chorionic somatomammotropin	491	82
10974	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	93
10975	D38112	Homo sapiens	NADH dehydrogenase subunit 4	236	85
10976	Y02785	Homo sapiens	Human secreted protein encoded by	108	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 51 clone HUKEX85.		
10977	J03071	Homo sapiens	chorionic somatomammotropin CS-2	435	73
10978	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	119	74
10979	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	137	73
10980	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	133	63
10981	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	90	65
10982	X92485	Plasmodium vivax	pval	119	47
10983	Y15913	Homo sapiens	COL1A1 and PDGFB fusion transcript	64	47
10984	D38112	Homo sapiens	cytochrome c oxidase subunit 1	463	77
10985	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	309	65
10986	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	145	87
10987	AF130089	Homo sapiens	PRO2550	88	31
10988	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	65
10989	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	137	75
10990	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	76
10991	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	118	72
10992	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	69
10993	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	120	92
10994	AJ277092	Oryctolagus cuniculus	translationally controlled tumor protein 3	172	49
10995	AF052831	Trypanosoma cruzi	unknown	92	37
10996	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	119	53
10997	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	123	43
10998	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	165	52
10999	S52010	Mus sp.	orf1 5' of EpoR	93	39
11000	AF130079	Homo sapiens	PRO2852	131	81
11001	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	111	75
11002	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	132	83
11003	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	151	60
11004	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	159	58
11005	K02401	Homo sapiens	chorionic somatomammotropin	579	89
11006	K02401	Homo sapiens	chorionic somatomammotropin	464	87
11007	M15894	Homo sapiens	chorionic somatomammotropin precursor	370	74
11008	K02401	Homo sapiens	chorionic somatomammotropin	467	88
11009	K02401	Homo sapiens	chorionic somatomammotropin	537	91
11010	K02401	Homo sapiens	chorionic somatomammotropin	475	87
11011	K02401	Homo sapiens	chorionic somatomammotropin	460	88

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11012	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	101	61
11013	AF266166	Gillichthys mirabilis	ribosomal protein S13	223	54
11014	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	176	61
11015	AF116715	Homo sapiens	PRO2829	121	69
11016	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	92	75
11017	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	113	78
11018	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	114	40
11019	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	48
11020	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	151	51
11021	X14963	Homo sapiens	collagen-like protein (447 AA)	107	47
11022	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	72
11023	AF116715	Homo sapiens	PRO2829	140	75
11024	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	125	70
11025	AP000001	Pyrococcus horikoshii	58aa long hypothetical protein	99	52
11026	D38112	Homo sapiens	cytochrome c oxidase subunit 3	601	81
11027	D38112	Homo sapiens	cytochrome c oxidase subunit 3	434	74
11028	Z97333	Homo sapiens	RHCE protein	149	51
11029	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	113	48
11030	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	120	77
11031	U61234	Homo sapiens	cofactor C	226	63
11032	M10546	Homo sapiens	cytochrome oxidase I	116	88
11033	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	584	93
11034	L10910	Homo sapiens	splicing factor	108	58
11035	M26361	Mus musculus	LINE/Ig H-chain fusion protein	140	48
11036	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	79
11037	AK024455	Homo sapiens	FLJ00047 protein	122	48
11038	AF126163	Homo sapiens	HHLA3 protein	96	68
11039	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	144	79
11040	AK024455	Homo sapiens	FLJ00047 protein	151	62
11041	L06498	Homo sapiens	ribosomal protein S20	321	73
11042	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	84
11043	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	125	68
11044	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	208	91
11045	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	79	62
11046	D38112	Homo sapiens	ATPase subunit 6	297	90
11047	D38112	Homo sapiens	cytochrome c oxidase subunit 3	416	73
11048	G00491	Homo sapiens	Human secreted protein, SEQ ID NO: 4572.	73	80
11049	AF090944	Homo sapiens	PRO0663	96	70
11050	AF130089	Homo sapiens	PRO2550	152	71
11051	Y02671	Homo sapiens	Human secreted protein encoded by	108	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 22 clone HMSJW18.		
11052	W89031	Homo sapiens	Polypeptide fragment encoded by gene 167.	254	95
11053	AF109907	Homo sapiens	S164	136	45
11054	AF217536	Homo sapiens	truncated mevalonate kinase	117	58
11055	X72004	Halichoerus grypus	ATP synthase subunit 6	160	78
11056	V00662	Homo sapiens	ATPase 6	300	71
11057	AF228021	Bos taurus	cyclophilin I	209	73
11058	L27428	Homo sapiens	reverse transcriptase	303	65
11059	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	464	80
11060	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	145	68
11061	D38112	Homo sapiens	cytochrome c oxidase subunit 3	301	85
11062	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	119	64
11063	Y08061	Homo sapiens	Human c-myb protein fragment.	128	76
11064	U50188	Cavia porcellus	CGRP-receptor component protein	152	88
11065	G03107	Homo sapiens	Human secreted protein, SEQ ID NO: 7188.	104	44
11066	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	112	64
11067	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	71
11068	AE003499	Drosophila melanogaster	CG12706 gene product	145	43
11069	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	160	65
11070	D38112	Homo sapiens	cytochrome c oxidase subunit 1	416	67
11071	D38112	Homo sapiens	cytochrome c oxidase subunit 3	220	86
11072	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	144	63
11073	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	115	60
11074	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	117	65
11075	D38112	Homo sapiens	cytochrome c oxidase subunit 1	589	87
11076	D38112	Homo sapiens	cytochrome c oxidase subunit 1	588	83
11077	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	106	86
11078	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	90	50
11079	AF132200	Homo sapiens	PRO1751	97	89
11080	AF116661	Homo sapiens	PRO1438	109	51
11081	AK024455	Homo sapiens	FLJ00047 protein	93	48
11082	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	84	73
11083	J02963	Homo sapiens	platelet glycoprotein IIb precursor	108	80
11084	AF068294	Homo sapiens	HDcMB45P	229	59
11085	M10546	Homo sapiens	cytochrome oxidase I	137	73
11086	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	49
11087	L26953	Homo sapiens	chromosomal protein	122	75
11088	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	103	46
11089	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	112	56
11090	AF130089	Homo sapiens	PRO2550	172	60
11091	K02576	Homo sapiens	salivary proline-rich protein 1	107	35

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11092	AF090930	Homo sapiens	PRO0478	146	75
11093	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	163	82
11094	V00662	Homo sapiens	ATPase 6	130	87
11095	B01372	Homo sapiens	Neuron-associated protein.	122	82
11096	D38112	Homo sapiens	ATPase subunit 6	152	62
11097	U18339	Varicella virus	D4L	96	60
11098	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	60
11099	AF130089	Homo sapiens	PRO2550	128	75
11100	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	218	62
11101	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	232	79
11102	AF090930	Homo sapiens	PRO0478	154	73
11103	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	133	65
11104	K03036	Mus musculus	alpha-1 type I procollagen	105	43
11105	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	142	59
11106	L13129	Mus musculus	synexin	119	35
11107	AF280111	Homo sapiens	cytochrome P450 subfamily IIIA polypeptide 43	122	52
11108	J00314	Homo sapiens	beta-tubulin	606	94
11109	X05196	Homo sapiens	aldolase C	412	89
11110	D00570	Mus musculus	open reading frame (196 AA)	127	85
11111	D50532	Homo sapiens	macrophage lectin 2	165	65
11112	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	125	74
11113	M15530	Homo sapiens	B-cell growth factor	163	82
11114	V00662	Homo sapiens	ATPase 6	217	91
11115	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	100
11116	K02576	Homo sapiens	salivary proline-rich protein 1	119	36
11117	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	132	59
11118	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	103	67
11119	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	94	42
11120	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	127	75
11121	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	104	64
11122	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	90	59
11123	AF161356	Homo sapiens	HSPC093	119	64
11124	J02963	Homo sapiens	platelet glycoprotein IIb precursor	102	70
11125	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	149	60
11126	AF068294	Homo sapiens	HDCMB45P	272	59
11127	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	120	79
11128	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	101	78
11129	AF130089	Homo sapiens	PRO2550	124	80
11130	A1359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	109	51
11131	U40265	Trypanosoma cruzi	ATPase subunit 6	102	31

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11132	X01677	Homo sapiens	glyceraldehyde-3-phosphate dehydrogenase	555	88
11133	K02576	Homo sapiens	salivary proline-rich protein 1	108	37
11134	M81757	Homo sapiens	S19 ribosomal protein	232	76
11135	U93565	Homo sapiens	putative p150	173	51
11136	AF061944	Homo sapiens	kinase deficient protein KDP	369	100
11137	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	145	61
11138	AB030255	Homo sapiens	serine/threonine phosphatase 1 gamma	404	83
11139	AL049610	Homo sapiens	dJ1055C14.2 (KIAA0026 (transcription factor-like protein MRGX))	248	77
11140	Y36421	Homo sapiens	Fragment of human secreted protein encoded by gene 8.	81	53
11141	M13692	Homo sapiens	alpha-1 acid glycoprotein precursor	112	41
11142	M16961	Homo sapiens	alpha-2-HS-glycoprotein	543	89
11143	D38112	Homo sapiens	cytochrome c oxidase subunit 3	605	88
11144	AF090944	Homo sapiens	PRO0663	137	67
11145	X92485	Plasmodium vivax	pval	102	57
11146	AF130089	Homo sapiens	PRO2550	113	58
11147	U63542	Homo sapiens	FAP protein	154	57
11148	W03988	Homo sapiens	SH2 domain from human SH-PTP2 (amino acids 1-106).	162	73
11149	AF116695	Homo sapiens	PRO2221	173	44
11150	M15530	Homo sapiens	B-cell growth factor	105	45
11151	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	160	64
11152	M15530	Homo sapiens	B-cell growth factor	124	75
11153	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	117	67
11154	AF118082	Homo sapiens	PRO1902	79	52
11155	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	123	72
11156	Y27893	Homo sapiens	Human secreted protein encoded by gene No. 116.	266	96
11157	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	148	84
11158	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	72
11159	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	105	58
11160	X60376	Brassica napus	proline-rich protein	111	39
11161	S79410	Mus musculus	nuclear localization signal binding protein	111	37
11162	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	53
11163	AF090930	Homo sapiens	PRO0478	146	73
11164	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	90	60
11165	AF242772	Homo sapiens	mesenchymal stem cell protein DSCD28	141	51
11166	X82629	Homo sapiens	Mox-2	307	83
11167	D38112	Homo sapiens	NADH dehydrogenase subunit 4	168	91
11168	X55684	Lycopersicon esculentum	extensin (class I)	71	66
11169	AC079041	Arabidopsis thaliana	hypothetical protein	98	45
11170	AF090930	Homo sapiens	PRO0478	156	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11171	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	99	70
11172	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	124	54
11173	D38112	Homo sapiens	cytochrome c oxidase subunit 1	587	82
11174	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	127	66
11175	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	157	68
11176	AF090931	Homo sapiens	PRO0483	146	87
11177	M15530	Homo sapiens	B-cell growth factor	153	75
11178	AF090930	Homo sapiens	PRO0478	129	52
11179	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	98	77
11180	AF194537	Homo sapiens	NAG13	163	48
11181	AF068294	Homo sapiens	HDCMB45P	146	53
11182	AF090931	Homo sapiens	PRO0483	153	78
11183	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	141	65
11184	Y13336	Homo sapiens	Amino acid sequence of protein PR...332.	452	92
11185	AF090930	Homo sapiens	PRO0478	132	51
11186	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	178	79
11187	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	237	70
11188	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	117	83
11189	AL080206	Homo sapiens	hypothetical protein	103	71
11190	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	77
11191	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	112	65
11192	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	127	54
11193	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	150	65
11194	M92046	Trypanosoma cruzi	surface antigen	160	26
11195	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	126	72
11196	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	98	75
11197	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	117	50
11198	D88548	Homo sapiens	24-kDa subunit of complex I	160	47
11199	AF090852	Antilocapra americana	prion protein	115	38
11200	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	136	62
11201	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	139	75
11202	U93563	Homo sapiens	putative p150	239	43
11203	U93570	Homo sapiens	putative p150	173	45
11204	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	166	68
11205	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	68
11206	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	87	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11207	W48808	Homo sapiens	Homo sapiens clone CG109_1 protein.	123	89
11208	D38112	Homo sapiens	cytochrome c oxidase subunit 3	619	87
11209	W48808	Homo sapiens	Homo sapiens clone CG109_1 protein.	125	89
11210	D38112	Homo sapiens	cytochrome c oxidase subunit 3	521	83
11211	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	90	76
11212	D38112	Homo sapiens	cytochrome c oxidase subunit 1	547	81
11213	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	92	74
11214	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	126	63
11215	AF162149	Mycoplasma bovis	variable surface lipoprotein	118	34
11216	AF130089	Homo sapiens	PRO2550	147	96
11217	AF090931	Homo sapiens	PRO0483	112	77
11218	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	70
11219	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	111	55
11220	AF130051	Homo sapiens	PRO0898	122	63
11221	AF130079	Homo sapiens	PRO2852	171	64
11222	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	146	55
11223	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	130	71
11224	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	69
11225	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	141	85
11226	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	103	90
11227	M15530	Homo sapiens	B-cell growth factor	122	55
11228	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	121	67
11229	M15317	Plasmodium falciparum	histidine-rich protein	116	43
11230	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	131	78
11231	W19932	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS55.	74	76
11232	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	134	67
11233	AK023045	Homo sapiens	unnamed protein product	100	69
11234	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	82
11235	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	125	65
11236	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	53
11237	AF029403	Homo sapiens	oxysterol 7alpha-hydroxylase	144	72
11238	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	112	44
11239	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	96
11240	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	127	43
11241	L36529	Homo sapiens	protein p84	343	90
11242	M15530	Homo sapiens	B-cell growth factor	122	55
11243	Y01158	Homo sapiens	Secreted protein encoded by gene 18	130	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HCACJ81.		
11244	U92698	Rattus norvegicus	ribosomal protein S2	229	74
11245	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	116	41
11246	W75859	Homo sapiens	Human secretory protein of clone DM340-1.	123	37
11247	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	132	73
11248	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	93	56
11249	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	132	56
11250	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	72
11251	S79410	Mus musculus	nuclear localization signal binding protein	115	46
11252	AK021455	Homo sapiens	unnamed protein product	146	81
11253	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	88.	56
11254	S80916	Homo sapiens	parotid "o" protein, Po=salivary proline-rich protein (exon 3)	113	43
11255	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	136	45
11256	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	107	67
11257	AF194537	Homo sapiens	NAG13	153	76
11258	M15530	Homo sapiens	B-cell growth factor	130	70
11259	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	131	72
11260	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	104	59
11261	G02922	Homo sapiens	Human secreted protein, SEQ ID NO: 7003.	316	92
11262	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	111	81
11263	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	142	71
11264	AF130089	Homo sapiens	PRO2550	111	66
11265	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	118	71
11266	M15530	Homo sapiens	B-cell growth factor	158	76
11267	AF130079	Homo sapiens	PRO2852	124	68
11268	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	104	50
11269	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	57
11270	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	107	63
11271	AF118082	Homo sapiens	PRO1902	87	47
11272	M10546	Homo sapiens	cytochrome oxidase I	305	74
11273	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	108	53
11274	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	235	81
11275	U93570	Homo sapiens	putative p150	182	54
11276	X03145	Homo sapiens	pot. ORF V	144	60
11277	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	103	57
11278	AL035681	Homo sapiens	dJ756G23.1 (novel Leucine Rich	269	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			Protein)		
11279	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	103	61
11280	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	115	70
11281	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	87	71
11282	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	162	81
11283	AF116715	Homo sapiens	PRO2829	141	71
11284	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	111	76
11285	U52077	Homo sapiens	mariner transposase	198	78
11286	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	62
11287	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	103	45
11288	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	63	60
11289	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	123	72
11290	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	120	70
11291	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	106	46
11292	AF116715	Homo sapiens	PRO2829	130	63
11293	AF090930	Homo sapiens	PRO0478	134	60
11294	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	119	65
11295	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	102	50
11296	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	141	49
11297	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	154	72
11298	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO: 75.	126	54
11299	AK025270	Homo sapiens	unnamed protein product	150	54
11300	AF118078	Homo sapiens	PRO1848	121	63
11301	AF090942	Homo sapiens	PRO0657	81	43
11302	AF116715	Homo sapiens	PRO2829	131	60
11303	AF090931	Homo sapiens	PRO0483	121	71
11304	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	108	82
11305	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	122	59
11306	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	93	89
11307	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	108	65
11308	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	114	51
11309	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	67	55
11310	J02963	Homo sapiens	platelet glycoprotein IIb precursor	105	71
11311	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	104	73
11312	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	88	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11313	U40265	Trypanosoma cruzi	ATPase subunit 6	94	31
11314	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	157	53
11315	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	113	54
11316	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	165	90
11317	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	149	74
11318	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	144	55
11319	AF161356	Homo sapiens	HSPC093	112	56
11320	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	102	53
11321	AF116661	Homo sapiens	PRO1438	131	74
11322	AK000496	Homo sapiens	unnamed protein product	137	59
11323	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	74	57
11324	U63542	Homo sapiens	FAP protein	151	79
11325	M15530	Homo sapiens	B-cell growth factor	192	45
11326	AF116715	Homo sapiens	PRO2829	164	78
11327	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	127	62
11328	AF090895	Homo sapiens	PRO0117	116	69
11329	AF090942	Homo sapiens	PRO0657	132	62
11330	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	190	72
11331	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	112	49
11332	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	119	38
11333	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	131	52
11334	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	145	53
11335	X92485	Plasmodium vivax	pval	105	38
11336	M15530	Homo sapiens	B-cell growth factor	148	73
11337	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	100
11338	AF118086	Homo sapiens	PRO1992	123	80
11339	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	79	66
11340	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	162	73
11341	AF130079	Homo sapiens	PRO2852	145	80
11342	M19419	Mus musculus	proline-rich salivary protein	104	44
11343	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	123	62
11344	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	120	91
11345	U94832	Homo sapiens	KSRP	122	51
11346	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	139	56
11347	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	188	87
11348	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	173	59
11349	W48351	Homo sapiens	Human breast cancer related protein	111	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
11350	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	149	62
11351	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	267	68
11352	AF161356	Homo sapiens	HSPC093	134	51
11353	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	139	47
11354	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	115	64
11355	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	126	67
11356	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	123	59
11357	AF130089	Homo sapiens	PRO2550	114	62
11358	AK000496	Homo sapiens	unnamed protein product	126	41
11359	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	173	81
11360	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	64
11361	AF130056	Homo sapiens	PRO1367	74	57
11362	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	116	63
11363	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	104	91
11364	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	137	53
11365	Z30643	Homo sapiens	chloride channel (putative)	409	98
11366	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	107	68
11367	AF068294	Homo sapiens	HDCMB45P	281	57
11368	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	110	71
11369	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	136	89
11370	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	129	79
11371	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	137	57
11372	U18339	Variola virus	D4L	95	61
11373	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	100	52
11374	M15530	Homo sapiens	B-cell growth factor	135	61
11375	X92485	Plasmodium vivax	pva1	111	50
11376	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	177	71
11377	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	111	68
11378	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	96	53
11379	G02567	Homo sapiens	Human secreted protein, SEQ ID NO: 6648.	83	54
11380	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	85
11381	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	156	64
11382	R96800	Homo sapiens	Human histiocyte-secreted factor HSF	121	79
11383	R13556	Homo sapiens	Protein encoded downstream of hbc_M oncoprotein.	104	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11384	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	86	53
11385	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	40
11386	AF068294	Homo sapiens	HDCMB45P	158	48
11387	B08976	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:133.	136	46
11388	AF090931	Homo sapiens	PRO0483	123	74
11389	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	156	75
11390	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	102	48
11391	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	117	54
11392	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	134	43
11393	S79410	Mus musculus	nuclear localization signal binding protein	111	46
11394	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	49
11395	AF090930	Homo sapiens	PRO0478	148	70
11396	AF210651	Homo sapiens	NAG18	100	62
11397	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	121	56
11398	AF063243	Bos taurus	ribosomal protein L30	165	77
11399	AF162149	Mycoplasma bovis	variable surface lipoprotein	104	37
11400	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	175	71
11401	D38112	Homo sapiens	NADH dehydrogenase subunit 4	341	92
11402	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	137	90
11403	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	115	70
11404	M10126	Leishmania tarentolae	NH2 terminus uncertain	101	41
11405	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	126	69
11406	X82385	Homo sapiens	RNA polymerase II subunit	296	100
11407	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	68
11408	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	44
11409	J02963	Homo sapiens	platelet glycoprotein IIb precursor	118	77
11410	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	169	77
11411	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	169	82
11412	AK025116	Homo sapiens	unnamed protein product	133	44
11413	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	113	63
11414	AK024455	Homo sapiens	FLJ00047 protein	127	65
11415	AK024455	Homo sapiens	FLJ00047 protein	87	63
11416	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	94	57
11417	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	123	58
11418	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	148	69

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11419	S79410	Mus musculus	nuclear localization signal binding protein	113	53
11420	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	166	68
11421	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	124	51
11422	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	113	70
11423	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	88	62
11424	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	136	72
11425	AK002154	Homo sapiens	unnamed protein product	292	75
11426	Y02887	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	98	75
11427	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	143	64
11428	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	81
11429	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	130	81
11430	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	172	61
11431	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	112	74
11432	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	52
11433	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	128	58
11434	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	147	63
11435	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	139	83
11436	X63220	Bos taurus	NADH dehydrogenase	154	57
11437	AF090895	Homo sapiens	PRO0117	122	59
11438	J04655	Ascaris suum	collagen	90	46
11439	AF090942	Homo sapiens	PRO0657	166	52
11440	AK024455	Homo sapiens	FLJ00047 protein	100	55
11441	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	116	49
11442	M15530	Homo sapiens	B-cell growth factor	105	75
11443	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	133	64
11444	Y19730	Homo sapiens	SEQ ID NO 448 from WO9922243.	115	67
11445	AF090895	Homo sapiens	PRO0117	79	61
11446	AF118086	Homo sapiens	PRO1992	109	63
11447	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	160	80
11448	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	97	75
11450	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	136	72
11451	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	89	55
11452	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	144	71
11453	AF090931	Homo sapiens	PRO0483	140	78
11454	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	129	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11455	G00383	Homo sapiens	Human secreted protein, SEQ ID NO: 4464.	104	63
11456	AF118086	Homo sapiens	PRO1992	151	71
11457	U73168	Homo sapiens	partial CDS, human putative tumor suppressor (U23946)	121	95
11458	S79410	Mus musculus	nuclear localization signal binding protein	96	73
11459	AK000496	Homo sapiens	unnamed protein product	233	63
11460	AK024455	Homo sapiens	FLJ00047 protein	90	73
11461	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	64
11462	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	103	86
11463	K03207	Homo sapiens	salivary proline-rich protein precursor	135	36
11464	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	127	88
11465	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	104	77
11466	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	141	48
11467	AF090942	Homo sapiens	PRO0657	89	58
11468	AC005698	Arabidopsis thaliana	T3P18.6	128	47
11469	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	101	48
11470	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	136	81
11471	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	91	45
11472	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	102	77
11473	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	145	55
11474	AF210651	Homo sapiens	NAG18	117	57
11475	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	117	62
11476	AF116715	Homo sapiens	PRO2829	124	77
11477	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	45
11478	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	85	78
11479	X91940	Homo sapiens	WNT-8B protein	204	97
11480	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	71
11481	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	117	63
11482	X92485	Plasmodium vivax	pval	98	52
11483	AF217518	Homo sapiens	uncharacterized bone marrow protein BM042	895	100
11484	U79260	Homo sapiens	unknown	104	80
11485	L27428	Homo sapiens	reverse transcriptase	169	52
11486	M15530	Homo sapiens	B-cell growth factor	122	67
11487	U49974	Homo sapiens	mariner transposase	156	62
11488	AF090942	Homo sapiens	PRO0657	110	44
11489	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	156	65
11490	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	52
11491	G03133	Homo sapiens	Human secreted protein, SEQ ID NO:	95	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7214		
11492	AF090930	Homo sapiens	PRO0478	145	58
11493	X63726	Phoca vitulina	cytochrome c oxidase subunit I	556	87
11494	AL021897	Mycobacterium tuberculosis	pra	119	56
11495	X98485	Plasmodium vivax	putative	92	35
11496	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	156	73
11497	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	129	72
11498	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	115	66
11499	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	58
11500	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	113	36
11501	AE003568	Drosophila melanogaster	CG12566 gene product	105	32
11502	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	141	78
11503	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	102	51
11504	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	138	60
11505	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	109	85
11506	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	101	59
11507	M81321	Macaca fascicularis	proline-rich protein	128	48
11508	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	110	78
11509	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	98	60
11510	X07882	Homo sapiens	Po protein	118	41
11511	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	133	79
11512	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	68
11513	AF000381	Homo sapiens	non-functional folate binding protein	203	93
11514	X92485	Plasmodium vivax	pval	115	44
11515	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH 8c)	109	51
11516	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	141	78
11517	AF090894	Homo sapiens	PRO0113	108	58
11518	M15530	Homo sapiens	B-cell growth factor	93	72
11519	G03084	Homo sapiens	Human secreted protein, SEQ ID NO: 7165.	66	73
11520	AF117065	Homo sapiens	male-specific lethal-3 homolog 1	200	61
11521	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	335	87
11522	M15530	Homo sapiens	B-cell growth factor	104	74
11523	AF116715	Homo sapiens	PRO2829	122	64
11524	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	145	68
11525	Y02671	Homo sapiens	Human secreted protein encoded by	103	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 22 clone HMSJW18.		
11526	X92485	Plasmodium vivax	pval	111	42
11527	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	101	80
11528	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	134	58
11529	AF090931	Homo sapiens	PRO0483	163	76
11530	AF119900	Homo sapiens	PRO2822	139	44
11531	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	73
11532	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	126	50
11533	S79410	Mus musculus	nuclear localization signal binding protein	107	46
11534	AF090930	Homo sapiens	PRO0478	120	81
11535	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	105	64
11536	X92485	Plasmodium vivax	pval	123	56
11537	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	122	72
11538	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	108	64
11539	AE003834	Drosophila melanogaster	CG8054 gene product	456	84
11540	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	135	53
11541	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	99	70
11542	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	77	63
11543	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	123	73
11544	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	78	58
11545	U79260	Homo sapiens	unknown	128	43
11546	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	122	56
11547	X92485	Plasmodium vivax	pval	116	46
11548	S79410	Mus musculus	nuclear localization signal binding protein	111	55
11549	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	95	75
11550	U67056	Acanthamoeba castellanii	myosin I heavy chain kinase	111	44
11551	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	159	60
11552	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	127	50
11553	Z34975	Homo sapiens	IdiCp	470	86
11554	AF210651	Homo sapiens	NAG18	101	65
11555	X78677	Homo sapiens	ketoheokinase	241	92
11556	G04039	Homo sapiens	Human secreted protein, SEQ ID NO: 8120.	254	72
11557	AB032976	Homo sapiens	KIAA1150 protein	565	75
11558	U93572	Homo sapiens	p40	127	37

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11559	U27488	Pseudorabies virus	glycoprotein gX	88	38
11560	R80095	Homo sapiens	Human superoxide-dismutase-4 polypeptide.	113	63
11561	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	83	65
11562	AF130089	Homo sapiens	PRO2550	111	33
11563	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	146	60
11564	AF090895	Homo sapiens	PRO0117	172	77
11566	V01512	Homo sapiens	c-fos	416	82
11567	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	72	33
11568	X16074	Mus sp.	L-34 protein (AA 1-264)	117	35
11569	Y45381	Homo sapiens	Human secreted protein fragment encoded from gene 28.	131	77
11570	AK025395	Homo sapiens	unnamed protein product	683	98
11571	D78255	Mus musculus	PAP-1	134	80
11572	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	110	70
11573	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	78
11574	J01415	Homo sapiens	cytochrome oxidase subunit 3	141	59
11575	S79410	Mus musculus	nuclear localization signal binding protein	102	58
11576	AC007842	Homo sapiens	BC331191_1	409	86
11577	Z22636	Sinorhizobium meliloti	Thi	103	36
11578	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	83	36
11579	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	115	60
11580	AF162149	Mycoplasma bovis	variable surface lipoprotein	167	44
11581	AF130079	Homo sapiens	PRO2852	117	77
11582	AF229067	Homo sapiens	PADI-H protein	136	75
11583	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	132	72
11584	Z70292	Homo sapiens	chemokine CC-1	386	93
11585	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	107	67
11586	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	134	75
11587	X05006	Homo sapiens	S-protein	237	100
11588	Y21850	Homo sapiens	Human signal peptide-containing protein (SIGP) (clone ID 1880830).	365	77
11589	U43959	Homo sapiens	beta 4 aducan	114	54
11590	AF030162	Homo sapiens	inner mitochondrial membrane translocase Tim23	104	95
11591	X03557	Homo sapiens	56-KDa protein (aa 1-478)	491	74
11592	AF151074	Homo sapiens	HSPC240	151	73
11593	AF116719	Homo sapiens	PRO2987	558	89
11594	AF090942	Homo sapiens	PRO0657	120	41
11595	X55039	Homo sapiens	centromere autoantigen B (CENP-B)	160	32
11596	X98475	Mus musculus	vasodilator-stimulated phosphoprotein	101	43
11597	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	140	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11598	U07151	Homo sapiens	ARL3	113	35
11599	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	123	79
11600	AL050084	Homo sapiens	hypothetical protein	119	100
11601	AF090931	Homo sapiens	PRO0483	124	73
11602	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	132	60
11603	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	156	82
11604	AF224494	Mus musculus	arsenite inducible RNA associated protein	473	79
11605	M60047	Homo sapiens	heparin binding protein	597	95
11606	G00933	Homo sapiens	Human secreted protein, SEQ ID NO: 5014.	721	97
11607	W12091	Homo sapiens	C57S derivative of antigen non-specific human G1F.	573	98
11608	AF229439	Mus musculus	zinc finger protein 289	535	80
11609	M86637	Brugia pahangi	unknown	104	38
11610	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	93	70
11611	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	508	94
11612	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	108	51
11613	AK024372	Homo sapiens	unnamed protein product	105	77
11614	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein sequence SEQ ID NO:42.	310	62
11615	Y48547	Homo sapiens	Human breast tumour-associated protein 8.	641	96
11616	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	108	81
11617	L34081	Homo sapiens	bile acid CoA: Amino acid N-acyltransferase	356	82
11618	G01399	Homo sapiens	Human secreted protein, SEQ ID NO: 5480.	570	98
11619	AF020038	Homo sapiens	NADP-dependent isocitrate dehydrogenase	272	83
11620	AB051901	Homo sapiens	VDUP1	247	98
11621	Y48547	Homo sapiens	Human breast tumour-associated protein 8.	691	92
11622	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	382	71
11623	A06977	Homo sapiens	albumin	562	92
11624	X73460	Homo sapiens	ribosomal protein L3	502	84
11625	AL035398	Homo sapiens	dj796117.1 (PUTATIVE novel protein)	373	98
11626	D50310	Homo sapiens	cyclin I	175	100
11627	AE000950	Archaeoglobus fulgidus	thermosome, subunit alpha (thsA)	131	25
11628	D88315	Mus musculus	tetracycline transporter-like protein	137	81
11629	Y36204	Homo sapiens	Human secreted protein #76.	406	100
11630	AF130089	Homo sapiens	PRO2550	110	63
11631	J02982	Homo sapiens	glycophorin B precursor	95	100
11632	AF116719	Homo sapiens	PRO2987	558	93
11633	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	137	92
11634	U09823	Oryctolagus	elongation factor I alpha	483	85

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			cuniculus		
11635	G01922	Homo sapiens	Human secreted protein, SEQ ID NO: 6003.	157	73
11636	AF116719	Homo sapiens	PRO2987	491	90
11637	D14421	Rattus norvegicus	b isotype of B regulatory subunit of protein phosphatase 2A	208	86
11638	AF116719	Homo sapiens	PRO2987	544	93
11639	AF130079	Homo sapiens	PRO2852	127	81
11640	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	150	59
11641	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	100	66
11642	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	119	71
11643	Y86574	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:491.	64	100
11644	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	82	70
11645	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	109	74
11646	AF130089	Homo sapiens	PRO2550	128	52
11647	AK024455	Homo sapiens	FLJ00047 protein	138	61
11648	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	73	84
11649	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	128	60
11650	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	83	78
11651	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	105	64
11652	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	103	62
11653	AF130089	Homo sapiens	PRO2550	116	69
11654	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	176	54
11655	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	129	63
11656	AF130089	Homo sapiens	PRO2550	135	77
11657	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	146	93
11658	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	123	61
11659	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	117	47
11660	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	92	84
11661	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	70	75
11662	U00029	Saccharomyces cerevisiae	Yhr217cp	101	50
11663	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	107	88
11664	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	110	90
11665	U63542	Homo sapiens	FAP protein	119	69
11666	AF130114	Homo sapiens	PRO2459	78	38
11667	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	106	64
11668	G00397	Homo sapiens	Human secreted protein, SEQ ID NO:	137	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4478.		
11669	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	77	63
11670	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	116	68
11671	AK021618	Homo sapiens	unnamed protein product	97	43
11672	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	108	55
11673	S75997	Rattus sp.	nucleoporin p62 homolog	95	40
11674	AF229163	Homo sapiens	natural resistance-associated macrophage protein 1	104	54
11675	M15530	Homo sapiens	B-cell growth factor	89	81
11676	M92357	Homo sapiens	B94 protein	143	100
11677	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	132	74
11678	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	126	64
11679	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	66
11680	U16359	Rattus norvegicus	nitric oxide synthase	108	85
11681	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	92
11682	M15530	Homo sapiens	B-cell growth factor	127	64
11683	AF090931	Homo sapiens	PRO0483	152	60
11684	AF130087	Homo sapiens	PRO2411	150	68
11685	U18339	Varola virus	D4L	94	70
11686	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	104	80
11687	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	134	68
11688	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	131	70
11689	AF090944	Homo sapiens	PRO0663	129	73
11690	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	111	67
11691	U79260	Homo sapiens	unknown	98	44
11692	W78226	Homo sapiens	Fragment of human secreted protein encoded by gene 1.	361	64
11693	G00962	Homo sapiens	Human secreted protein, SEQ ID NO: 5043.	269	100
11694	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	132	83
11695	Y94526	Homo sapiens	Human lysine-rich statherin protein.	136	82
11696	AF116637	Homo sapiens	PRO1489	232	95
11697	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	108	50
11698	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	120	81
11699	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	150	80
11700	AK024455	Homo sapiens	FLJ00047 protein	148	68
11701	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	131	72
11702	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	105	45
11703	AC005545	Homo sapiens	delta-adaptin, partial CDS	127	38
11704	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	143	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11705	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	67
11706	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	153	67
11707	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	129	88
11708	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	89	69
11709	AB047600	Macaca fascicularis	hypothetical protein	95	63
11710	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	100	76
11711	J02963	Homo sapiens	platelet glycoprotein IIb precursor	112	80
11712	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	117	58
11713	AF008196	Homo sapiens	bax epsilon	140	71
11714	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	113	56
11715	G00397	Homo sapiens	Human secreted protein; SEQ ID NO: 4478.	125	67
11716	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	121	74
11717	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	125	51
11718	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	96	81
11719	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	106	85
11720	AJ243883	Periplaneta americana	putative transcription factor	118	57
11721	AF220264	Homo sapiens	MOST-1	121	74
11722	AF130051	Homo sapiens	PRO0898	169	72
11723	K02401	Homo sapiens	chorionic somatomammotropin	507	95
11724	K02401	Homo sapiens	chorionic somatomammotropin	461	85
11725	U93564	Homo sapiens	p40	340	90
11726	AF130089	Homo sapiens	PRO2550	107	73
11727	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	128	79
11728	J02963	Homo sapiens	platelet glycoprotein IIb precursor	109	90
11729	Y51824	Homo sapiens	Human OSBH protein.	182	89
11730	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	107	80
11731	K02401	Homo sapiens	chorionic somatomammotropin	459	94
11732	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	93	42
11733	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	111	67
11734	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	103	43
11735	S79410	Mus musculus	nuclear localization signal binding protein	98	75
11736	AF090931	Homo sapiens	PRO0483	123	88
11737	K02401	Homo sapiens	chorionic somatomammotropin	340	92
11738	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	73
11739	G02624	Homo sapiens	Human secreted protein, SEQ ID NO: 6705.	131	57
11740	X55695	Lycopersicon esculentum	glycine-rich protein	164	48
11741	AK024455	Homo sapiens	FLJ00047 protein	89	77

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11742	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	415	90
11743	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	105	94
11744	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	116	87
11745	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	131	69
11746	W13831	Homo sapiens	Human cyclin E delta 9 mutant.	140	52
11747	AB001431	Mus musculus	motor domain of KIF14	179	84
11748	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	141	72
11749	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	99	63
11750	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	88	64
11751	AF090931	Homo sapiens	PRO0483	118	68
11752	AF150105	Homo sapiens	small zinc finger-like protein	194	68
11753	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	127	69
11754	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	100	80
11755	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	109	65
11756	K02401	Homo sapiens	chorionic somatomammotropin	427	87
11757	U52077	Homo sapiens	mariner transposase	113	82
11758	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	133	54
11759	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	111	80
11760	AF090944	Homo sapiens	PRO0663	143	76
11761	D38112	Homo sapiens	NADH dehydrogenase subunit 6	529	99
11762	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	171	58
11763	AF132200	Homo sapiens	PRO1751	127	66
11764	AK025116	Homo sapiens	unnamed protein product	141	80
11765	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	75	62
11766	AF090930	Homo sapiens	PRO0478	106	59
11767	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	127	80
11768	AF090931	Homo sapiens	PRO0483	164	60
11769	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	102	81
11770	AF161356	Homo sapiens	HSPC093	131	68
11771	AF130089	Homo sapiens	PRO2550	160	82
11772	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	140	79
11773	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	136	71
11774	AF090942	Homo sapiens	PRO0657	153	78
11775	AJ223410	Homo sapiens	EBI1-ligand chemokine	108	52
11776	K02401	Homo sapiens	chorionic somatomammotropin	395	91
11777	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	107	70
11778	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	99	62
11779	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	84	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11780	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	116	68
11781	AF194537	Homo sapiens	NAG13	201	65
11782	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	139	68
11783	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	149	59
11784	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	112	78
11785	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	68
11786	AF130089	Homo sapiens	PRO2550	108	83
11787	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	124	88
11788	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	103	100
11789	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	146	60
11790	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	73
11791	AL035494	Homo sapiens	dJ635G19.2.3 (novel protein (PUTATIVE PARTIAL isoform 3))	106	56
11792	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	100	66
11793	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	125	61
11794	A20770	synthetic construct	(Asp1-Thr161)-EPI	95	76
11795	S74221	Homo sapiens	IK factor=cytokine down-regulating HLA class II	108	61
11796	K01664	Drosophila melanogaster	Bkm-like protein	96	77
11797	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	111	65
11798	Y75995	Homo sapiens	Human skin cell protein, SEQ ID NO:173.	324	87
11799	J03071	Homo sapiens	chorionic somatomammotropin CS-5	120	75
11800	L00693	Homo sapiens	carcinoembryonic antigen	96	85
11801	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	80	44
11802	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	125	64
11803	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	142	82
11804	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	107	85
11805	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	152	80
11806	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	122	61
11807	U91985	Homo sapiens	DNA fragmentation factor-45	585	92
11808	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	60
11809	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	170	89
11810	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	191	76
11811	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11812	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	156	55
11813	P92219	Homo sapiens (human)	CR1 protein.	121	84
11814	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	107	75
11815	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	74	78
11816	M15530	Homo sapiens	B-cell growth factor	148	68
11817	AF090942	Homo sapiens	PRO0657	139	60
11818	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	117	100
11819	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	73
11820	Z72853	Saccharomyces cerevisiae	ORF YGR069w	94	42
11821	G03710	Homo sapiens	Human secreted protein, SEQ ID NO: 7791.	176	65
11822	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	60
11823	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	104	68
11824	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	99	51
11825	W90172	Homo sapiens	Human heart muscle specific protein.	256	34
11826	AB017007	Homo sapiens	PMS2L16	248	89
11827	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	127	86
11828	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	135	71
11829	AF119851	Homo sapiens	PRO1722	129	60
11830	AF132200	Homo sapiens	PRO1751	120	77
11831	Y08061	Homo sapiens	Human c-myb protein fragment.	133	83
11832	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	128	64
11833	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	152	100
11834	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	73
11835	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	88
11836	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	95
11837	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	411	91
11838	AK000496	Homo sapiens	unnamed protein product	113	78
11839	AF119855	Homo sapiens	PRO1847	84	68
11840	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	88
11841	S79410	Mus musculus	nuclear localization signal binding protein	113	69
11842	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	151	55
11843	AF090942	Homo sapiens	PRO0657	139	65
11844	AF220264	Homo sapiens	MOST-1	88	69
11845	AF184612	Drosophila melanogaster	split ends	95	47
11846	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	136	82

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11847	AB017007	Homo sapiens	PMS2L16	310	100
11848	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	100	79
11849	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	111	61
11850	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	110	72
11851	AF090931	Homo sapiens	PRO0483	164	80
11852	AF116661	Homo sapiens	PRO1438	124	67
11853	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	119	72
11854	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	135	59
11855	U63332	Homo sapiens	super cysteine rich protein; SCRP	100	84
11856	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	120	54
11857	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	68
11858	AK024455	Homo sapiens	FLJ00047 protein	123	69
11859	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	66
11860	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	94	66
11861	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	108	75
11862	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	108	86
11863	AF130050	Homo sapiens	PRO0872	81	58
11864	AF119900	Homo sapiens	PRO2822	152	90
11865	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	78	45
11866	J03071	Homo sapiens	chorionic somatomammotropin CS-2	526	93
11867	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	80
11868	G00591	Homo sapiens	Human secreted protein, SEQ ID NO: 4672.	119	58
11869	Y10830	Homo sapiens	Amino acid sequence of a human secreted protein.	246	100
11870	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	101	59
11871	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	120	59
11872	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	84
11873	D28113	Homo sapiens	MOBP	458	80
11874	D28114	Homo sapiens	MOBP	306	68
11875	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	101	85
11876	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	110	64
11877	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	57
11878	M15530	Homo sapiens	B-cell growth factor	98	62
11879	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	100
11880	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	99	70
11881	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	101	53

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11882	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	219	75
11883	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	131	61
11884	U93563	Homo sapiens	putative p150	139	75
11885	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	154	52
11886	AF090944	Homo sapiens	PRO0663	149	80
11887	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	107	94
11888	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	138	62
11889	L26953	Homo sapiens	chromosomal protein	123	75
11890	U16359	Rattus norvegicus	nitric oxide synthase	105	69
11891	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	129	83
11892	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	126	78
11893	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	82	70
11894	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	149	90
11895	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	118	75
11896	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	167	86
11897	D38112	Homo sapiens	NADH dehydrogenase subunit 6	136	77
11898	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	126	58
11899	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	158	78
11900	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	137	71
11901	G00613	Homo sapiens	Human secreted protein, SEQ ID NO: 4694.	85	62
11902	G02558	Homo sapiens	Human secreted protein, SEQ ID NO: 6639.	242	73
11903	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	127	59
11904	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	182	85
11905	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	135	75
11906	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	128	79
11907	U93574	Homo sapiens	putative p150	169	64
11908	AF090944	Homo sapiens	PRO0663	128	75
11909	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	100	84
11910	AF090930	Homo sapiens	PRO0478	159	76
11911	J03071	Homo sapiens	chorionic somatomammotropin CS-2	496	88
11912	J03071	Homo sapiens	chorionic somatomammotropin CS-2	551	92
11913	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	168	76
11914	K02401	Homo sapiens	chorionic somatomammotropin	450	85
11915	K02401	Homo sapiens	chorionic somatomammotropin	478	87
11916	K02401	Homo sapiens	chorionic somatomammotropin	454	82

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11917	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	121	73
11918	X65121	Mus musculus	alpha1 (X) collagen	112	35
11919	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	115	62
11920	AK024455	Homo sapiens	FLJ00047 protein	102	76
11921	AF150087	Homo sapiens	small zinc finger-like protein	181	52
11922	U55376	Caenorhabditis elegans	F16H11.2 gene product	122	78
11923	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	256	80
11924	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	127	74
11925	AF090944	Homo sapiens	PRO0663	144	75
11926	AJ223475	Escherichia coli	InsA protein	477	100
11927	M15386	Homo sapiens	gamma-globin	616	92
11928	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	105	72
11929	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	122	92
11930	AF090895	Homo sapiens	PRO0117	80	71
11931	AF130089	Homo sapiens	PRO2550	129	68
11932	AK025116	Homo sapiens	unnamed protein product	113	53
11933	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	114	70
11934	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	69	76
11935	AF116695	Homo sapiens	PRO2221	336	70
11936	AF090931	Homo sapiens	PRO0483	133	77
11937	AF130089	Homo sapiens	PRO2550	135	72
11938	L06237	Homo sapiens	microtubule-associated protein 1B	143	36
11939	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	124	72
11940	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	158	76
11941	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	130	53
11942	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	111	65
11943	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	106	59
11944	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	65
11945	D28113	Homo sapiens	MOBP	186	62
11946	D38112	Homo sapiens	NADH dehydrogenase subunit 1	353	76
11947	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	113	72
11948	D38112	Homo sapiens	NADH dehydrogenase subunit 6	139	87
11949	AJ006591	Homo sapiens	cysteine-rich protein	148	76
11950	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	88
11951	AF116695	Homo sapiens	PRO2221	205	57
11952	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	158	75
11953	AF113685	Homo sapiens	PRO0974	107	72
11954	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	107	80
11955	AK026107	Homo sapiens	unnamed protein product	129	84
11956	AF109907	Homo sapiens	S164	140	96

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11957	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	99	100
11958	K02576	Homo sapiens	salivary proline-rich protein 1	124	41
11959	K02401	Homo sapiens	chorionic somatomammotropin	497	90
11960	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	155	69
11961	J02963	Homo sapiens	platelet glycoprotein IIb precursor	126	85
11962	M15530	Homo sapiens	B-cell growth factor	114	86
11963	K02401	Homo sapiens	chorionic somatomammotropin	472	87
11964	AK024455	Homo sapiens	FLJ00047 protein	95	61
11965	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	145	78
11966	L27428	Homo sapiens	reverse transcriptase	144	50
11967	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	187	76
11968	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	124	81
11969	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	112	64
11970	AK024455	Homo sapiens	FLJ00047 protein	120	70
11971	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	103	61
11972	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	106	70
11973	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	70	75
11974	G00491	Homo sapiens	Human secreted protein, SEQ ID NO: 4572.	86	60
11975	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	161	72
11976	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	105	42
11977	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	121	58
11978	AK024372	Homo sapiens	unnamed protein product	104	80
11979	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	137	77
11980	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	96	90
11981	S79410	Mus musculus	nuclear localization signal binding protein	100	56
11982	R59842	Homo sapiens	ApoE4L1 protease.	129	62
11983	K01664	Drosophila melanogaster	Bkm-like protein	132	53
11984	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	105	90
11985	M15530	Homo sapiens	B-cell growth factor	117	43
11986	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	99	65
11987	R59843	Homo sapiens	ApoE4L2 protease.	117	84
11988	L26953	Homo sapiens	chromosomal protein	124	79
11989	U93564	Homo sapiens	p40	523	88
11990	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	82
11991	AF090894	Homo sapiens	PRO0113	126	56
11992	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	129	63
11993	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	144	67
11994	U71363	Homo sapiens	zinc finger protein zfp6	213	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11995	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	82	65
11996	AF130089	Homo sapiens	PRO2550	145	68
11997	R95913	Homo sapiens	Neural thread protein.	114	88
11998	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	122	56
11999	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	147	81
12000	AF090931	Homo sapiens	PRO0483	152	81
12001	AF090931	Homo sapiens	PRO0483	145	81
12002	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	124	64
12003	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	103	78
12004	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	51
12005	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	108	63
12006	L19527	Homo sapiens	ribosomal protein L27	547	93
12007	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	127	82
12008	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	127	82
12009	M55409	Homo sapiens	pancreatic tumor-related protein	257	98
12010	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	127	64
12011	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	291	89
12012	X03717	Homo sapiens	pot. unidentified reading frame	126	43
12013	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	131	80
12014	AB011148	Homo sapiens	KIAA0576 protein	135	84
12015	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	114	87
12016	AK024455	Homo sapiens	FLJ00047 protein	102	70
12017	L27428	Homo sapiens	reverse transcriptase	144	87
12018	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	135	87
12019	D38112	Homo sapiens	NADH dehydrogenase subunit 1	137	93
12020	AK001363	Homo sapiens	unnamed protein product	490	100
12021	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	111	79
12022	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	106	87
12023	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	157	58
12024	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	87	66
12025	R95913	Homo sapiens	Neural thread protein.	157	45
12026	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	138	52
12027	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	116	60
12028	V00488	Homo sapiens	alpha globin	191	100
12029	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	102	87
12030	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	114	79
12031	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	142	86
12032	X01703	Homo sapiens	alpha-tubulin	534	93
12033	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	557	90

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12034	X01703	Homo sapiens	alpha-tubulin	619	94
12035	AF255556	Notothenia corticeps	alpha tubulin	430	85
12036	X53618	Paracentrotus lividus	alpha-tubulin (AA 1-452)	437	87
12037	M62810	Homo sapiens	mitochondrial transcription factor 1	433	95
12038	Y36156	Homo sapiens	Human secreted protein #28.	157	75
12039	X01703	Homo sapiens	alpha-tubulin	604	97
12040	X01703	Homo sapiens	alpha-tubulin	517	90
12041	S70154	Homo sapiens	cytosolic acetoacetyl-coenzyme A thiolase, CT {EC 2.3.1.9}	533	94
12042	X01703	Homo sapiens	alpha-tubulin	472	85
12043	M23613	Homo sapiens	nucleophosmin	428	80
12044	AL031174	Schizosaccharomyces pombe	hypothetical protein	102	52
12045	Y94653	Homo sapiens	Human netrin-like protein (NEL) amino acid sequence.	152	82
12046	AF016507	Homo sapiens	C-terminal binding protein 2	172	100
12047	X05196	Homo sapiens	aldolase C	454	93
12048	X03796	Mus musculus	aldolase C (aa 1-227)	351	74
12049	X05196	Homo sapiens	aldolase C	408	88
12050	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	147	70
12051	S58722	Homo sapiens	X-linked retinopathy protein [C-terminal, clone XEH.8c]	169	55
12052	AF090944	Homo sapiens	PRO0663	119	59
12053	V01577	Homo sapiens	variable region	223	93
12054	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	144	74
12055	AF090931	Homo sapiens	PRO0483	121	74
12056	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	105	76
12057	U18339	Variola virus	D4L	100	52
12058	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	135	62
12059	AB001684	Chlorella vulgaris	ORF41c	81	75
12060	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	128	74
12061	AK024455	Homo sapiens	FLJ00047 protein	70	46
12062	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	130	69
12063	AF090944	Homo sapiens	PRO0663	110	66
12064	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	109	53
12065	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	94	79
12066	AF090931	Homo sapiens	PRO0483	123	70
12067	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	111	75
12068	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	144	77
12069	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	145	76
12070	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	114	81
12071	AF116715	Homo sapiens	PRO2829	138	63
12072	J02963	Homo sapiens	platelet glycoprotein IIb precursor	127	82
12073	U79260	Homo sapiens	unknown	98	73
12074	W88627	Homo sapiens	Secreted protein encoded by gene 94	132	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HPMBQ32.		
12075	J02459	bacteriophage lambda	T (tail component;144)	555	98
12076	AK024455	Homo sapiens	FLJ00047 protein	127	65
12077	X00911	Rattus norvegicus	pot. MSA-precursor	190	73
12078	AF164797	Homo sapiens	ribosomal protein L17 isolog	538	95
12079	A06977	Homo sapiens	albumin	602	87
12080	AF000198	Caenorhabditis elegans	Similar to cuticular collagen	118	38
12081	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	142	86
12082	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhala.	103	50
12083	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	142	86
12084	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	64	54
12085	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	132	53
12086	A14829	Homo sapiens	preproapolipoprotein	619	82
12087	AF119900	Homo sapiens	PRO2822	107	76
12088	U52077	Homo sapiens	mariner transposase	277	74
12089	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	100
12090	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	92
12091	W05278	Homo sapiens	Tumour necrosis factor-related gene product CL6.5.40.	115	42
12092	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	112	81
12093	G03343	Homo sapiens	Human secreted protein, SEQ ID NO: 7424.	114	64
12094	AJ237660	Bacteriophage 21	Ren protein	187	94
12095	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	135	80
12096	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	49
12097	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	122	92
12098	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	148	59
12099	AF090942	Homo sapiens	PRO0657	115	70
12100	AF090931	Homo sapiens	PRO0483	112	74
12101	AF090944	Homo sapiens	PRO0663	103	37
12102	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	76	58
12103	J02963	Homo sapiens	platelet glycoprotein IIb precursor	130	80
12104	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	106	84
12105	R95913	Homo sapiens	Neural thread protein.	105	75
12106	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	149	75
12107	Y09561	Homo sapiens	ATP receptor	188	85
12108	AF090895	Homo sapiens	PRO0117	107	83
12109	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	117	65
12110	G02211	Homo sapiens	Human secreted protein, SEQ ID NO:	130	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6292.		
12111	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	117	69
12112	Y12478	Homo sapiens	congenital heart disease 5 protein	291	62
12113	AF220264	Homo sapiens	MOST-1	142	76
12114	Y12077	Homo sapiens	Human 5' EST secreted protein SEQ ID NO: 390.	109	95
12115	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	171	63
12116	AF064869	Rattus norvegicus	brain-enriched guanylate kinase-associated protein 2; BEGA2	294	98
12117	S79410	Mus musculus	nuclear localization signal binding protein	128	36
12119	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	102	73
12120	U79260	Homo sapiens	unknown	98	65
12121	AF161356	Homo sapiens	HSPC093	118	67
12122	AF130087	Homo sapiens	PRO2411	115	80
12123	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	280	75
12124	S48406	Mus sp.	alpha 1 (XII) collagen (triple-helical domain COL2)	59	41
12125	AB030816	Homo sapiens	H-REV107 protein-related protein	420	79
12126	R96418	Homo sapiens	Partial human transforming growth factor beta receptor type II.	169	100
12127	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	91	46
12128	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	109	83
12129	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	127	57
12130	AF119900	Homo sapiens	PRO2822	108	79
12131	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	127	70
12132	AF303828	Mus musculus	ubc-like protein MMS2	131	43
12133	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	127	58
12134	U49974	Homo sapiens	mariner transposase	124	80
12135	X52164	Mus musculus	Q300 protein (AA 1-77)	106	94
12136	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	151	69
12137	AF192913	Homo sapiens	zinc finger protein ZNF180	581	94
12138	X58907	Homo sapiens	steroid 21-monooxygenase	128	58
12139	AF090931	Homo sapiens	PRO0483	121	70
12140	AK024455	Homo sapiens	FLJ00047 protein	84	60
12141	AF090931	Homo sapiens	PRO0483	122	71
12142	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	153	60
12143	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	121	100
12144	G02922	Homo sapiens	Human secreted protein, SEQ ID NO: 7003.	191	62
12145	U57092	Homo sapiens	Rab30	257	87
12146	AF130089	Homo sapiens	PRO2550	129	74
12147	AF090931	Homo sapiens	PRO0483	138	80
12148	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	135	60
12149	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	138	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12150	U51723	Plasmodium vivax	V-SERA 1	107	37
12151	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	82	68
12152	Y23884	Homo sapiens	Amino acid sequence of FK506 binding protein 65 (FKBP65).	124	69
12153	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	93	70
12154	AF229067	Homo sapiens	PADI-H protein	162	68
12155	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	125	86
12157	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	113	39
12158	U89439	Bos taurus	ubiquitin-like protein	146	76
12159	G03725	Homo sapiens	Human secreted protein, SEQ ID NO: 7806.	677	98
12160	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	124	90
12161	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	109	80
12162	AF090931	Homo sapiens	PRO0483	125	76
12163	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	191	64
12164	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	96	61
12165	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	115	68
12166	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	219	93
12167	AF118086	Homo sapiens	PRO1992	155	78
12168	X12789	Mus musculus	cytokeratin 8 (AA 1 - 489)	174	63
12169	S79410	Mus musculus	nuclear localization signal binding protein	94	48
12170	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	57
12171	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	78
12172	AF068294	Homo sapiens	HDCMB45P	184	56
12173	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	116	50
12174	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	107	59
12175	X92485	Plasmodium vivax	pva1	108	44
12176	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	102	84
12177	X83703	Homo sapiens	nuclear protein	330	68
12178	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	147	50
12179	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	103	73
12180	AF132200	Homo sapiens	PRO1751	131	64
12181	AC005514	Homo sapiens	CTF5	261	90
12182	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	156	75
12183	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	75
12184	P92219	Homo sapiens (human)	CR1 protein.	101	74
12185	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	156	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12186	G02213	Homo sapiens	Human secreted protein, SEQ ID NO: 6294.	626	97
12187	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	96	51
12188	AF118067	Homo sapiens	PRO1578	89	73
12189	M63154	Homo sapiens	intrinsic factor	130	96
12190	AF090942	Homo sapiens	PRO0657	144	72
12191	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	76
12192	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	134	63
12193	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	159	76
12194	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	76
12195	AF090931	Homo sapiens	PRO0483	134	62
12196	AF130089	Homo sapiens	PRO2550	117	74
12197	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	57
12198	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	126	70
12199	J02459	bacteriophage lambda	Fi (DNA packaging;117)	203	95
12200	Y08061	Homo sapiens	Human c-myc protein fragment.	135	58
12201	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	132	86
12202	AF119900	Homo sapiens	PRO2822	148	68
12203	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	59
12204	R59842	Homo sapiens	ApoE4L1 protease.	118	91
12205	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	121	72
12206	S75997	Rattus sp.	nucleoporin p62 homolog	131	65
12207	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	145	65
12208	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	145	86
12209	AJ242956	Homo sapiens	E1 fusion protein	96	88
12210	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	132	78
12211	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	81
12212	K03179	Homo sapiens	pro-alpha-1 type-I collagen	96	37
12213	G01895	Homo sapiens	Human secreted protein, SEQ ID NO: 5976.	310	57
12214	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	493	82
12215	R13144	Homo sapiens	Deleted in Colorectal Carcinomas.	700	98
12216	AF132200	Homo sapiens	PRO1751	109	61
12217	AB013897	Homo sapiens	HKR1	324	64
12218	AF071172	Homo sapiens	HERC2	123	86
12219	L38593	Homo sapiens	integral membrane protein	78	62
12220	AF036233	Homo sapiens	cdc25B phosphatase	204	51
12221	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	107	60
12222	AL049795	Homo sapiens	d1622L5.9 (eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) (TRIP-1, TGF-beta receptor interacting protein 1))	163	86
12223	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	120	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12224	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	64
12225	AF130079	Homo sapiens	PRO2852	103	80
12226	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	163	86
12227	AF119855	Homo sapiens	PRO1847	96	78
12228	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	195	87
12229	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	103	90
12230	U49957	Homo sapiens	LIM protein	212	100
12231	AK022759	Homo sapiens	unnamed protein product	646	100
12232	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	110	70
12233	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	109	74
12234	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	123	76
12235	AF220264	Homo sapiens	MOST-1	104	85
12236	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH 8c}	113	87
12237	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	143	84
12238	AF090942	Homo sapiens	PRO0657	103	66
12239	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	129	72
12240	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	135	75
12241	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	136	95
12242	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH 8c}	148	72
12243	K02576	Homo sapiens	salivary proline-rich protein 1	118	39
12244	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	78	100
12245	AC005200	Homo sapiens	plasmalemmal porin	131	79
12246	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	150	65
12247	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	90	55
12248	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	77	64
12249	U63542	Homo sapiens	FAP protein	108	56
12250	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH 8c}	101	75
12251	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	139	63
12252	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	122	71
12253	AF118086	Homo sapiens	PRO1992	73	70
12254	AF083929	Mus musculus	ES18	108	44
12255	AF130089	Homo sapiens	PRO2550	124	88
12256	AF090931	Homo sapiens	PRO0483	132	80
12257	X95190	Homo sapiens	branched chain acyl-CoA oxidase	166	86
12258	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	131	53
12259	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	124	88
12260	G00328	Homo sapiens	Human secreted protein, SEQ ID NO:	128	85

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4409.		
12261	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	133	72
12262	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	110	70
12263	Y08061	Homo sapiens	Human c-myc protein fragment.	125	85
12264	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	65
12265	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	95
12266	AK024455	Homo sapiens	FLJ00047 protein	108	63
12267	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	166	73
12268	AF090931	Homo sapiens	PRO0483	108	82
12269	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	120	68
12270	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	120	66
12271	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	74
12272	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	129	60
12273	AF130089	Homo sapiens	PRO2550	134	79
12274	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	118	80
12275	AF194537	Homo sapiens	NAG13	151	52
12276	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	75	68
12277	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	113	60
12278	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	111	70
12279	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	119	92
12280	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	90
12281	U66464	Homo sapiens	hematopoietic progenitor kinase	102	83
12282	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	118	65
12283	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	162	82
12284	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	130	77
12285	AF116661	Homo sapiens	PRO1438	104	74
12286	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	98	66
12287	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	105	74
12288	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	129	78
12289	X53581	Rattus norvegicus	ORF7	111	47
12290	AF090931	Homo sapiens	PRO0483	147	87
12291	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	106	69
12292	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	53
12293	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12294	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	60
12295	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	112	66
12296	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	140	62
12297	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	144	70
12298	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	95	51
12299	S79410	Mus musculus	nuclear localization signal binding protein	108	70
12300	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	122	85
12301	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	117	73
12302	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	115	62
12303	AF130051	Homo sapiens	PRO0898	116	65
12304	J02963	Homo sapiens	platelet glycoprotein IIb precursor	119	60
12305	V00662	Homo sapiens	ATPase 6	118	100
12306	AF107406	Homo sapiens	GW128	98	66
12307	A05308	synthetic construct	glioblastoma-derived T-cell suppressor factor	376	93
12308	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	173	71
12309	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	140	74
12310	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	98	47
12311	Y27571	Homo sapiens	Human secreted protein encoded by gene No. 5.	130	42
12312	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	134	76
12313	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	98	82
12314	U79260	Homo sapiens	unknown	97	64
12315	L27428	Homo sapiens	reverse transcriptase	214	44
12316	D00570	Mus musculus	open reading frame (196 AA)	115	83
12317	AF090931	Homo sapiens	PRO0483	104	74
12318	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	123	84
12319	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	107	70
12320	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	97	62
12321	S79410	Mus musculus	nuclear localization signal binding protein	95	58
12322	G00362	Homo sapiens	Human secreted protein, SEQ ID NO: 4443.	104	59
12323	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	115	75
12324	AF286472	Homo sapiens	retinitis pigmentosa GTPase regulator	121	53
12325	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	162	75
12326	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	129	75
12327	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	125	88

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12328	AF090944	Homo sapiens	PRO0663	122	76
12329	AF090931	Homo sapiens	PRO0483	156	81
12330	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	107	80
12331	AF116715	Homo sapiens	PRO2829	127	72
12332	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	145	49
12333	S80862	Western equine encephalomyelitis virus, Western equine encephalomyelitis virus, Peptide Partial, 259 aa	nucleocapsid gene C	108	35
12334	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	141	83
12335	AK024455	Homo sapiens	FLJ00047 protein	133	71
12336	AF090944	Homo sapiens	PRO0663	139	84
12337	J02963	Homo sapiens	platelet glycoprotein IIb precursor	124	71
12338	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	102	69
12339	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	121	81
12340	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	149	54
12341	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	134	66
12342	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	102	60
12343	AF118086	Homo sapiens	PRO1992	80	63
12344	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	104	80
12345	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	145	72
12346	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	143	75
12347	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	116	37
12348	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	176	76
12349	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	103	48
12350	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	81
12351	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	108	70
12352	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	101	84
12353	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	105	42
12354	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	147	66
12355	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	125	65
12356	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	96	68
12357	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	122	43
12358	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	132	38
12359	G00397	Homo sapiens	Human secreted protein, SEQ ID NO:	94	90

SEQ ID NO.	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4478.		
12360	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	56
12361	AB001684	Chlorella vulgaris	ORF49b	92	44
12362	U93564	Homo sapiens	p40	257	84
12363	U60269	Homo sapiens	putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	427	84
12364	G03064	Homo sapiens	Human secreted protein, SEQ ID NO: 7145.	102	73
12365	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	102	68
12366	AF090944	Homo sapiens	PRO0663	94	45
12367	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	150	55
12368	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	105	85
12369	AF130089	Homo sapiens	PRO2550	112	78
12370	AF090895	Homo sapiens	PRO0117	125	64
12371	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	121	95
12372	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	145	72
12373	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	72
12374	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	133	79
12375	AP000001	Pyrococcus horikoshii	58aa long hypothetical protein	96	51
12376	U16359	Rattus norvegicus	nitric oxide synthase	105	76
12377	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	123	78
12378	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	126	83
12379	Y53643	Homo sapiens	A bone marrow secreted protein designated BMS6.	329	98
12380	U64094	Homo sapiens	soluble type II interleukin-1 receptor	114	100
12381	J02459	bacteriophage lambda	D (head-DNA stabilization;110)	467	100
12382	L10908	Mus musculus	Gcap1 gene product	100	89
12383	AF220264	Homo sapiens	MOST-1	113	68
12384	U79260	Homo sapiens	unknown	94	60
12385	B01372	Homo sapiens	Neuron-associated protein.	148	52
12386	R13556	Homo sapiens	Protein encoded downstream of hbc_M oncoprotein.	116	63
12387	G00952	Homo sapiens	Human secreted protein, SEQ ID NO: 5033.	125	92
12388	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	130	65
12389	S79410	Mus musculus	nuclear localization signal binding protein	150	62
12390	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	102	38
12391	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	113	56
12392	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	73	92

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12393	M69297	Homo sapiens	ORF 3	167	75
12394	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	142	43
12395	AF220264	Homo sapiens	MOST-1	131	57
12396	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	139	62
12397	AF130089	Homo sapiens	PRO2550	120	62
12398	AK023117	Homo sapiens	unnamed protein product	529	97
12399	AF123652	Homo sapiens	FEZ1	157	96
12400	D38112	Homo sapiens	NADH dehydrogenase subunit 6	139	87
12401	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	306	60
12402	AC005031	Homo sapiens	neuronal apoptosis inhibitory protein	143	96
12403	J03071	Homo sapiens	chorionic somatomammotropin CS-2	583	100
12405	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	125	100
12406	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	150	63
12407	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	157	85
12408	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	120	75
12409	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	141	50
12410	G03465	Homo sapiens	Human secreted protein, SEQ ID NO: 7546.	103	51
12411	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	71
12412	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	159	70
12413	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	129	79
12414	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	156	72
12415	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	74	72
12416	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	102	50
12417	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	171	75
12418	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	137	55
12419	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	111	52
12420	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	129	53
12421	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	110	55
12422	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	126	87
12423	U93564	Homo sapiens	p40	350	93
12424	M17885	Homo sapiens	acidic ribosomal phosphoprotein (P0)	484	88
12425	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	130	69
12426	X60376	Brassica napus	proline-rich protein	89	47
12427	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	83	88
12428	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	117	75
12429	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	107	67

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12430	AK027208	Homo sapiens	unnamed protein product	108	64
12431	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	154	68
12432	AF130089	Homo sapiens	PRO2550	118	88
12433	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	90	55
12434	AK024455	Homo sapiens	FLJ00047 protein	113	75
12435	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	107	80
12436	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	114	75
12437	AC005498	Homo sapiens	R31665_2	163	75
12438	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
12439	G03116	Homo sapiens	Human secreted protein, SEQ ID NO: 7197.	145	84
12440	AK024455	Homo sapiens	FLJ00047 protein	136	73
12441	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	122	69
12442	AF090942	Homo sapiens	PRO0657	120	72
12443	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	159	53
12444	AF130089	Homo sapiens	PRO2550	110	73
12445	AL021395	Homo sapiens	dJ269M15.1 (similar to peptidylprolyl isomerase (cyclophilin))	225	64
12446	AF090931	Homo sapiens	PRO0483	155	79
12447	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	130	81
12448	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	122	74
12449	AF119855	Homo sapiens	PRO1847	88	72
12450	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	84
12451	AK024455	Homo sapiens	FLJ00047 protein	78	68
12452	AF116712	Homo sapiens	PRO2738	118	62
12453	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	109	67
12454	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	59
12455	AK024455	Homo sapiens	FLJ00047 protein	146	64
12456	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	72
12457	AF090944	Homo sapiens	PRO0663	129	79
12458	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	119	70
12459	R22278	Homo sapiens	Human gp.-specific component phenotype Gc1.	250	65
12460	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	143	58
12461	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	111	61
12462	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	84
12463	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	94	38
12464	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	134	74
12465	AF200715	Homo sapiens	PTB domain adaptor protein CED-6	332	95
12466	G03786	Homo sapiens	Human secreted protein, SEQ ID NO:	139	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7867.		
12467	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	55
12468	AF199023	Homo sapiens	phospholipid scramblase 4	476	98
12469	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	104	89
12470	AF108841	Homo sapiens	pol protein	306	87
12471	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	111	79
12472	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	124	78
12473	U18339	Variola virus	D4L	117	60
12474	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	124	63
12475	AF130089	Homo sapiens	PRO2550	105	52
12476	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	80	62
12477	M91242	Rattus norvegicus	calcium channel alpha-1 subunit	156	68
12478	AF130089	Homo sapiens	PRO2550	154	79
12479	M15530	Homo sapiens	B-cell growth factor	154	70
12480	U39904	Mus musculus	citron	718	97
12481	R99364	Homo sapiens	Human REST protein DNA binding domain.	229	37
12482	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	97	54
12483	AF161356	Homo sapiens	HSPC093	94	55
12484	Y69166	Homo sapiens	A mature human N-acetylglycosaminyl transferase protein.	97	75
12485	AF090942	Homo sapiens	PRO0657	103	55
12486	U79260	Homo sapiens	unknown	98	74
12487	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	96	53
12488	U37100	Homo sapiens	aldose reductase-like peptide	400	97
12489	U93569	Homo sapiens	putative p150	141	56
12490	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	104	66
12491	R59842	Homo sapiens	ApoE4L1 protease.	86	89
12492	Y00876	Homo sapiens	Human LAPH-1 protein sequence.	219	45
12493	AK024455	Homo sapiens	FLJ00047 protein	85	53
12494	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	95	63
12495	Y36722	Homo sapiens	Fragment of human secreted protein encoded by gene 98.	216	60
12496	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	102	57
12497	Y77551	Homo sapiens	C-terminal domain of beta1c integrin.	132	67
12498	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	122	69
12499	AF161356	Homo sapiens	HSPC093	98	51
12500	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	150	81
12501	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	97	52
12502	AF132200	Homo sapiens	PRO1751	94	69
12503	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	76	65
12504	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	99	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12505	M19651	Rattus norvegicus	fos-related antigen	132	92
12506	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	113	48
12507	U94832	Homo sapiens	KSRP	117	48
12508	W47029	Homo sapiens	Human N-proteinase (70 kDa short form).	121	62
12509	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	66
12510	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	90	80
12511	AF042384	Homo sapiens	BC-2 protein	516	98
12512	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	96	50
12513	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	121	45
12514	AL162044	Homo sapiens	hypothetical protein	174	48
12515	AF130079	Homo sapiens	PRO2852	96	73
12516	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	113	77
12517	D32202	Homo sapiens	alpha 1C adrenergic receptor isoform 2	164	86
12518	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	99	85
12519	U00694	Gallus gallus	vitamin D3 hydroxylase associated protein	187	45
12520	AB030829	Rattus norvegicus	carbonic anhydrase III	503	63
12521	J04204	Bos taurus	32 kd accessory protein	618	95
12522	M36341	Homo sapiens	ADP-ribosylation factor 4	374	93
12523	AF090931	Homo sapiens	PRO0483	163	82
12524	AB007925	Homo sapiens	KIAA0456 protein	130	62
12525	G02314	Homo sapiens	Human secreted protein, SEQ ID NO: 6395.	162	79
12526	AF178948	Homo sapiens	TALE homeobox protein Meis2a	321	93
12527	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	156	85
12528	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	126	57
12529	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	145	68
12530	AK024372	Homo sapiens	unnamed protein product	112	56
12531	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	76	65
12532	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	132	66
12533	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	146	53
12534	AF090942	Homo sapiens	PRO0657	83	60
12535	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	136	65
12536	R95913	Homo sapiens	Neural thread protein.	106	52
12537	AF130089	Homo sapiens	PRO2550	148	84
12538	AF102826	Homo sapiens	RD114/simian type D retrovirus receptor	605	91
12539	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	52
12540	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	87	65
12541	G03600	Homo sapiens	Human secreted protein, SEQ ID NO: 7681.	209	92

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12542	M31964	Saimiriine herpesvirus 2	collagen-like protein	92	52
12543	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	76
12544	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	155	72
12545	AC004912	Homo sapiens	similar to CR16, SH3 domain binding protein; similar to 2205340A (PID:g1587070)	442	98
12546	V00662	Homo sapiens	URF A6L (NADH dehydrogenase subunit)	175	91
12547	AF130089	Homo sapiens	PRO2550	112	40
12548	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	48
12549	X55110	Homo sapiens	neurite outgrowth-promoting protein	479	72
12550	X98296	Homo sapiens	ubiquitin hydrolase	500	88
12551	R94317	Homo sapiens	Hepatocyte proliferation substance HP-041V.	390	92
12552	G01623	Homo sapiens	Human secreted protein, SEQ ID NO: 5704.	142	90
12553	D86966	Homo sapiens	similar to human ZFY protein.	161	56
12554	D00570	Mus musculus	open reading frame (196 AA)	122	67
12555	AF130089	Homo sapiens	PRO2550	94	88
12556	AF043184	Homo sapiens	T cell receptor beta chain	607	84
12557	U93564	Homo sapiens	p40	154	100
12558	U42026	Homo sapiens	plasma membrane Ca ²⁺ -ATPase variant 4a PMCA4a	200	97
12559	S79410	Mus musculus	nuclear localization signal binding protein	103	50
12560	U90552	Homo sapiens	butyrophilin	356	98
12561	K02576	Homo sapiens	salivary proline-rich protein 1	156	37
12562	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	138	41
12563	X16454	Homo sapiens	carcinoembryonic antigen subdomain B	353	98
12564	AL031186	Homo sapiens	bK984G1.4 (Ewing sarcoma breakpoint region 1 protein)	119	100
12565	M68941	Homo sapiens	protein-tyrosine phosphatase	223	93
12566	Y14487	Homo sapiens	cytosolic serine hydroxymethyltransferase	145	84
12567	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	149	61
12568	AB005047	Homo sapiens	SH3 binding protein	124	52
12569	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	102	53
12570	X68142	Oryctolagus cuniculus	elongation factor 1 gamma	678	93
12571	L20315	Mus musculus	MPS1 protein	337	77
12572	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	114	50
12573	AF130089	Homo sapiens	PRO2550	124	71
12574	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	146	51
12575	AF005902	Monodelphis domestica	kinesin homolog	534	82
12576	Y56021	Homo sapiens	Human CD40 receptor interacting protein 4C4.	711	96
12577	Y99662	Homo sapiens	Human GTPase associated protein-13.	634	100
12578	Z48008	Saccharomyces cerevisiae	Sok1p	225	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12579	AF112207	Homo sapiens	translation initiation factor eIF-2b delta subunit	195	97
12580	M22538	Homo sapiens	NADH-ubiquinone reductase	224	82
12581	AB034730	Mus musculus	This gene is isolated by means of differential display method using twt, an excellent mouse model for ectopic ossification.; similar to megakaryocyte stimulating factor precursor and cartilage superficial zone protein	112	44
12582	U93567	Homo sapiens	p40	364	93
12583	AY007233	Homo sapiens	phosphoinositol 3-phosphate binding protein-1	475	100
12584	L07592	Homo sapiens	peroxisome proliferator activated receptor	113	81
12585	AE003682	Drosophila melanogaster	CG8135 gene product	191	38
12586	AF119851	Homo sapiens	PRO1722	88	64
12587	AF090895	Homo sapiens	PRO0117	144	59
12588	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	144	57
12589	U73199	Mus musculus	Rho-guanine nucleotide exchange factor	111	32
12590	J04615	Homo sapiens	small nuclear ribonucleoprotein	383	97
12591	L77967	Ovis aries	small proline-rich protein with paired repeat	60	33
12592	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	118	78
12593	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	123	83
12594	AF090944	Homo sapiens	PRO0663	152	82
12595	Y15243	Homo sapiens	ULBP-3 amino acid sequence.	852	100
12596	X98235	Drosophila melanogaster	type 1	159	42
12597	AF191309	Mus musculus	zinc finger protein	407	66
12598	W82841	Homo sapiens	Human cerebral protein-1.	107	91
12599	AF070664	Homo sapiens	HSPC008	128	89
12600	U03688	Homo sapiens	cytochrome P450	237	96
12601	AB015798	Homo sapiens	DnaJ homolog	226	73
12602	AC003058	Arabidopsis thaliana	unknown protein	88	40
12603	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	80	35
12604	AF200187	cercopithecine herpesvirus 15	EBNA2-like protein	109	28
12605	AF161532	Homo sapiens	HSPC047	720	100
12606	M21302	Homo sapiens	small proline rich protein	60	59
12607	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	107	47
12608	AJ302650	Rattus norvegicus	RP59 protein	599	54
12609	J05401	Homo sapiens	sarcomeric mitochondrial creatine kinase precursor (EC 2.7.3.2)	763	96
12610	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	216	87
12611	W78175	Homo sapiens	Human secreted protein encoded by gene 50 clone HSTAG52.	337	100
12612	S79410	Mus musculus	nuclear localization signal binding protein	145	66
12613	AF119855	Homo sapiens	PRO1847	157	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12614	U82303	Homo sapiens	unknown	107	62
12615	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	146	49
12616	AF130051	Homo sapiens	PRO0898	254	56
12617	AF037350	Rattus norvegicus	NF-E2-related factor 2	807	59
12618	Y02168	Homo sapiens	A facilitative glucose transporter protein GLUT8.	452	100
12619	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	158	84
12620	G03812	Homo sapiens	Human secreted protein, SEQ ID NO: 7893.	246	60
12621	X55683	Lycopersicon esculentum	extensin (class I)	79	43
12622	AF109907	Homo sapiens	SI64	93	40
12623	Y36156	Homo sapiens	Human secreted protein #28.	114	61
12624	AF116712	Homo sapiens	PRO2738	104	48
12625	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	81	65
12626	AF113685	Homo sapiens	PRO0974	104	43
12627	AL160371	Leishmania major	probable (hhv-5) u1 102, variant a DNA, complete virion genome	116	45
12628	AF107406	Homo sapiens	GW128	133	58
12629	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	100	57
12630	AB047600	Macaca fascicularis	hypothetical protein	172	66
12631	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	136	63
12632	AF118082	Homo sapiens	PRO1902	138	45
12633	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	151	62
12634	X52164	Mus musculus	Q300 protein (AA 1-77)	95	58
12635	AF064597	Homo sapiens	LINE-1 like protein	108	46
12636	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	116	49
12637	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	110	52
12638	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	79	70
12639	M29622	Mus musculus	open reading frame 2	81	60
12640	M26460	Homo sapiens	retinoblastoma 1	100	45
12641	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	110	63
12642	AB047936	Macaca fascicularis	hypothetical protein	100	52
12643	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	146	41
12644	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	143	48
12645	AF090942	Homo sapiens	PRO0657	157	54
12646	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	130	56
12647	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	267	65
12648	AF130079	Homo sapiens	PRO2852	109	57
12649	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	99	61
12650	X55686	Lycopersicon	extensin (class II)	65	35

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		esculentum			
12651	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795	87	84
12652	AF119851	Homo sapiens	PRO1722	150	70
12653	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	133	50
12654	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	146	70
12655	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	136	63
12656	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	93	52
12657	U93563	Homo sapiens	putative p150	1046	50
12658	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	346	70
12659	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	104	70
12660	AF119851	Homo sapiens	PRO1722	98	56
12661	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	90	65
12662	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	59	64
12663	AF118082	Homo sapiens	PRO1902	91	66
12664	L10908	Mus musculus	Gcap1 gene product	113	50
12665	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	124	37
12666	AF090895	Homo sapiens	PRO0117	76	57
12667	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	103	43
12668	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	90	61
12669	M15530	Homo sapiens	B-cell growth factor	90	80
12670	AF198447	Aspergillus nidulans	60S ribosomal protein L3	217	69
12671	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	137	51
12672	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	77	68
12673	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	67	40
12674	X79417	Sus scrofa	40S ribosomal protein S12	377	75
12675	AF107406	Homo sapiens	GW128	74	51
12676	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	99	62
12677	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	127	65
12678	G00590	Homo sapiens	Human secreted protein, SEQ ID NO: 4671.	99	62
12679	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	128	85
12680	AF194537	Homo sapiens	NAG13	142	59
12681	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	155	77
12682	AF161356	Homo sapiens	HSPC093	104	50
12683	AF107406	Homo sapiens	GW128	84	54
12684	U83303	Homo sapiens	line-1 reverse transcriptase	90	39
12685	V40883_cdl	Homo sapiens	03-DEC-1997 Coding sequence of clone BG366.2.	728	100
12686	M24732	Homo sapiens	lamin-like protein	94	54
12687	X00824	Gallus gallus	collagen	66	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12688	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	184	64
12689	AF118086	Homo sapiens	PRO1992	140	61
12690	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	131	54
12691	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	180	72
12692	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	104	72
12693	AF130089	Homo sapiens	PRO2550	204	51
12694	K01664	Drosophila melanogaster	Bkm-like protein	92	52
12695	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	110	52
12696	L39103	Homo sapiens	glycoprotein lb alpha	61	45
12697	M15530	Homo sapiens	B-cell growth factor	121	64
12698	M36913	Zea mays	cell wall protein (put.); putative	75	40
12699	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	101	68
12700	M24732	Homo sapiens	lamin-like protein	95	35
12701	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	67	50
12702	AF298594	Nicotiana glauca	arabinogalactan protein	105	30
12703	X92485	Plasmodium vivax	pva1	97	38
12704	AF210651	Homo sapiens	NAG18	89	64
12705	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	190	53
12706	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	93	78
12707	U52077	Homo sapiens	mariner transposase	451	51
12708	AC003058	Arabidopsis thaliana	unknown protein	244	77
12709	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	138	65
12710	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	99	82
12711	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	104	34
12712	AF242772	Homo sapiens	mesenchymal stem cell protein DSCD28	106	45
12713	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	116	36
12714	AF116715	Homo sapiens	PRO2829	139	68
12715	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	89	62
12716	X55684	Lycopersicon esculentum	extensin (class I)	86	54
12717	Z93891	Hegeter politus	cytochrome oxidase	72	48
12718	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	105	46
12719	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	74	46
12720	U30221	Crithidia fasciculata	NADH dehydrogenase subunit 5	92	39
12721	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	131	82
12722	AF107406	Homo sapiens	GW128	72	54
12723	G02639	Homo sapiens	Human secreted protein, SEQ ID NO:	131	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6720.		
12724	AF116661	Homo sapiens	PRO1438	145	59
12725	Y53871	Homo sapiens	A human brain-derived signalling factor polypeptide.	584	98
12726	L10908	Mus musculus	Gcap1 gene product	95	37
12727	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	124	37
12728	X55686	Lycopersicon esculentum	extensin (class II)	66	36
12729	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	110	55
12730	L23852	Homo sapiens	Putative 3' end of coding region; putative	83	37
12731	Y13141	Bromheadia finlaysoniana	extensin	59	48
12732	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	88	69
12733	AF090895	Homo sapiens	PRO0117	130	55
12734	R95913	Homo sapiens	Neural thread protein.	162	45
12735	U72355	Homo sapiens	Hsp27 ERE-TATA-binding protein	972	57
12736	AF247039	porcine adenovirus 3	163R*	108	35
12737	M22332	Homo sapiens	unknown protein	148	45
12738	AF090895	Homo sapiens	PRO0117	89	72
12739	B08525	Homo sapiens	Protein encoded by a novel gene associated with colon disease.	296	86
12740	X90872	Homo sapiens	associated to Golgi apparatus	116	54
12741	M26460	Homo sapiens	retinoblastoma 1	75	37
12742	S52010	Mus sp.	orf1 5' of EpoR	104	31
12743	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	88	50
12744	AB047600	Macaca fascicularis	hypothetical protein	111	47
12745	AF090944	Homo sapiens	PRO0663	152	65
12746	Y21106	Homo sapiens	Human bcl2 proto-oncogene wild type protein fragment 3.	62	64
12747	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	97	76
12748	X66861	Mus musculus	Hox-1.4	92	34
12749	AF166125	Homo sapiens	selenoprotein N	978	98
12750	W87504	Homo sapiens	Human N-methyl-D-aspartate receptor subunit encoded by clone NMDA24.	98	29
12751	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	91	78
12752	X72963	Nicotiana tabacum	pAP8 product	80	45
12753	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	123	61
12754	AF146191	Homo sapiens	FRG1	208	85
12755	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	154	75
12756	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	72	48
12757	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	111	51
12758	U83280	Leishmania donovani	39 kDa antigen	106	60
12759	AF116661	Homo sapiens	PRO1438	73	48
12760	AF164615	Homo sapiens	envelope protein.	257	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12761	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	135	70
12762	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	111	50
12763	M29622	Mus musculus	open reading frame 2	73	68
12764	L27428	Homo sapiens	reverse transcriptase	111	60
12765	S79410	Mus musculus	nuclear localization signal binding protein	106	45
12766	AK024455	Homo sapiens	FLJ00047 protein	108	66
12767	M36914	Zea mays	cell wall protein (put.); putative	78	36
12768	L27428	Homo sapiens	reverse transcriptase	159	59
12769	AJ005567	Mus musculus	SPR21 protein	55	39
12770	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	115	82
12771	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	76	64
12772	AF217374	Acanthaster planci	cytochrome oxidase subunit I	126	85
12773	AF130114	Homo sapiens	PRO2459	129	50
12774	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	220	71
12775	AF287482	Chlorobium tepidum	Orf122	166	68
12776	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	84	50
12777	AF130079	Homo sapiens	PRO2832	258	58
12778	AF090931	Homo sapiens	PRO0483	65	76
12779	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	152	66
12780	AB047948	Macaca fascicularis	hypothetical protein	59	37
12781	AF119900	Homo sapiens	PRO2822	132	59
12782	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	97	51
12783	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	77	77
12784	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	84
12785	L27428	Homo sapiens	reverse transcriptase	183	39
12786	AF119851	Homo sapiens	PRO1722	128	61
12787	AF116715	Homo sapiens	PRO2829	111	72
12788	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	147	77
12789	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	84	66
12790	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	71
12791	AF124729	Mus musculus	acinus ^S	122	50
12792	AC003058	Arabidopsis thaliana	unknown protein	86	52
12793	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	108	74
12794	M62415	Pseudopleuronectes americanus	HPLC6	82	35
12795	Y36156	Homo sapiens	Human secreted protein #28.	133	48
12796	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	74
12797	L22030	Glycine max	hydroxyproline-rich glycoprotein	170	32
12798	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	114	43
12799	Y76184	Homo sapiens	Human secreted protein encoded by	90	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 61.		
12800	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	102	38
12801	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	98	69
12802	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	177	69
12803	AF130089	Homo sapiens	PRO2550	94	74
12804	S77772	Homo sapiens	aspartylglucosaminidase, AGA (C-terminal, alternatively spliced) {EC 3.5.1.26}	83	68
12805	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	82	28
12806	AF026689	Homo sapiens	prostate-specific transglutaminase	80	60
12807	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	122	47
12808	X03145	Homo sapiens	pot. ORF V	150	34
12809	L10908	Mus musculus	Gcap1 gene product	111	34
12810	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	170	55
12811	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	101	62
12812	AJ233591	Mus musculus	reverse transcriptase	287	67
12813	U82303	Homo sapiens	unknown	149	52
12814	AF107406	Homo sapiens	GW128	103	58
12815	U82303	Homo sapiens	unknown	93	83
12816	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	161	54
12817	B01390	Homo sapiens	Neuron-associated protein.	81	38
12818	AF287482	Chlorobium tepidum	Orf122	174	69
12819	AE003499	Drosophila melanogaster	CG12706 gene product	166	28
12820	M15530	Homo sapiens	B-cell growth factor	124	71
12821	U83303	Homo sapiens	line-1 reverse transcriptase	161	53
12822	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	150	77
12823	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	103	66
12824	AF064597	Homo sapiens	LINE-1 like protein	64	45
12825	X71442	Rattus norvegicus	ORF 1; putative	113	45
12826	U62039	Elephantulus edwardii	reverse transcriptase	74	46
12827	M15530	Homo sapiens	B-cell growth factor	127	54
12828	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	94	84
12829	U63332	Homo sapiens	super cysteine rich protein; SCRP	59	57
12830	AF229067	Homo sapiens	PADI-H protein	184	61
12831	K02576	Homo sapiens	salivary proline-rich protein 1	69	34
12832	AF144054	Homo sapiens	apoptosis related protein APR-4	83	46
12833	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	61
12834	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	142	40
12835	U19098	Lycopersicon chilense	proline-rich protein	81	38
12836	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	229	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12837	Y13141	Bromheadia finlaysoniana	extensin	81	60
12838	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	88	71
12839	X72963	Nicotiana tabacum	pAP8 product	94	40
12840	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	315	56
12841	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	94	55
12842	AK025947	Homo sapiens	unnamed protein product	124	57
12843	AF159055	Homo sapiens	leucine zipper-like protein	69	55
12844	AF040257	Homo sapiens	TNF receptor homolog	98	50
12845	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	94	76
12846	X88799	Oryza sativa	DNA binding protein	94	37
12847	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	98	48
12848	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	164	56
12849	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	75	59
12850	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	122	54
12851	M31964	Saimiriine herpesvirus 2	collagen-like protein	79	50
12852	AF118082	Homo sapiens	PRO1902	94	77
12853	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	139	54
12854	R59842	Homo sapiens	ApoE4L1 protease.	108	82
12855	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	99	66
12856	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	89	56
12857	D29833	Homo sapiens	proline rich peptide P-B	64	52
12858	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	80
12859	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	88	61
12860	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	66	33
12861	Y13141	Bromheadia finlaysoniana	extensin	75	47
12862	M29622	Mus musculus	open reading frame 2	74	62
12863	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	141	70
12864	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	117	54
12865	AF090894	Homo sapiens	PRO0113	108	63
12866	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	121	54
12867	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	103	44
12868	S68106	Ascaris suum, Peptide Partial, 100 aa	type IV collagen alpha 2 chain, alpha 2 (IV) {alternatively spliced}	75	35
12869	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	97	56
12870	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	146	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12871	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	78	76
12872	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	105	56
12873	AB030234	Canis familiaris	D4 dopamine receptor	61	58
12874	M22332	Homo sapiens	unknown protein	128	41
12875	U05313	Trypanosoma brucei	CR3	67	48
12876	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	65
12877	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	66	54
12878	X55684	Lycopersicon esculentum	extensin (class I)	78	34
12879	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	51
12880	AF130079	Homo sapiens	PRO2852	125	75
12881	AF090895	Homo sapiens	PRO0117	142	59
12882	AF181251	Rattus norvegicus	lung Kruppel-like factor	93	39
12883	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	167	74
12884	M26460	Homo sapiens	retinoblastoma 1	136	41
12885	AJ277557	Homo sapiens	mitochondrial 5(3')-deoxyribonucleotidase (dNT-2)	280	100
12886	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	119	62
12887	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	43
12888	AF119851	Homo sapiens	PRO1722	94	50
12889	K02576	Homo sapiens	salivary proline-rich protein 1	121	39
12890	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	95	68
12891	AK024455	Homo sapiens	FLJ00047 protein	77	51
12892	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	115	83
12893	L27428	Homo sapiens	reverse transcriptase	89	29
12894	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WO9901020.	112	72
12895	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	72	62
12896	AK023563	Homo sapiens	unnamed protein product	260	64
12897	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	76	66
12898	AC002304	Arabidopsis thaliana	F14J16.29	111	36
12899	Y86445	Homo sapiens	Human gene 42-encoded protein fragment, SEQ ID NO:360.	83	53
12900	AF116638	Homo sapiens	PRO1546	123	57
12901	AB010561	Mus musculus	mszf47	64	43
12902	R59842	Homo sapiens	ApoE4L1 protease.	130	86
12903	L06498	Homo sapiens	ribosomal protein S20	249	56
12904	L13635	Rattus norvegicus	growth response protein	176	69
12905	AF156961	Homo sapiens	gag	183	44
12906	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	207	67
12907	AF107406	Homo sapiens	GW128	99	50
12908	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	93	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12909	AF263540	Homo sapiens	MIB006	1809	100
12910	Y48292	Homo sapiens	Human prostate cancer-associated protein 78.	60	50
12911	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	179	87
12912	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	108	72
12913	Z72499	Homo sapiens	herpesvirus associated ubiquitin-specific protease (HAUSP)	5242	99
12914	AF092136	Homo sapiens	PTD015	297	100
12915	AF161356	Homo sapiens	HSPC093	123	42
12916	AF044670	Homo sapiens	33 kDa Vapn-associated protein; VAP-33	506	90
12917	W27087	Homo sapiens	Human transforming growth factor alpha HIII.	1243	100
12918	Y59807	Homo sapiens	Human normal ovarian tissue derived protein 84.	111	43
12919	AJ388518	Canis familiaris	non-histone chromosomal protein HMG-17	108	84
12920	AK023392	Homo sapiens	unnamed protein product	119	60
12921	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	104	87
12922	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	124	81
12923	X78444 cd1	Homo sapiens	21-MAY-1997 Human UCSP-2 cDNA.	1090	100
12924	AF116661	Homo sapiens	PRO1438	89	52
12925	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	82	80
12926	AF119855	Homo sapiens	PRO1847	120	63
12927	AF090931	Homo sapiens	PRO0483	92	90
12928	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	119	88
12929	Y91429	Homo sapiens	Human secreted protein sequence encoded by gene 21 SEQ ID NO:150.	108	38
12930	Y12661	Homo sapiens	neuro-endocrine specific protein VGF	2506	99
12931	Y84546	Homo sapiens	Amino acid sequence of a fragment of human collagen type 1 protein.	61	50
12932	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	121	53
12933	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	104	52
12934	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	104	60
12935	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	331	77
12936	M15530	Homo sapiens	B-cell growth factor	83	71
12937	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	146	64
12938	R59842	Homo sapiens	ApoE4L1 protease.	112	61
12939	AF090895	Homo sapiens	PRO0117	94	80
12940	X73459	Homo sapiens	signal recognition particle subunit 14	549	98
12941	L23545	Homo sapiens	putative	141	45
12942	AF054178	Homo sapiens	Cl-B14.5a homolog	238	84
12943	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	55
12944	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	143	55
12945	D00570	Mus musculus	open reading frame (251 AA)	166	34
12946	U62039	Elephantulus	reverse transcriptase	63	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		edwardii			
12947	AE003499	Drosophila melanogaster	CG12706 gene product	104	31
12948	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	65	100
12949	X70343	Nicotiana sylvestris	extensin	102	38
12950	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	103	45
12951	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	85	56
12952	AF090895	Homo sapiens	PRO0117	139	68
12953	AF090896	Homo sapiens	PRO0131	93	85
12954	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	101	75
12955	M96982	Homo sapiens	U2 snRNP auxiliary factor small subunit	292	68
12956	X71087	Homo sapiens	monocyte chemoattractant protein (MCP-3)	408	96
12957	S80864	Homo sapiens	cytochrome c-like polypeptide	591	68
12958	AF109907	Homo sapiens	S164	188	63
12959	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	173	50
12960	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	168	62
12961	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	98	56
12962	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	106	84
12963	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	125	44
12964	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	107	57
12965	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	71	65
12966	AC009853	Arabidopsis thaliana	hypothetical protein	102	44
12967	AF090942	Homo sapiens	PRO0657	99	62
12968	M15530	Homo sapiens	B-cell growth factor	90	65
12969	AF090895	Homo sapiens	PRO0117	83	54
12970	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	119	54
12971	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	123	57
12972	L32558	Homo sapiens	sequence is expressed in human Tera-2 clone 13 (embryonal carcinoma) cells. The sequence may contain mismatches (one strand sequenced only once). 97% identical in 320 bp overlap with human 54 kDa prot; ORF	426	85
12973	AF008196	Homo sapiens	bax epsilon	78	87
12974	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	96	80
12975	AL031848	Homo sapiens	dJ20208.2.2 (novel rodent HES2 (hair and Enhancer of Split 2) LIKE protein (isoform 2))	176	100
12976	AJ245905	Chlorocebus aethiops	HSBP1-like protein	94	100
12977	AF067519	Homo sapiens	PITSLRE protein kinase beta SV1 isoform	1923	93

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12978	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	168	73
12979	X52164	Mus musculus	Q300 protein (AA 1-77)	105	39
12980	Y13141	Bromheadia finlaysoniana	extensin	53	36
12981	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	87	77
12982	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	83	89
12983	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	92	46
12984	AF113685	Homo sapiens	PRO0974	111	67
12985	U31086	Gallus gallus	neuron-glia adhesion molecule	52	50
12986	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	132	68
12987	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	91	71
12988	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	135	81
12989	AB029042	Homo sapiens	ATPase inhibitor precursor	364	100
12990	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	174	72
12991	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	174	57
12992	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	158	57
12993	AF118082	Homo sapiens	PRO1902	77	78
12994	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	76	60
12995	M15530	Homo sapiens	B-cell growth factor	105	76
12996	AJ005562	Mus musculus	SPR2D protein	104	36
12997	Y48346	Homo sapiens	Human prostate cancer-associated protein 43.	184	77
12998	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	82	53
12999	L11645	Homo sapiens	alpha-tubulin	196	68
13000	AF113685	Homo sapiens	PRO0974	123	52
13001	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	78	53
13002	AJ005564	Mus musculus	SPR2F protein	76	44
13003	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	101	76
13004	AL159178	Streptomyces coelicolor A3(2)	putative secreted protein	89	37
13005	L77967	Ovis aries	small proline-rich protein with paired repeat	64	36
13006	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	85	70
13007	AF068294	Homo sapiens	HDCMB45P	237	52
13008	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	128	50
13009	AF144054	Homo sapiens	apoptosis related protein APR-4	100	75
13010	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	148	67
13011	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	152	66
13012	B01390	Homo sapiens	Neuron-associated protein.	99	32
13013	A27282	Homo sapiens	TGR-CL3C	69	42
13014	G00689	Homo sapiens	Human secreted protein, SEQ ID NO:	135	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4770.		
13015	AF130089	Homo sapiens	PRO2550	88	60
13016	AF266223	Gillichthys mirabilis	ribosomal protein L27	122	50
13017	S79410	Mus musculus	nuclear localization signal binding protein	116	40
13018	U82303	Homo sapiens	unknown	64	60
13019	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	70	57
13020	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	169	91
13021	V00488	Homo sapiens	alpha globin	213	100
13022	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	59
13023	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	109	86
13024	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	151	84
13025	U82303	Homo sapiens	unknown	86	52
13026	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	124	61
13027	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	83	50
13028	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	74	63
13029	Y84546	Homo sapiens	Amino acid sequence of a fragment of human collagen type I protein.	59	46
13030	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	96	68
13031	S71494	Mus sp.	SmD homolog (Gly-Arg repeat)	93	55
13032	AF113685	Homo sapiens	PRO0974	100	48
13033	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	242	85
13034	AL390114	Leishmania major	extremely cysteine/valine rich protein	178	41
13035	G01129	Homo sapiens	Human secreted protein, SEQ ID NO: 5210.	228	81
13036	X66285	Mus musculus	HCl ORF	103	44
13037	AF026689	Homo sapiens	prostate-specific transglutaminase	90	55
13038	U47924	Homo sapiens	RPL13-2	424	63
13039	AF090942	Homo sapiens	PRO0657	111	44
13040	AK025116	Homo sapiens	unnamed protein product	131	52
13041	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	92	72
13042	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	100	69
13043	AF130089	Homo sapiens	PRO2550	109	45
13044	G02879	Homo sapiens	Human secreted protein, SEQ ID NO: 6960.	116	52
13045	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	162	70
13046	L10908	Mus musculus	Gcap1 gene product	162	40
13047	L02321	Homo sapiens	glutathione S-transferase GSTM5-5	1072	93
13048	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	89	60
13049	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	153	60
13050	U33547	Homo sapiens	MHC class II antigen	69	85
13051	AC006014	Homo sapiens	similar to mismatch repair proteins; similar to PID:g1304125	652	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13052	A27282	Homo sapiens	TGR-CL3C	65	51
13053	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	106	60
13054	M20030	Homo sapiens	small proline rich protein	57	33
13055	AF022117	Balaena mysticetus	metallothionein	119	62
13056	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	78	43
13057	R20305	Homo sapiens	Val(1) to Met, His(2) deleted, Ala(76) to Lys beta-globin mutant.	274	98
13058	X55686	Lycopersicon esculentum	extensin (class II)	56	39
13059	U10696	Zea mays	Ec metallothionein class II protein	66	26
13060	Y40417	Homo sapiens	A human N-acetylneuraminate lyase (hNANL) protein.	1183	80
13061	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	123	41
13062	AF002210	Homo sapiens	copper chaperone for superoxide dismutase	702	61
13063	AF118086	Homo sapiens	PRO1992	69	84
13064	M24097	Homo sapiens	MHC HLA-C-alpha-2 chain	1550	96
13065	AC003113	Arabidopsis thaliana	F24O1.6	51	40
13066	AF161531	Homo sapiens	HSPC046	488	97
13067	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	141	50
13068	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	116	46
13069	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	145	69
13070	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	224	71
13071	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	153	52
13072	AF216965	Homo sapiens	ancient conserved domain protein 3	876	100
13073	Y15917	Homo sapiens	COL1A1 and PDGFB fusion transcript	108	35
13074	X77664	Homo sapiens	retinoic acid receptor beta isoform 1	53	71
13075	AF156961	Homo sapiens	gag	136	37
13076	R59842	Homo sapiens	ApoE4L1 protease.	117	75
13077	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	121	65
13078	U23183	Caenorhabditis elegans	gene lies in inverted repeat and exon 1 overlaps tRNA; may be pseudogene	100	79
13079	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	56
13080	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	138	65
13081	Y12473	Homo sapiens	centrin	359	79
13082	G01518	Homo sapiens	Human secreted protein, SEQ ID NO: 5599.	375	98
13083	Y57891	Homo sapiens	Human transmembrane protein HTMPN-15.	1030	99
13084	AB046765	Homo sapiens	KIAA1545 protein	161	93
13085	X55686	Lycopersicon esculentum	extensin (class II)	66	40
13086	AF130079	Homo sapiens	PRO2852	137	45
13087	K01664	Drosophila melanogaster	Bkm-like protein	86	33
13088	G03812	Homo sapiens	Human secreted protein, SEQ ID NO:	105	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7893.		
13089	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	114	63
13090	AL121905	Homo sapiens	dJ534B8.3 (novel protein similar to an aspartic protease)	963	100
13091	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	95	47
13092	AB030236	Canis familiaris	D4 dopamine receptor	65	38
13093	AF161356	Homo sapiens	HSPC093	119	48
13094	Z14014	Nicotiana tabacum	Pistil extensin like protein, partial CDS only	67	50
13095	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	124	56
13096	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	73
13098	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	62
13099	AF130051	Homo sapiens	PRO0898	194	61
13100	Y86445	Homo sapiens	Human gene 42-encoded protein fragment, SEQ ID NO:360.	80	70
13101	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	111	43
13102	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	120	71
13103	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	116	63
13104	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	90	64
13105	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	176	56
13106	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	101	75
13107	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	100	65
13108	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	137	77
13109	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	94	88
13110	AF119855	Homo sapiens	PRO1847	103	49
13111	AF119851	Homo sapiens	PRO1722	142	80
13112	Y00311	Homo sapiens	Human secreted protein encoded by gene 54.	107	51
13113	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	104	54
13114	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	144	71
13115	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	138	50
13116	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	110	56
13117	AK025653	Homo sapiens	unnamed protein product	188	100
13118	AF130089	Homo sapiens	PRO2550	129	68
13119	AF161356	Homo sapiens	HSPC093	131	59
13120	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	121	45
13121	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	82	55
13122	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	87	45

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4718.		
13123	Y38394	Homo sapiens	Human secreted protein encoded by gene No. 9.	213	100
13124	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	108	55
13125	AF119855	Homo sapiens	PRO1847	109	45
13126	R95913	Homo sapiens	Neural thread protein.	137	47
13127	B01390	Homo sapiens	Neuron-associated protein.	101	47
13128	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	122	67
13129	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	105	52
13130	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	72
13131	D38112	Homo sapiens	NADH dehydrogenase subunit 3	500	90
13132	AF138957	Bos taurus	type II collagen cyanogen bromide fragment CB8	99	38
13133	AF084256	Homo sapiens	beta glucuronidase isoform d	157	69
13134	U92817	Homo sapiens	unnamed HERV-H protein	113	48
13135	Y19743	Homo sapiens	SEQ ID NO 461 from WO9922243.	967	99
13136	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	155	52
13137	AF090928	Homo sapiens	PRO0470	133	69
13138	AF090931	Homo sapiens	PRO0483	150	60
13139	AF116661	Homo sapiens	PRO1438	146	57
13140	AL022318	Homo sapiens	bK150C2.2 (Phorbol in 3)	443	56
13141	S79410	Mus musculus	nuclear localization signal binding protein	114	80
13142	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	86	43
13143	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	62
13144	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	146	66
13145	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	123	71
13146	AF107406	Homo sapiens	GW128	120	50
13147	L10908	Mus musculus	Gcap1 gene product	91	42
13148	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	66
13149	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	119	67
13150	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	168	86
13151	G00418	Homo sapiens	Human secreted protein, SEQ ID NO: 4499.	74	58
13152	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	108	61
13153	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	131	67
13154	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	113	54
13155	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	84
13156	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	167	80
13157	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	125	68
13158	D38112	Homo sapiens	cytochrome c oxidase subunit 3	514	71
13159	Y86248	Homo sapiens	Human secreted protein HCHPF68,	130	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SEQ ID NO:163.		
13160	AF116661	Homo sapiens	PRO1438	152	63
13161	AB046048	Macaca fascicularis	unnamed portein product	105	53
13162	AF107406	Homo sapiens	GW128	159	62
13163	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	132	59
13164	M15530	Homo sapiens	B-cell growth factor	97	80
13165	K02576	Homo sapiens	salivary proline-rich protein 1	67	36
13166	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	126	57
13167	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	95	53
13168	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	96	57
13169	AL049795	Homo sapiens	dj622L5.7.2 (novel protein (isoform 2))	250	95
13170	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	116	56
13171	L10908	Mus musculus	Gcap1 gene product	75	53
13172	S73853	Homo sapiens	NF2=neurofibromatosis type 2 [alternatively spliced, form A4]	160	73
13173	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	76
13174	A52568	Homo sapiens	HMGL-C	84	44
13175	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	91	49
13176	AK025116	Homo sapiens	unnamed protein product	130	44
13177	AF090901	Homo sapiens	PRO0195	103	84
13178	AF090894	Homo sapiens	PRO0113	92	62
13179	AF130079	Homo sapiens	PRO2852	118	38
13180	AK025047	Homo sapiens	unnamed protein product	141	67
13181	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	87	59
13182	AC003058	Arabidopsis thaliana	unknown protein	220	74
13183	S79980	Bos taurus	ribosomal protein L37	186	94
13184	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	90
13185	AF155232	Pisum sativum	extensin	95	36
13187	U16359	Rattus norvegicus	nitric oxide synthase	90	78
13188	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	113	79
13189	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	158	53
13190	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	130	59
13191	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	131	66
13192	D38112	Homo sapiens	NADH dehydrogenase subunit 3	439	86
13193	Z66499	Caenorhabditis elegans	T01B7.8	127	35
13194	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	126	61
13195	Y13141	Bromheadia finlaysoniana	extensin	58	43
13196	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	95	76
13197	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	116	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13198	X58236	Homo sapiens	36/8-8 fusion protein with epitope for anti-lectin antibody	98	41
13199	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	102	58
13200	AF220264	Homo sapiens	MOST-1	141	45
13201	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	112	58
13202	Y17221	Homo sapiens	Human secreted protein (clone R317-3).	115	57
13203	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	91	39
13204	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	65
13205	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	98	68
13206	M15530	Homo sapiens	B-cell growth factor	105	76
13207	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	84	45
13208	L27428	Homo sapiens	reverse transcriptase	205	49
13209	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	77	57
13210	M81321	Macaca fascicularis	proline-rich protein	104	48
13211	X55685	Lycopersicon esculentum	extensin (class I)	122	33
13212	M15530	Homo sapiens	B-cell growth factor	159	61
13213	AF130089	Homo sapiens	PRO2550	126	56
13214	AF210651	Homo sapiens	NAG18	125	68
13215	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	76
13216	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	157	70
13217	R59842	Homo sapiens	ApoE4L1-protease.	102	72
13218	K01664	Drosophila melanogaster	Bkm-like protein	123	37
13219	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	101	55
13220	D14167	Gallus gallus	ribosomal protein L37a	126	40
13221	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	178	82
13222	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	141	55
13223	L10908	Mus musculus	Gcap1 gene product	114	53
13224	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	216	73
13225	G03259	Homo sapiens	Human secreted protein, SEQ ID NO: 7340.	104	76
13226	AF130079	Homo sapiens	PRO2852	158	66
13227	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	60
13228	S77772	Homo sapiens	aspartylglucosaminidase, AGA {C-terminal, alternatively spliced} {EC 3.5.1.26}	100	46
13229	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	72
13230	M15530	Homo sapiens	B-cell growth factor	162	72
13231	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	161	66
13232	AL160371	Leishmania major	probable (hhv-6) u1 102, variant a DNA, complete virion genome	80	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13233	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	126	51
13234	AF126163	Homo sapiens	HHLA3 protein	131	78
13235	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	125	85
13236	AB001684	Chlorella vulgaris	ORF49b	55	45
13237	M15530	Homo sapiens	B-cell growth factor	114	66
13238	AL355929	Neurospora crassa	conserved hypothetical protein	99	46
13239	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	63
13240	S79410	Mus musculus	nuclear localization signal binding protein	110	40
13241	AF119851	Homo sapiens	PRO1722	167	63
13242	S79410	Mus musculus	nuclear localization signal binding protein	147	68
13243	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	95	65
13244	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	99	84
13245	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	104	62
13246	AF161356	Homo sapiens	HSPC093	116	67
13247	X61046	Hydra sp.	mini-collagen	108	49
13248	V00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	458	89
13249	M11900	Mus musculus	15-kDa proline-rich salivary protein	92	37
13250	AB017362	Bombyx mori	fibroin H-chain	70	43
13251	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	125	58
13252	G00360	Homo sapiens	Human secreted protein, SEQ ID NO: 4441.	122	58
13253	AF210651	Homo sapiens	NAG18	151	73
13254	AF224494	Mus musculus	arsenite inducible RNA associated protein	299	50
13255	AK026107	Homo sapiens	unnamed protein product	102	60
13256	Y02571	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	113	61
13257	AK024455	Homo sapiens	FLJ00047 protein	115	59
13258	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	155	51
13259	AJ251579	Arabidopsis thaliana	cef protein	115	39
13260	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	360	82
13261	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	151	61
13262	D38112	Homo sapiens	NADH dehydrogenase subunit 3	413	87
13263	D23661	Homo sapiens	ribosomal protein L37	487	94
13264	AF130079	Homo sapiens	PRO2852	153	43
13265	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	109	61
13266	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WO9901020.	133	79
13267	L10908	Mus musculus	Gcap1 gene product	103	43
13268	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	151	70
13269	G04064	Homo sapiens	Human secreted protein, SEQ ID NO: 8145.	97	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13270	AF130089	Homo sapiens	PRO2550	95	47
13271	AF130075	Homo sapiens	PRO2532	90	60
13272	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	103	54
13273	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	77	91
13274	AF130089	Homo sapiens	PRO2550	104	57
13275	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	94	45
13276	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	122	52
13277	AF113685	Homo sapiens	PRO0974	98	36
13278	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	85	68
13279	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	139	89
13280	G01129	Homo sapiens	Human secreted protein, SEQ ID NO: 5210.	243	79
13281	AF116715	Homo sapiens	PRO2829	108	56
13282	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	105	60
13283	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	194	78
13284	AL359782	Trypanosoma brucei	probable granule cell antiserum positive 8	104	47
13285	S79410	Mus musculus	nuclear localization signal binding protein	104	72
13286	AF130089	Homo sapiens	PRO2550	147	58
13287	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	133	58
13288	AF119855	Homo sapiens	PRO1847	115	45
13289	AF161356	Homo sapiens	HSPC093	131	50
13290	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	104	43
13291	K01664	Drosophila melanogaster	Bkm-like protein	112	49
13292	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	150	69
13293	M36647	Homo sapiens	mitochondrial hinge protein precursor	284	76
13294	D38112	Homo sapiens	NADH dehydrogenase subunit 3	444	85
13295	D38112	Homo sapiens	cytochrome c oxidase subunit 3	633	93
13296	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	164	76
13297	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	147	80
13298	Y13141	Bromheadia finlaysoniana	extensin	84	38
13299	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	139	49
13300	AF130079	Homo sapiens	PRO2852	98	60
13301	AF090894	Homo sapiens	PRO0113	114	52
13302	AF130079	Homo sapiens	PRO2852	161	83
13303	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	154	76
13304	AF118086	Homo sapiens	PRO1992	120	75
13305	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	100	73
13306	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	108	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13307	Y74110	Homo sapiens	Human prostate tumor EST fragment derived protein #297.	448	100
13308	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	85	65
13309	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	104	47
13310	AF116715	Homo sapiens	PRO2829	124	76
13311	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	142	63
13312	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	61
13313	AF116661	Homo sapiens	PRO1438	142	67
13314	AF161356	Homo sapiens	HSPC093	121	46
13315	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	169	52
13316	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	98	90
13317	AF130079	Homo sapiens	PRO2852	109	58
13318	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	113	80
13319	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	81	61
13320	AF130089	Homo sapiens	PRO2550	106	77
13321	AF090931	Homo sapiens	PRO0483	143	63
13322	D29833	Homo sapiens	proline rich peptide P-B	59	33
13323	D38112	Homo sapiens	NADH dehydrogenase subunit 3	417	78
13324	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	119	82
13325	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	168	59
13326	A31038	Nicotiana glauca	PRP3	88	41
13327	AF090895	Homo sapiens	PRO0117	87	55
13328	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	88	51
13329	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	103	66
13330	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	101	67
13331	AF090930	Homo sapiens	PRO0478	93	36
13332	AF159055	Homo sapiens	leucine zipper-like protein	118	71
13333	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	89	57
13334	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	121	80
13335	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	160	73
13336	AJ005562	Mus musculus	SPR2D protein	86	44
13337	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	169	66
13338	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	78	57
13339	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	102	91
13340	AF090895	Homo sapiens	PRO0117	137	47
13341	K01664	Drosophila melanogaster	Bkm-like protein	115	46
13342	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	100	76
13343	G03714	Homo sapiens	Human secreted protein, SEQ ID NO:	134	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7795.		
13344	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhla.	76	76
13345	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	72
13346	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	143	69
13347	AF119900	Homo sapiens	PRO2822	93	58
13348	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	169	75
13349	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	83	68
13350	AF116715	Homo sapiens	PRO2829	134	64
13351	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	115	65
13352	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	118	59
13353	Y02887	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	139	77
13354	AF116661	Homo sapiens	PRO1438	112	75
13355	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	170	73
13356	AF126163	Homo sapiens	HHLA3 protein	116	55
13357	U18339	Variola virus	D4L	101	58
13358	AF130089	Homo sapiens	PRO2550	127	52
13359	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	184	82
13360	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	78	50
13361	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	126	71
13362	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	174	76
13363	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	176	51
13364	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	99	41
13365	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	118	56
13366	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	158	50
13367	Y19467	Homo sapiens	Amino acid sequence of a human secreted protein.	65	64
13368	M15530	Homo sapiens	B-cell growth factor	132	77
13369	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	63
13370	AF130079	Homo sapiens	PRO2852	108	61
13371	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	150	76
13372	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	117	65
13373	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	118	57
13374	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	121	63
13375	AF118086	Homo sapiens	PRO1992	147	74
13376	AF130089	Homo sapiens	PRO2550	149	48
13377	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	123	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13378	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	53
13379	AF090894	Homo sapiens	PRO0113	101	52
13380	AF107406	Homo sapiens	GW128	126	51
13381	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	156	84
13382	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	119	80
13383	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	84	70
13384	S79410	Mus musculus	nuclear localization signal binding protein	107	53
13385	S79410	Mus musculus	nuclear localization signal binding protein	107	53
13386	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	141	65
13387	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	113	63
13388	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	155	77
13389	AF130089	Homo sapiens	PRO2550	159	62
13390	AF161356	Homo sapiens	HSPC093	154	74
13391	AC006135	Arabidopsis thaliana	putative vicilin storage protein (globulin-like)	171	28
13392	AF113685	Homo sapiens	PRO0974	226	57
13393	AF118082	Homo sapiens	PRO1902	69	68
13394	D23661	Homo sapiens	ribosomal protein L37	498	96
13395	AF130079	Homo sapiens	PRO2852	109	54
13396	AF119851	Homo sapiens	PRO1722	107	57
13397	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	165	68
13398	AF130089	Homo sapiens	PRO2550	145	68
13399	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	134	54
13400	J03798	Homo sapiens	small nuclear riboprotein Sm-D	451	93
13401	D29833	Homo sapiens	proline rich peptide P-B	64	39
13402	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	99	76
13403	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	159	76
13404	AF090894	Homo sapiens	PRO0113	152	70
13405	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	45
13406	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	172	72
13407	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	135	84
13408	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	63
13409	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	138	58
13410	AF130089	Homo sapiens	PRO2550	101	70
13411	AK024455	Homo sapiens	FLJ00047 protein	112	73
13412	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	48
13413	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	95	50
13414	AF090942	Homo sapiens	PRO0657	171	72
13415	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	120	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13416	M15530	Homo sapiens	B-cell growth factor	121	45
13417	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	115	58
13418	AF026689	Homo sapiens	prostate-specific transglutaminase	146	70
13419	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	85	64
13420	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	77	73
13421	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	149	62
13422	AF130089	Homo sapiens	PRO2550	111	39
13423	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	106	42
13424	AF119882	Homo sapiens	PRO2492	110	70
13425	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	104	59
13426	AF118082	Homo sapiens	PRO1902	129	48
13427	X70771	Chironomus tentans	Sp17	95	56
13428	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	66
13429	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	149	80
13430	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	103	63
13431	AF116661	Homo sapiens	PRO1438	128	54
13432	AK024455	Homo sapiens	FLJ00047 protein	117	69
13433	Y13141	Bromheadia finlaysoniana	extensin	91	40
13434	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	118	64
13435	AF090944	Homo sapiens	PRO0663	115	50
13436	X55687	Lycopersicon esculentum	extensin (class II)	73	32
13437	AF090942	Homo sapiens	PRO0657	77	50
13438	AP000061	Aeropyrum pernix	104aa long hypothetical protein	82	41
13439	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	94	51
13440	AF161356	Homo sapiens	HSPC093	115	53
13441	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	125	44
13442	Y59784	Homo sapiens	Human normal ovarian tissue derived protein 61.	1096	100
13443	U33547	Homo sapiens	MHC class II antigen	120	73
13444	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	106	71
13445	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	115	34
13446	G02256	Homo sapiens	Human secreted protein, SEQ ID NO: 6337.	486	100
13447	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	155	60
13448	AF130079	Homo sapiens	PRO2852	167	56
13449	AB047890	Macaca fascicularis	hypothetical protein	171	62
13450	AK025326	Homo sapiens	unnamed protein product	111	67
13451	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	93	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13452	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	109	91
13453	U65650	Arabidopsis thaliana	blue-copper binding protein III	103	35
13454	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	123	69
13455	AF090894	Homo sapiens	PRO0113	122	56
13456	D38585	Homo sapiens	TSC-22	710	99
13457	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene I21.	113	45
13458	X55686	Lycopersicon esculentum	extensin (class II)	64	51
13459	AF107406	Homo sapiens	GW128	162	54
13460	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	145	65
13461	X61045	Hydra sp.	mini-collagen	107	34
13462	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	130	46
13463	Y35970	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 219.	189	80
13464	L47668	Homo sapiens	alpha-2 collagen type I	64	39
13465	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	155	65
13466	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	76
13467	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	109	70
13468	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	144	69
13469	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	121	39
13470	M15530	Homo sapiens	B-cell growth factor	144	57
13471	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	116	83
13472	V00488	Homo sapiens	alpha globin	704	96
13473	AJ012166	Canis familiaris	brain-specific synapse associated protein, Bassoon	56	45
13474	AF116661	Homo sapiens	PRO1438	128	45
13475	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	99	78
13476	V00488	Homo sapiens	alpha globin	278	91
13477	W65762	Homo sapiens	Human HDCAF protein.	490	98
13478	AB033767	Homo sapiens	brain-selective and closely mapped on the counter allele of CMAP in cystatin cluster	2184	97
13479	AB033767	Homo sapiens	brain-selective and closely mapped on the counter allele of CMAP in cystatin cluster	2184	97
13480	Y42382	Homo sapiens	Amino acid sequence of Fx317_11.	613	95
13481	D29833	Homo sapiens	proline rich peptide P-B	61	58
13482	AK023277	Homo sapiens	unnamed protein product	488	98
13483	X67703	Drosophila melanogaster	Mst84Da	53	60
13484	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	135	54
13485	AF210350	Sceloporus siniferus	NADH dehydrogenase subunit 4	149	79
13486	Y14544	Danio rerio	Hoxc8 protein	98	36
13487	AP002032	Arabidopsis		111	27

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		thaliana			
13488	AB047846	Homo sapiens	gamma1-COP	4463	100
13489	M37194	Rattus norvegicus	clathrin-associated protein 17	739	100
13490	Y59743	Homo sapiens	Human normal ovarian tissue derived protein 20.	138	96
13491	U01317	Homo sapiens	G-gamma globin	198	90
13492	W04180	Homo sapiens	Cellubrevin-1.	459	98
13493	AL121585	Homo sapiens	ba504H3.1 (SNX5 (sorting nexin 5))	2058	100
13494	X53777	Homo sapiens	putative ribosomal protein (AA 1-184)	970	100
13495	AJ271881	Homo sapiens	bromodomain containing protein	3378	99
13496	AF132970	Homo sapiens	CGI-36 protein	878	100
13497	V73498 cd1	Homo sapiens	21-AUG-1997 Human S100P1 DNA.	273	100
13498	AL121585	Homo sapiens	ba504H3.1 (SNX5 (sorting nexin 5))	2058	100
13499	X82456	Homo sapiens	LIM and SH3 domain protein	1420	100
13500	AJ277932	Homo sapiens	RPB1 Ia protein	588	98
13501	Y53569	Homo sapiens	Consensus sequence for human RAD1 binding proteins.	633	84
13502	W73434	Homo sapiens	Human secreted protein encoded by Gene No. 2.	1903	100
13503	AJ005981	Sus scrofa	cAMP-regulated phosphoprotein	577	100
13504	AF116715	Homo sapiens	PRO2829	143	65
13505	U97553	murid herpesvirus 4	unknown	84	35
13506	X06323	Homo sapiens	put. ribosomal protein L3 (AA 1 - 348)	1903	100
13507	W82397	Homo sapiens	Human UBP protein #3.	4264	99
13508	M86246	Homo sapiens	EHS-2	110	71
13509	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	121	50
13510	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	91	44
13511	G03812	Homo sapiens	Human secreted protein, SEQ ID NO: 7893.	591	100
13512	Y04369	Homo sapiens	Human HUCEP-14 protein.	1389	100
13513	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	60
13514	AE000232	Escherichia coli K12	orf, hypothetical protein	1480	100
13515	X76717	Homo sapiens	MT-11 protein	382	100
13516	Y00919	Homo sapiens	Human Rab protein, RABP-2, protein sequence.	1039	100
13517	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	67
13518	AF090895	Homo sapiens	PRO0117	109	56
13519	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	109	65
13520	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	145	71
13521	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	93	60
13522	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	140	72
13523	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	130	73
13524	M15530	Homo sapiens	B-cell growth factor	112	67
13525	AF119851	Homo sapiens	PRO1722	135	57
13526	G00541	Homo sapiens	Human secreted protein, SEQ ID NO: 4622.	98	82
13527	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	117	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13528	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	100
13529	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	79	78
13530	AJ000536	Arabidopsis thaliana	COP1 protein	98	32
13531	U50403	Homo sapiens	breast cancer suppressor element Ishmael Upper RP2	101	62
13532	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	156	56
13533	Z80779	Homo sapiens	histone H2B	628	100
13534	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	62
13535	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	82	63
13536	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	93	56
13537	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	139	81
13538	AF130051	Homo sapiens	PRO0898	90	53
13539	X16832	Homo sapiens	preprocathepsin H (AA -22 to 314)	1835	99
13540	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	100	80
13541	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	131	82
13542	G00452	Homo sapiens	Human secreted protein, SEQ ID NO: 4533.	94	65
13543	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	141	86
13544	AF130089	Homo sapiens	PRO2550	107	72
13545	M36647	Homo sapiens	mitochondrial hinge protein precursor	435	89
13546	U63810	Homo sapiens	WD40 protein Ciao 1	505	100
13547	AF090931	Homo sapiens	PRO0483	126	73
13548	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	143	65
13549	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	82	62
13550	AF113685	Homo sapiens	PRO0974	126	48
13551	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	89	53
13552	AF116661	Homo sapiens	PRO1438	109	69
13553	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	101	85
13554	X16832	Homo sapiens	preprocathepsin H (AA -22 to 314)	1835	99
13555	Y73435	Homo sapiens	Human secreted protein clone yd73_1 protein sequence SEQ ID NO:92.	528	84
13556	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	126	65
13557	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	67
13558	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	189	75
13559	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	131	53
13560	AF118086	Homo sapiens	PRO1992	157	71
13561	Y00320	Homo sapiens	Human secreted protein encoded by gene 64.	101	64
13562	AF159055	Homo sapiens	leucine zipper-like protein	119	74

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13563	AF118082	Homo sapiens	PRO1902	83	86
13564	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	234	97
13565	Y59778	Homo sapiens	Human normal ovarian tissue derived protein 55.	66	100
13566	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	103	60
13567	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	96
13568	X83703	Homo sapiens	nuclear protein	1633	99
13569	G02473	Homo sapiens	Human secreted protein, SEQ ID NO: 6554.	242	45
13570	G00521	Homo sapiens	Human secreted protein, SEQ ID NO: 4602.	105	90
13571	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	80
13572	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	46
13573	X92744	Homo sapiens	hBD-1	290	83
13574	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	107	68
13575	AF107406	Homo sapiens	GW128	356	100
13576	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	101	48
13577	AF220264	Homo sapiens	MOST-1	95	73
13578	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	68
13579	AK024455	Homo sapiens	FLJ00047 protein	81	76
13580	AF130051	Homo sapiens	PRO0898	128	64
13581	AF084256	Homo sapiens	beta glucuronidase isoform d	142	58
13582	AF118082	Homo sapiens	PRO1902	85	51
13583	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	114	52
13584	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	66	54
13585	X52164	Mus musculus	Q300 protein (AA 1-77)	109	64
13586	AL359782	Trypanosoma brucei	possible (hvh-6) u1102, variant a dna, complete virion genome.	109	77
13587	AF090901	Homo sapiens	PRO0195	114	53
13588	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	95	66
13589	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	117	58
13590	AK000521	Homo sapiens	unnamed protein product	1313	100
13591	AL357374	Homo sapiens	bA353C18.2 (novel protein)	421	100
13592	AL357374	Homo sapiens	bA353C18.2 (novel protein)	421	100
13593	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	139	62
13594	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	103	56
13595	U16359	Rattus norvegicus	nitric oxide synthase	109	76
13596	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	88
13597	G00325	Homo sapiens	Human secreted protein, SEQ ID NO: 4406.	275	100
13598	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	108	63
13599	AF116661	Homo sapiens	PRO1438	128	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13600	X55682	Lycopersicon esculentum	extensin (class I)	58	43
13601	X52164	Mus musculus	Q300 protein (AA 1-77)	106	45
13602	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	122	92
13603	AF149419	Oryctolagus cuniculus	eye sodium bicarbonate cotransport protein NBC2	126	75
13604	AJ005567	Mus musculus	SPK21 protein	63	40
13605	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	150	96
13606	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	121	60
13607	G02867	Homo sapiens	Human secreted protein, SEQ ID NO: 6948.	85	60
13608	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	57	35
13609	AF107406	Homo sapiens	GW128	108	42
13610	D82345	Homo sapiens	NB thymosin beta	167	100
13611	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	59
13612	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	50
13613	Y32193	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 044150.	490	80
13614	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	57
13615	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	124	58
13616	AF119900	Homo sapiens	PRO2822	95	53
13617	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	124	58
13618	S79978	Homo sapiens	prion protein, PrP {octapeptide repeats}	88	42
13619	AF220264	Homo sapiens	MOST-1	130	81
13620	U16359	Rattus norvegicus	nitric oxide synthase	95	65
13621	AL132841	Caenorhabditis elegans	Y15E3A.3	168	85
13622	K01664	Drosophila melanogaster	Bkm-like protein	118	65
13623	M86246	Homo sapiens	EHS-2	100	63
13624	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	104	46
13625	AF067205	Homo sapiens	vesicle transport related protein	198	69
13626	U39529	Echinometra mathaei	bindin	72	47
13627	S79410	Mus musculus	nuclear localization signal binding protein	102	52
13628	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	123	54
13629	K01664	Drosophila melanogaster	Bkm-like protein	113	46
13630	AF161536	Homo sapiens	HSPC051	582	100
13631	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	158	87
13632	AF130089	Homo sapiens	PRO2550	105	66
13633	AF116661	Homo sapiens	PRO1438	116	53
13634	AF116715	Homo sapiens	PRO2829	101	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13635	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	139	63
13636	U33547	Homo sapiens	MHC class II antigen	154	79
13637	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	107	75
13638	AF090895	Homo sapiens	PRO0117	87	62
13639	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	131	69
13640	AF026689	Homo sapiens	prostate-specific transglutaminase	128	60
13641	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	128	81
13642	AC003058	Arabidopsis thaliana	unknown protein	210	67
13643	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	287	76
13644	Y73483	Homo sapiens	Human secreted protein clone y118_1 protein sequence SEQ ID NO:188.	376	88
13645	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	130	83
13646	Y87212	Homo sapiens	Human secreted protein sequence SEQ ID NO:251.	423	97
13647	U50403	Homo sapiens	breast cancer suppressor element Ishmael Upper RP2	103	86
13648	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	128	55
13649	X58521	Homo sapiens	nucleoporin p62	2610	98
13650	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	69
13651	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	111	81
13652	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	140	60
13653	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	121	46
13654	U13066	Nicotiana glauca	arabinogalactan-protein precursor	92	33
13655	S79410	Mus musculus	nuclear localization signal binding protein	134	50
13656	Y07766	Homo sapiens	Human secreted protein fragment encoded from gene 23.	156	100
13657	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	48
13658	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	171	80
13659	AK000017	Homo sapiens	unnamed protein product	611	100
13660	U90446	Mus musculus	RNAse L inhibitor	3100	99
13661	AE000882	Methanothermobacter thermoautotrophicus	phosphoenolpyruvate synthase	88	38
13662	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	65
13663	K01664	Drosophila melanogaster	Bkm-like protein	97	34
13664	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	77	41
13665	Y94890	Homo sapiens	Human protein clone HP02798.	325	98
13666	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	65
13667	AF090930	Homo sapiens	PRO0478	119	88
13668	AF130089	Homo sapiens	PRO2550	120	77

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13669	AC006693	Caenorhabditis elegans	Hypothetical protein W02H5.e	165	85
13670	W80293	Homo sapiens	Human translocation associated protein designated Gp25L-H.	1003	95
13671	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	113	91
13672	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	160	60
13673	AL132841	Caenorhabditis elegans	Y15E3A.3	178	75
13674	AF118086	Homo sapiens	PRO1992	85	75
13675	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	132	55
13676	AF220264	Homo sapiens	MOST-1	133	85
13677	Y19730	Homo sapiens	SEQ ID NO 448 from WO9922243.	122	51
13678	Y65416	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1577.	467	98
13679	Y16589	Homo sapiens	A protein that interacts with presenilins.	2286	99
13680	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	104	52
13681	AF090931	Homo sapiens	PRO0483	117	67
13682	X55686	Lycopersicon esculentum	extensin (class II)	60	56
13683	AF090944	Homo sapiens	PRO0663	93	90
13684	AL096770	Homo sapiens	bA150A6.2 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein (hs6M1-21))	178	52
13685	AF116661	Homo sapiens	PRO1438	115	60
13686	U62039	Elephantulus edwardii	reverse transcriptase	86	53
13687	Y13141	Bromheadia finlaysoniana	extensin	77	36
13688	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	114	60
13689	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	53
13690	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	107	51
13691	AC003058	Arabidopsis thaliana	unknown protein	178	85
13692	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	94	35
13693	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	78
13694	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	98	50
13695	D63163	Rattus sp.	cyclin C	111	86
13696	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	118	95
13697	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	80
13698	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	70
13699	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	93	58
13700	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	100	73
13701	M76744	Homo sapiens	BGP	112	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13702	Y15155	Homo sapiens	phosphorylase kinase beta-subunit	206	100
13703	AF090901	Homo sapiens	PRO0195	100	70
13704	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	131	79
13705	R95913	Homo sapiens	Neural thread protein.	106	36
13706	M15073	Homo sapiens	MHC HLA-DR-beta-1 chain	74	77
13707	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	35
13708	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	150	56
13709	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	89	77
13710	X70775	Chironomus cinclus	Sp12 gene homologue	85	38
13711	X80265	Hordeum vulgare	structural protein	96	41
13712	AB007922	Homo sapiens	KIAA0453 protein	147	64
13713	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	124	60
13714	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	108	65
13715	AF116661	Homo sapiens	PRO1438	120	77
13716	AF118086	Homo sapiens	PRO1992	127	64
13717	AK024455	Homo sapiens	FLJ00047 protein	93	56
13718	AF116661	Homo sapiens	PRO1438	137	55
13719	W48352	Homo sapiens	Human breast cancer related protein BCFLT1.	93	59
13720	AF119851	Homo sapiens	PRO1722	94	58
13721	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	124	45
13722	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	117	58
13723	AF161361	Homo sapiens	HSPC098	115	50
13724	Y95829	Homo sapiens	Native human Tie receptor signal peptide.	108	100
13725	AF118086	Homo sapiens	PRO1992	166	75
13726	AF116636	Homo sapiens	PRO1488	95	70
13727	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	70
13728	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	60
13730	G00673	Homo sapiens	Human secreted protein, SEQ ID NO: 4754.	118	63
13731	U33547	Homo sapiens	MHC class II antigen	123	69
13732	R59843	Homo sapiens	ApoE4Lx2 protease.	135	88
13733	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	138	75
13734	AF026204	Caenorhabditis elegans	C30E1.1 gene product	102	51
13735	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	117	63
13736	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	112	87
13737	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	115	58
13738	AF130089	Homo sapiens	PRO2550	122	70
13739	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	124	74
13740	AF130051	Homo sapiens	PRO0898	85	70

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13741	AF093748	Homo sapiens	KH type splicing regulatory protein; KSRP	91	51
13742	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	150	77
13743	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	124	82
13744	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	91	48
13745	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	116	64
13746	AB001684	Chlorella vulgaris	ORF54d	70	66
13747	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	140	60
13748	AF090901	Homo sapiens	PRO0195	92	39
13749	AF090895	Homo sapiens	PRO0117	148	67
13750	AF119882	Homo sapiens	PRO2492	91	45
13751	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	60
13752	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	129	65
13753	AF161356	Homo sapiens	HSPC093	99	48
13754	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	70
13755	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	120	51
13756	AF130089	Homo sapiens	PRO2550	142	96
13757	AF130089	Homo sapiens	PRO2550	132	86
13758	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	50
13759	Y19609	Homo sapiens	SEQ ID NO 327 from WO9922243.	92	60
13760	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	154	52
13761	U62040	Elephantulus edwardii	reverse transcriptase	134	51
13762	AB001684	Chlorella vulgaris	ORF49b	100	45
13763	AF118082	Homo sapiens	PRO1902	129	50
13764	AF220264	Homo sapiens	MOST-1	129	66
13765	R59842	Homo sapiens	ApoE4L1 protease.	135	50
13766	AF220264	Homo sapiens	MOST-1	115	71
13767	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	139	73
13768	AF130089	Homo sapiens	PRO2550	97	34
13769	U80739	Homo sapiens	CAGH26	564	100
13770	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	55
13771	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	102	68
13772	AE004507	Pseudomonas aeruginosa	hypothetical protein of bacteriophage Pfl	93	44
13773	AB044885	Canis familiaris	dopamine receptor D4	78	52
13774	AF026246	Homo sapiens	HERV-E envelope glycoprotein	108	53
13775	S71805	Homo sapiens	RNA-binding protein=TLS/FUS-ERG	126	100
13776	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	82
13777	AB015727	Mus musculus	truncated granzyme M	86	37
13778	G02832	Homo sapiens	Human secreted protein, SEQ ID NO:	74	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6913.		
13779	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	137	61
13780	M14123	Homo sapiens	neutral protease large subunit	246	55
13781	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	99	67
13782	AF132972	Homo sapiens	CGI-38 protein	902	99
13783	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	147	63
13784	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	68
13785	AF130051	Homo sapiens	PRO0898	138	72
13786	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	95
13787	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	92	53
13788	U12206	Homo sapiens	unknown	84	42
13789	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	118	58
13790	S79410	Mus musculus	nuclear localization signal binding protein	102	50
13791	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	137	76
13792	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	104	72
13793	AB006006	Bos taurus	neurocalcin alpha	1000	100
13794	U63332	Homo sapiens	super cysteine rich protein; SCRP	183	95
13795	W34499	Homo sapiens	Obesity receptor C protein.	120	85
13796	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	127	67
13797	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	182	83
13798	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	112	71
13799	U63332	Homo sapiens	super cysteine rich protein; SCRP	91	84
13800	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	105	67
13801	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	134	72
13802	AF119900	Homo sapiens	PRO2822	131	50
13803	AK024435	Homo sapiens	FLJ00025 protein	117	95
13804	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	142	53
13805	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	48
13806	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	98	66
13807	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	98	66
13808	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	150	54
13809	M37679	Mus musculus	Ig heavy chain precursor	70	100
13810	AL451015	Neurospora crassa	putative protein	96	55
13811	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	88	77
13812	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	71

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13813	AF130089	Homo sapiens	PRO2550	93	75
13814	K01664	Drosophila melanogaster	Bkm-like protein	119	60
13815	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	64
13816	AJ011435	Blackstonia imperfoliata	maturase	93	48
13817	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH 8c)	130	76
13818	AF119851	Homo sapiens	PRO1722	141	50
13819	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	74	60
13820	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	76	72
13821	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	135	50
13822	K01664	Drosophila melanogaster	Bkm-like protein	95	52
13823	L10908	Mus musculus	Gcap1 gene product	103	50
13824	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	146	62
13825	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	125	83
13826	L10908	Mus musculus	Gcap1 gene product	96	43
13827	G02971	Homo sapiens	Human secreted protein, SEQ ID NO: 7052.	102	64
13828	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	135	53
13829	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	142	70
13831	AP000060	Aeropyrum pernix	101aa long hypothetical protein	79	50
13832	AF119900	Homo sapiens	PRO2822	94	46
13833	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	145	40
13834	AF218028	Homo sapiens	unknown	117	57
13835	L10908	Mus musculus	Gcap1 gene product	79	45
13836	Z26876	Homo sapiens	ribosomal protein	129	93
13837	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	124	76
13838	AF044311	Homo sapiens	gamma-synuclein	603	99
13839	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	100	82
13840	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	154	46
13841	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	64
13842	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	92	62
13843	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	93	60
13844	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	63
13845	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	145	79
13846	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	50
13847	G03469	Homo sapiens	Human secreted protein, SEQ ID NO: 7550.	101	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13848	G03240	Homo sapiens	Human secreted protein, SEQ ID NO: 7321.	107	43
13849	U05313	Trypanosoma brucei	CR3	98	40
13850	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	100	65
13851	AF159055	Homo sapiens	leucine zipper-like protein	103	55
13852	R59842	Homo sapiens	ApoE4L1 protease.	99	71
13853	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	142	65
13854	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	79
13855	R59842	Homo sapiens	ApoE4L1 protease.	93	69
13856	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	114	76
13857	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	94	57
13858	U63332	Homo sapiens	super cysteine rich protein; SCRP	105	58
13859	AF289022	Homo sapiens	formiminotransferase cyclodeaminase form C	467	100
13860	AF078844	Homo sapiens	hqp0376 protein	488	100
13861	AB032436	Homo sapiens	brain-specific Na-dependent inorganic phosphate cotransporter	2968	100
13862	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	91	72
13863	AF130079	Homo sapiens	PRO2852	131	63
13864	Z29701_cdl	Homo sapiens	29-MAY-1998 Wild-type human c-Src tyrosine kinase cDNA.	2380	100
13865	L77967	Ovis aries	small proline-rich protein with paired repeat	80	33
13866	AL050318	Homo sapiens	dj977B1.5 (myosin regulatory light chain 2, smooth muscle isoform)	904	100
13867	U37690	Homo sapiens	RNA polymerase II subunit	358	100
13868	X13923	Homo sapiens	cytochrome c oxidase subunit Vlb (AA 1-86)	491	100
13869	L13848	Homo sapiens	RNA helicase A	6669	99
13870	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	133	46
13871	K02064	Bos taurus	cytochrome c oxidase subunit IV precursor EC 1.9.3.1	96	72
13872	D31763	Homo sapiens	ha0946 protein is Kruppel-related.	4606	96
13873	Z14014	Nicotiana tabacum	Pistil extensin like protein, partial CDS only	83	43
13874	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	117	70
13875	Z52203_cdl	Homo sapiens	17-SEP-1998 Human PRO217 protein encoding cDNA, UNQ191.	2135	99
13876	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	106	64
13877	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	50
13878	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	104	60
13879	L25404	Brassica napus	cyclin	124	42
13880	AL390114	Leishmania major	extremely cysteine/valine rich protein	139	59
13881	AC003113	Arabidopsis thaliana	F24O1.6	70	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13882	AB000098	Rattus norvegicus	MIPP65	905	50
13883	Z95114	Homo sapiens	bK212A2.1 (TNF-inducible protein CG12-1 (similar to apolipoprotein L))	1639	100
13884	AF132984	Homo sapiens	Nuclear pore complex interacting protein NPIP	551	82
13885	AF121862	Homo sapiens	Sorting nexin 13	1453	99
13886	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	83	69
13887	K01664	Drosophila melanogaster	Bkm-like protein	109	77
13888	AF217197	Homo sapiens	FBP interacting repressor	2725	99
13889	D38112	Homo sapiens	NADH dehydrogenase subunit 6	187	94
13890	AF118086	Homo sapiens	PRO1992	85	62
13891	M58664	Homo sapiens	Signal transducer CD24	371	97
13892	AK023443	Homo sapiens	Unnamed protein product	125	45
13893	AB040972	Homo sapiens	KJAA1539 protein	2271	99
13894	U03750	Escherichia coli	DeaD	95	48
13895	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	73	53
13896	AF078851	Homo sapiens	Secretogranin III	2384	99
13897	U62039	Elephantulus edwardii	Reverse transcriptase	109	48
13898	X07816	Human herpesvirus 4	Epitope C13 (57 AA)	55	53
13899	AF116661	Homo sapiens	PRO1438	146	48
13900	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	77	60
13901	Y28643	Homo sapiens	Human serine protease inhibitor from cDNA clone HETDK50.	2191	100

TABLE 3

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1	13902	A	1	114	434	AIPRCVGMFRIAMVNVCFVSSGSLLI*PLTY/GVYDEWTHPAYMTIDLLEIPITG SHPVVLNALFCLEAP\WISPN TGSPAYP VYPKSLIAHDFAVEATMPYIRLSST
2	13903	A	2	124	466	KSNIPNLGDCGWESLFNR\QSWRSSLAV \NDTYSSKKSNAETFTFPHADLCTLSDKD RPITTIQTALAEVLVHKPKATYEQLIAVL DEF\ANFLKKWKKAYDKENLFCBEG*KL CNAEN
3	13904	A	4	1	427	ESFLELLRTRNNHSSNLSQLTGTGGLFLN EQLKLVDKFLEDV*K*YHSETFTFNESD TE*AMKHINDYVEKGTQGIKIVDLVKELD RDTVEDLANYIFFKGKWDPRFPEVMDTEE EDFHVDQVSTVNEPIKMLLS\MLNIHPC FKL
4	13905	A	5	1	464	KIKSFYASKDTTKRMVRVTDWKKIFAY*I SDKELIFTLRLTKT**K*GKQPNLKNQG EI*VPISPODIQIAHK\HLEGWSTSLVS ELAPCEAPV/RHPLTGLTIAGLQGFGEA GRLVGRGWGC*W/VHPF*KYI/WQFLSK LHISLPYDPTTELLGTCR
5	13906	A	6	308	3	HFVHSHKDLALAHGLIY/PREMKT*VH TKTKCT*IFTVALSVIARANNQPRPLCS EWL\KYNVHTME*HSAIKRLNYRYKNNC VNLFLGITLSEKSTONVI
6	13907	A	7	587	2	FLTRTGDPDTRGSSSHANTQSRFFPDD PG\PLNNLGNTHGCGRRAGRCPTGPDG P\AGCGGPRCWPSGHLAATGD*OPSCGR LGANRGEAGPAGPTACSPGSCRTPYTH HFPASRMSCHLNCASPRTRYSQNGRGCE RVAQSQGAGGERGAKSQVVPVAPARNK DPAKCRPRNRRPQSGGPVVRAYRRGR
7	13908	A	8	1	474	RLNEENGKYGELNE*EVKWHLYTKSPA FDLHLHCYQKDWNGISTASSPAGVCTG NMDDEDDPSKWNFYSPHSYDPK*LTG FKTESRVRESDEVQIKVNDWDEEVISGL LTSLKDNVLKATGVLKYDAYK\YLCEHT RSTLKEESLKLERNLQNH
8	13909	A	9	3	539	SQCSFFTS PACSLTALAEETEARVHPR LCLSPNLAPSSGPPRPRPELAPCPSSQA GLRTCHSWVKGLHQLPDLVASGMKSTFCN KTYTCYPYPP/DPLCPNHSPNALTLPDS VTHAVFFE/L*SPSAPPSSTA*ILGSPS \CGASPCNHPSHPGICPTPPGLWVPVC CAPRAWQRDGTQT
9	13910	A	10	2	453	RL*LGLEYALLVWGTFRV*H*GGFFPIY YIVLLLSYALHQVTEYSMYVSIMAFNAK VSDPLIVGTYMTLLNTVSNLIGNWPSTV SLWLNVFLTVKECV*TSYQNCCTPDAAE LCKLGGSCVTALDGYVESIIICVSI AF V/W*VFLVHKFK
10	13911	A	11	20	475	KMGVPLLMSDPNRFLLPKNFLEKRTIS PPKTF*PLKIWVKQGVNLFLGPGFKI FPPVFKFFFFFFFFFF/RDRVSLYHPGWA VSQSELTAALTSPGSGQVILPSQPPK* ENHNLNGRGCCSEFLPRAEFLDLRSFS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9/15,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11	13912	A	12	392	63	IIIVIFF HIRADPGLEPRPSARTGLGPGLGCTMN KLGDAGSATQSLGGSQSLWSRREQL EQARWEAQ*QVETLGRVAREKEALAKEH AGLAVQLAA\AEHECIRTVEEATHLQ
12	13913	A	13	18	338	APHGPVQLMPMLLPRTGPGQFSLPSS RHGCHLE/GKEHESVTLCGGEPPPTFP PRDPPGPF*ARRAPCGRPT*AHPRALS RAAPQEPRALAGPRARHPICPGSL
13	13914	A	14	2	371	TTKQ*KDNPIQTGAKSLKRHECFKEDMQN ASNHT\KRSLTSLVREMHIKTTRMAGI KKSNNKHV*GRGIRT/LLRCHWDCKV VQLLWKTVMQFL*GLQYIHPDVPISRL GISLILYIALRTF
14	13915	A	15	443	1	SRTFLDTDMKSMRGFKAS*NRDTLLGA NAAGD\KLKAMLTNHSENRKILQNVYKC TLFMYLKWNNKAWMTAYLFTTQCTEYFK PTVETHCSEKKISF\KILLTIYNAGHL RALMQIYKEITHVVFVNIPISLQPIVQ NVISTFKS
15	13916	A	16	375	38	HQONGFLKKTPTLLQLQETHFR/CKDT KRLKVRRY/QPNSNQKRR/VPILEDK IDFKTKKIFMMIKDLTIINI*ASNTRVP KSMKQLAGLKEEMDNSVIMVGGFSYPV SIRK
16	13917	A	17	448	189	NRDRVSLCCPGWS*TPGLKRSFHLGLFK CWDYRRDIY*LL\FARHTQMISTHS*QT TNICSYPAF*KSRP*EPGYNTHTTHSS DML
17	13918	A	18	1	426	GMSHARSLLTINQLFKKCSLTVL/REM QIKSKLLASSSSSSRNSVSGGFETVGT HCQKCKLVQDPF\WKAUV*YLLKLVFI LFLIYNRAHLEDTCEVDRALFVIVKM WKLKSPYPOVKWRILKLYSHSVESSTAV LPKV
18	13919	A	19	2	423	YFETFPFLRLRGYGGTFEPFF\KPNSSC LGIEYNSGPDSCA*FFLQNGIRLVNSAN IRLMAMTLKTNQVALAQFLECKESDQOF CIGVTHVKARTGWA*F*SAQGCDDLQNL QNVTO/GAKIPLUV*GDFNAETQEA*K HF
19	13920	A	20	10	443	LKVDSDGSEVRVYFVLQHTITLMCSAYM NQLLNI FVRPSLLAVALHMTPGTKEDV YSCFRFLRDVFADEFILPGNTL*DFEE SCYLLCKSEAIQVTTKDILFTEKNTVL *FLVGLFKPF/VESYHIIICKSLLEK*A PFIEEP
20	13921	A	21	11	426	VLVETNNLRMGQVTM*PELEDN/SPDAW TLSDSPSQKIGHAQQ/KYSIIKWNYTE DWAQACLEDTSKYEQVTQIPMAPNDATL /PSS/AHLAFTAS*GAPSDS*LRNTLGL ICDGT\KPSSTN*KQTVIALQSHAGLN MKEC
21	13922	A	22	1147	1768	QLSMHSGYSSKSMQKMLCFLFNHHLQK GHCLPFVLSNFPPIIKYALQDMLML SQYSPSRBOEVSLSQCPGHFNHTAIS RECLANLKGWTKLLYQSAANTNGRIS SSYPVEPKKINSFEETAFTPKSSQMFR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PSVPPLVKTSLFSSKSLSTPDVVSFFGTP FGSSVMNRMAGIDVNTCYGS*AT*HSE W\LLNLSSLHYHVMCGVLLTTWYVSWI LFKIYATKAHVFPVQPPFAEGS*VPSKS VK*QSSP\LIKYLALQDMLLSQYSPSR RQEVFSLSQPGGHPHNWTAISRECLNLL NGMTQKLILYQEAATNGRVSSSYVPEP KKLNSPEETAFTQTPKSSQMPRPVPEPLV KTSLFSSKSLSTPDVVSFFGTPFGSSVMN RMAGIDVNTCYGSPQSPQLIRRGPRLN TSAS
22	13923	A	23	421	3	KIIFRAFKA*KSFSMPGFKA*KDRLLILL LGTNADNDFKRKPM\LLYHSKNPRALKN YKSIQPLYE*KKA*MTAHLKLVNVTY FKPIVGYTC*KI/SFKILLNDAPG\H PKALIMYREINIFMSANTLFI LQPMK GVI
23	13924	A	24	226	2	THERTHSKIIHVIIIXITHPLNPSILRP QTTA*TKWRDLSSQLPLP/PG/LKRFPSY LLLPSSWDYRCPLRPANFCF
24	13925	A	25	2	611	FFFFLLGLLKHGIPDVSPTGKYITTLPL MILMISGKIVV/DHK*HGRQNS/VR NTKLL*QDSWDTFKWKEVNVGDTVAKN GELLPATDVPMCV\YIATSNPDRETN/VK TRQALPETASV
25	13926	A	26	1	443	ATQWRPFLVPSAENNVNKAESFAAGIHA LGGTNINDAMLMVQLLDSINQDELVT* GSVLLIILLTDGEPTAWETNLMISIQNV REAVRGRYSFLCGLGLGFDVCYAFLEKLA LDNGGLARRIHEDSDSALHMQDFY\QEV AHPLVTAV
26	13927	A	27	2	359	KAQSKQWLPRGSSGFPVK/ARVDEESAKV IVRVYWEAQGILLIDFLKQRRITAYYS ENILRKPEL**RNAWGSFSRVLHHDRA AHFSHQ/TRAIG/REF**KTIRHPHY/S PNLNPLDAFCF
27	13928	A	28	2	427	WRKTVKGHTDQCRKHAK/LGN*IHFL EYHIHKHSIQYSGIQATQEFGLKTSY CSKD*YITVLDLTKISKNQVSN*HENP ISMYKN/IPTVIYGSKVIKDRKLKA*I* CP/HRNKKF*YDFYVLLNTMTPLKLW RIITEI
28	13929	A	29	47	412	HCDVLLASSRYTCILPYSDRDDGPDQDL KMSVDFRSRRTS/WFPQNSWGHMGVCG WGGAGRTLLDLIHLRIPMRGLRSGGLFCR RKLVSSEYG*EPSP/L*K*KGWGSSEPS/ LTVPSOL
29	13930	A	30	336	419	RLCCSGMISAYCNLSLGLSDPENSASR
30	13931	A	32	1	408	KIALKLRISYKISGY/MANTOKLIIFL YTSNEQIEFEIKNTIPTTAPDKI*LC TNLTCK\VOELVEKIKYKVMGNIKELNK WRSSYVGKSGKIKIKINK*MDIACSNL RRLKIVKISVLHNLIVRFNIVPIEIP
31	13932	A	33	412	2	QGHLSLQKFL\LPVPVQLCAPRGGVYRG RQDSLSCGGLHPF*ASGLLCLPQTASAM VGTPPFASLLLCSSILDCASNERGVS VEPPEFGTGHNLVCRLLRPLEKRSIRW KSAVGVARFSRCRPSWLPLARKKNPS

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32	13933	A	35	304	33	KVWGKVMYVQKMTQIVCNDRTESPQID N*SLTKEIQWRKDSLFNK*GNNWTPF SS/RSNLNKLDTAVTKIKSWVTDLNV KHKTIKLL
33	13934	A	36	2	424	SKTYSIGHFTYEGKGTTISLNGKVNVED AVGETLGRLLVEYPWQRFDFSGKLSS ASAIMGPNPFVKAHGLKGLTSLGDALQHL DDLKG\TFAQLTELHCDKLHVDPENFFL LG*VLVTVALAHF/SRRPT/ELQAS/W PKM
34	13935	A	37	2	433	NKRLPGPGF*KRPNPFGEGGDAKYFNPL GGNREIPLQPEV*THFGQNRPPVFLK ILKISGAFWGPFGVPTWCG*EGLNRCG PGYN*P/R/PPAPPPWG*SQAPFPKPAP PP/TGIKPNP
35	13936	A	38	3	425	GAQOLLVPSLPSAQRALDQLLITPWEN WTSIASLQHKTTIGRSWLTGPISATSS TPTSCVTASP\TRGHV*RSASWKYDV LQ HSSHMMVVHTAVYLGEAFHQVHATGSC H RVLSCCPTIGRSRDLA*QLLPL/HAL TEA
36	13937	A	39	2	463	LNEVRDILKSSDHWPSKTNFLHSPGFL SRFFEPQASVA/PR*SQQSLPGKAST SLWPPNPVFPVTSLSLSALPGLFLWLP SIPLPLPGSPFFSPE*PEVPLFGPTYHN PPSPPD/PTVLEAHQDQALP/PGVPTAE QRETPAP*AHRPS/LPLPP
37	13938	A	40	223	408	RNTV*NIGTDKDFMT*TPQAIATKAQID KWNLIPEMFSFC/TYRETIIGVTDRTYRD KIFESGR
38	13939	A	41	3	427	NLKMKSRTSKENIGEHIYDFDIGRFVNT *SKPKERKRLSKFTSVQEKTP*L*GHKK *MCLPE\LPYPKINSKWIHDNVRSKAHL LEEENRESSIWQRL/SIMPKAQAIKEK VNDLDFKIKNCVSKDTIKKALDRPSEK EKI
39	13940	A	42	30	448	FEMREIYVAPHSILLRYHGLINLRKFG* MDRYSKEVQDLLETWKLFARIVGPL*H DKFIESHALEFEILREIKLQYERTAGI TNFCSARTYDHLKKT*ERLKRMTLSE VLOQYQDSNACQWLRETY\IESGPNF
40	13941	A	43	1	928	LRQRMPQGLQCPWPFPPEY/PDSPLGC PGGLA*PPNPSWPKLASLAGSGSSAP PGVWGLVATGA*PLQRPSAPPPCP/R/LC PGREPCMCP
41	13942	A	44	2	409	SKSPDPTQQPLRGGLSLTHSAPGFSLOP LAQLTTPAFGPSTSSSLFNQKSSLSARH PQRKRRGGPSEPTPGSRQDQATVHPACQ IFPHYTP/VWHILGPQRHTP*SVD/HPG LDKRLLPETPGPCYSNSQPVWLCLTP
42	13943	A	45	3	136	LPMTLTFELE*ATLRFIWNHITIGIAKA ILTNQ\NKARGITNIC
43	13944	A	46	365	2	AWGSLRAPRASVPEPTGPVPMGNLAHR QFSPCLDGLSCPSFLRG*NSPPHGPS PG LPKHA*APAAVSPWVDPRTPVQPPPPAP PSTD*PHCSPPCCTPWCPRRLGSAVPM GCFASVPRR
44	13945	A	47	1	456	AELSLEYESSDLQNDVMPGEGDLPRK\

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						EEATGTRAAPFWVPATGAQQLLEEGPM EE\BEAQPMAPGKRS\LANGPNAGEQP GQSPGRRTSRAEDEA\EEFDDWEDDYD F\FREEPVKGARLRLFLPS*KTTPSPWE NRNTPLWGLKIFY
45	13946	A	48	116	442	PQNMGMERKPGPPKGLSWASGDLEDLG VMSVGFLSSPDDAVINRGPRKTGLIKQ FLRNGTGKVDYPMGDTQLGTSDEHLSS VATWAKAHLGEPGAFTFPORVSLRE
46	13947	A	49	434	3	FTVFGPLLTVTPIFISVFFKFLSPQIF NFTPFPGFPQIRV\TIIPISLRFFRKKP LFFFF\NKVELCSPYWNISARSWVPAAS VFQV\KESFYLNLLSVFPQVPLNVFLTF FFFFFLGRDR/SLPLFRMVWNSWAQAI LPLWL
47	13948	A	50	1	482	ERFPVQCSDFGKAFNMKTQ\LVVHQGVHT GNPNPYCRECGKAGRKQ\TAHLIAHA R*KPYGCSCEGKAFSSKSYLVTHRRTH GERPYECSSCDRAFCKGSQLIHQITHS TENHYECNECENTYPRKASLKHQKIDL GKKPF/ECNEWGKALLK
48	13949	A	51	1	470	REFLWQEGHRAFTVDEAGEEVLQILDL YADVVELLAIPIVANGTKTDKDLAGGD YATTEAFICASGRAIQGSTSHLQGNF SAWSEI\VLDEPEI\PGENQAFANSWLT TRTTVMVTIGHQDNMGL/LTTPRVA*VQ /MVIIPGGPKPAFLKQKQT
49	13950	A	52	26	448	SPGTEREYRIGQGSVTVGTVSVDDNSYV RIRGKSATVCERGTP*IK*GQDIRLTHVN TGRNLHSHHFTSPYGN/QVAL*GDIVI IL*RRKQRLKGFTEEGIKLRFKEVSFAF DEGEEDYLDWTVL\CNPGYVWRDGEVRF NT
50	13951	A	53	3	495	AMEVKFAETHIRGFTLNDAAANSRLITP QVRRHYLKEAATLTKTVLDHQHTPSRLA VTRVJQALAMKGV\DN1*VFHKLNLGL EDSIGLSKXMDFINNIALAQI*NSNLDA V*HIENMLTS*NNVIEPQYFGSAYLFRQ VLEEQLPTVEKISIMAERLAKPLO
51	13952	A	55	1	428	QERGTKKEMEDRMFLBETK\EQILKLEE KL*ALQEEKHQLFLQKKVLHEEERRRR KEQSDLTTLTSAAYQOSLTVHTGTHLS VQGSPPGHNRPQT\MAADRAKQMYGPQV LTTRRYVGIAAFAFGTP\PEHGQFGGRPGG VYG
52	13953	A	56	2	453	EDGDLDAFSSDEGLTMAMSYLKDDIFRI YITETQECRRYHRP\CAQAEAPCMVHFPI VICGCGYGPVGTTRYVSCVCPDYDLSSS CKGKGLHRGHKTALFSPFPHLSEGFH SRWLNRNVKHLLRWS*WEMGPPGNWSPR TSCA/GEARLGP
53	13954	A	57	3	435	ELNTSIFSRRTIEGLGLNTVLT\DNSNL VI\NRIGIV\PSVTEKEYTDPSSDQTYA WKIFSHETITKQA\LLKFLSYDYAVNNP WLAYPHYKSPEKCPSTILHDLRYLNLGL *CAASAMVMIAIVTYMVALLAYHRNGL TYMID
54	13955	A	59	409	1	LCCEHRGKTV\CVPRGKFTTLN\ASINKER

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						SKI SVLSFRLMKLKKEYVK*K*VEKEKINNRIRIEKINKARS/WFL*HNKIE*TIRMINHQKRENIQITDFRNERTELPDSDTIKKAIRKY*K*FYNNIFNPEENKFK
55	13956	A	60	1	393	GNVSSCGDHPCEG*LEPVDKNS*F*VPEACQTCIGEDGVHGFLESVWDHQ PCHICTSLNGRKDNCCTTQTCPTGKASTGLCELARLRQNAQDCCPENECVCDPESC DLPPVPN*ERGLQSTLTNP
56	13957	A	61	250	1	REDCKRVLYKDKVSLCCAGPCSAV*SLCKAASTFO/VKHFSLQSSVVRHAPPLA NFFHFLQORQLTTPDGLVLNSVWHAI
57	13958	A	62	365	3	IKKKLILWRLFPTFFPSWGGKTKKGIFPF*GPKKIPGIFKFPQGIKKAFGKRN*TLGNGN*KKKKKKKCGFGGDI PCS*IG/RNIVKILIPKAIYSFNTIHKIPKTFTEIETTILKFL*NH
58	13959	A	63	245	558	FLPTQVISYVKRLAEGAQI*CGEGVDKLSLPARNQAGYFMLPTEITDIDESCMTTEEIFGPMTCDFPFDEEDVIERANNVKG YGLAATVW/SSNVARV
59	13960	A	64	106	532	ERACQSGTSGGGVQPRRAIGAPR/E/DAFTGAVYIYHGDAGGI V PQYSMHPPA*SLYPSGQ/SVAARGNLGSDSFNCHN*GLQG LLLASSV*RPVMLLNDPIIYTTKN/ISGPKCHE
60	13961	A	65	2	548	VQKYPQQRKSCVPPVAEAWVPQSSRLKY RQLFNSHDKTMSGHLTGPOARTILMQSSLEQOQLASIWNLSDIDQDKLTAREFILLAMHLIDVAMSQPLPPVLPVYIIPPSF/RRVRS CSGISVISTSTVDQLRPEPVERDEQOQLEKKLPOTTFEDKKRENS*RGNLELKKRQALLQOORQG
61	13962	A	66	72	952	SRRTYTTSLFLFLKKEVTRKIRKYFTLNN*NTTYHNLNDLTKVVSFGKLLF*RSR*EYRKDKISDLCFYIOMLE/QRQVKKPKVSTRKEINKSRTO*SGKETMERPKLEDKFLVNINNINNP*NLN*RKKEGHICIFYRH*KDNKGYIYANNFNILDMQDKFFERYVTKMD/QEQIVSLNIPADKSNA*LNFPSSSSSSSSSSSS
62	13963	A	67	139	422	VNGNEPEPL*KGISRHEHRROPHNGFRPKXGGAQKQ*ASLGMKTPEAPAHSDKPERRQHAAYSS*AMPFLGICISFSQCNL/C PPKLVN
63	13964	A	68	274	1	NLKNKAVITKTA*H*QNTDQWNRIKNPEIN/HPFYGQLIFDIDAKNTM/WKR/DSNPNK*CWEN*ILTCKKQQLHP/SLTTNTKLNSQWIKDL
64	13965	A	69	22	419	KTIGEDGDT/PLSENAKSQRQIFSKDLVKLDSTINGVDIIDIYKLHHP/KWTVYTFSSH*GTFSKIDHILLDKTYPNNL*RTGTWQHMLSDIKVFKLEISTARKVTKS*HTMSLCKLTLEHPSGNDASAYLK
65	13966	A	70	57	423	KDKNSQVTSSEEEQSGKIKENLSNRDTR/CH/WIGRWIVIRLSFLPKLIFPNTVPKIRTOFPMKLNKPKVLKFIY*TKRTRIAKSLKKK/ROEGKISPTNRTTYEAYS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, Y=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
66	13967	A	71	394	1	TLESIGASMPSLDLG KHFRCLMQEDCRILLWFFSETGSPCAV SPRIECSSKIIVHSLKLLGSSDPRASLS *VAGTIGVHHHTQP*GI/CNI*GSGRR SEKQNIKEKNVSSSEAKRRRTF*NE*SV* KGDYNDQGLRLGTVAHAYN
67	13968	A	72	485	1707	SALGLSQRPFPGASDAADFSTPAGV*TA SSSAPAGEKDAQMEWARDPGPLHQAA PAPH*SHLVRDKRAQERLRKTSRGPFA HRSGPVDLSRSSHSDSTPVHGPYFRS APDPRGSAPAFRGPPIATRG/R/RAPRA TASHVPLSSSSWKEPEATAPR*ASAC MKWRLEAGCPGHRGVWPGPSSRLFMWA TATGKEKSTSPPTGVWRPGVEACT*AGS PTAHQHSQRTWQVPPTCINGSRSPKTS SYPKNQSKVGTVPKRGWACQPIPETAVR QATI SQ*ARKGAARPHHQARQVEHSTQ/ QRPSGDSGKFDORSLCEASTLLQPERPE VQKICKFRV/GERRRTASPNASVPEKR TRTQTMVGTAFIGCSGKMRVYSVRR/R SSPRIPPPVGSS\PLKTPPPP
68	13969	A	73	1	462	QDHRSSKSHSNRPSGLASSLSENFPCRA ADKPLGVNKKLSTELLAIPFCMGPRV HDKVRFVLVPLDQSLQSLDVSQKGV LTKRSVLKVACPLNALKSSLSKMSWYVG RVT*KYLL*F/YR/TNRL*SMGFAPR YLPBGDPAHLERN
69	13970	A	74	307	436	LP*VGCITGIEPGDMVRGKHLRQEK TRLIGPNCPGVINPGECKI GIMPGHINX KGRIGIASRSGTLTYEAVHOTTQVGLGQ SLCVGIGGDPFNGTEFIDCLEIFVND SA TEGII LIGENGA/NAEDNAECL
70	13971	A	75	1	435	EISDSKAQLAAMALI IDTWERMNCFS* NHEPLRTHCALAASKLLKKPD/QAB*RE HLCTSL\WSGTNTDKNGEELHGGKRVME RLKKALIIAHQGMDSLQVRVFIEILNR YIYFYEKENDAVTIQV/LNOLIQKILEDL PNLESWK
71	13972	A	76	58	366	EFPELVKDMNLHIEQAQCIPKNKINLKL MNRHRII/RLNTTTKKRILKAAQK*N I/T/IRGSSICMMDFSSEITDRRKNH SI*KILK/EKTQNCPLRVFCVKI
72	13973	A	77	1	445	YHETGCFLMGAI DVTLTFTNTYVHFQK MKGFSLLADPQCFVVDNSTSMSAPMLSG MGTQFQWSDIH\DNLSVTHVPFTDSACL LLIQPHYAFDLKVEGLTFHQNSLNMWK KLSSRTIHTMPQLALQGSYDL*DLDDQ A*LSDIITP
73	13974	A	78	53	444	ERKGYGAGPVAQQLVSTAPMLQSPPL GFADHTTPVPAPAN*ACPLPYA*RI TGPWHIIAHLDTTFTGDTTHPSSPASP STPMLPADFPCELPND/RPCLQPLLS SLTPRLPPLFCPELLAPAP
74	13975	A	79	1	353	HIRTELDYGLTVVYISDT*EAYNYIY IMVT*NVYKPOLWNI FDRATMHSQDVRH HLLCIRLMKINPKHAFV*/VLNGHYAFV SR/SFKHALVQYVQAFRTHPDEFLYSFC IGLTFIHM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
75	13976	A	80	1	350	LYFYALLFLSSG/CVAVYATRDNCICILD ERFGSYCPTTCGIAYFLSYHIKVDKDL QTLEDILHQVEDKTS*FKQLIKAIQLTY NPDDSLKPNMIDAATLKSMMKL*IMTY EASILT
76	13977	A	81	76	386	PAYPQVRGPASTFASCIRPTNARVLSTT PRKSVAEHSHVSPAHGVTISVIKLWS AKRLH*YGA/KVRPNS/VGCTP
77	13978	A	82	1	360	ESTLQEDTYLVNGAPNNRASKYMRQ/H LVELQRQIDESIICEDFNILISEMDST RPKISKDIVGLNGTIN*LDIIDIVRL* PTTAEKTFPSSSRGAFT*MDHILCYETH IYFKLHE
78	13979	A	83	39	344	WGTLGEGEYIWHVGGKSLRASGGLSQ PPRQPDSDRPLVLVPVCHLPHWIGPTD LGHKRQN/MGPQVAHVHCNPSTLGG*GE WIT*GREFETSLANMVKPC
79	13980	A	84	1	427	QQAHLAGHHRIHTGEKF*KCEACDRVYR GKSSL/MK/HRRRIHTGEKAYKCECHKV YSR/N/SQTVKDRRIHTGEKP*KCKS\C DKAFGHDSHLAQHARIHTGEKPYQCNGC GKAFSRQSLVYRQAIHGVGKLY*GNDC HKVFSNAT
80	13981	A	85	88	307	TWTORRAKLVRRIGWALLFPFRPSGSKP PP*TPPALPPCV/P/QSSPWTPPQPAP DSREVSQDWTQMRSFKEN
81	13982	A	86	5	375	NSLNTSHSRGPGASHCTFWLHERASSRD LTGAESYICRLRLRLISLIVFSKSIHG LACISILFLFLFLFFVKTGSMWLCPP WPQAFELRQSSLLSLSSWNYRR*PPHQ LIF\DPFCRN
82	13983	A	87	2	342	VTKNEDHYIMIKCLT*QEDQTLLNLHST NKTININIKHMTLQKAVKITITV* TCTSLSIIVACRLKWL/VEDLSNIN KLDM/DNIYKTLHLNIRDYTFLKHTWN IYKN
83	13984	A	88	1	338	CNEPRSHHCTPAWRQSKTSPSKKKKKKK LTTS/CIKASMKSRVQG*LR/CWAGVQG **GGVWLFLVK/REFPTSLINLSKQHS RRVPLGLCKKKKKKKKKKKKKKKKK KKFF
84	13985	A	89	931	2	VASPNALPE*LLPVSGHTDLERVGVAR LGQPHHTLTACRARMESRDTCPGVTILH P*PPSPSSSSPSGGPRTLTHQAGL EGSQGLQSQNSAA/PLGACRGWNEP QGPGSGS*GG*IMLRELRE/WQEAARVQ PTPG*PS*ESGRPLSSASGPTPGSP/ SP*PGTQGLCGHPSGLCATAAGPDGS GPTPTPH\VPQSCDRDSGPGQRLSTP LTSWPNTRSPPTGPGPGGRATW/PG S/PSPPQRESFSPQLPCCPTPGSFAGHPC AP\AAPSSVACPLP/PDGFRAPASSGI TTAPSPGDP
85	13986	A	90	66	464	LWVSSFFRLFLSHGSAESPEGDILWGL TLPLSPSPPLSCSHLSSTCARPRES PRFLCWRHPHPSKPPQ*VKRDCPS DPRVLSVGENPSAGPR/VFLRPP
86	13987	A	91	197	2	NAEIIAPQKVGFFIKIWINFFPPFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
						FFF*DRVLLCHPGMSAVQS*LTVASNF*F*AK*SSCLT
87	13988	A	92	317	2	SRTPTDFR*STRGLGPKCWDYRCEPPCPD TSSF*HLSLC*QGNL/VVGPDSIRMG AG/TRKTKWEGCHFLFLLRSL/NSVA QAGVOWRDLCPLOSLTFRFKRLS
88	13989	A	93	1163	0	FAPGFEM*YCSVAQAS/VOWYDLTLLOP PLPGVQSDSPASSLPNKLGLQGTSHHAW LNFL
89	13990	A	94	3	363	VLMFCRPAFSLGLNFFLYSWLRLOTFA AIRPGSTGRRLCLPNWVPTRNSLPFH*L VC/CSSRHNTYLQECTGHRPTYQLNIH DIKLLFLRFAMEQSFSAADTGGGGRESNI HLIPYIIHT
90	13991	A	95	17	353	PEPRYVGFISGGKVDIKTKWTKQRLE TVYTYGMVFINCH/VLKNITDSSWGTS*P *IQQHAGKRDNNYQLL/KLQG/QFSBAY TKCYSNPDSHTDVRKVYQDCPLLAFLND TS
91	13992	A	96	3	355	ANYPRDLCKVTDDEGGYTKQOIFNADQTA LYWKMP/SRTLMEREKSVSGVQASKD RLTLGLGGSVAGDVK/LKPMLIYHSENP RRC*SYSLPVLCKNN/KMTWMTAHLFTT WTECLNPL
92	13993	A	97	367	2	SLHFRARGKGVGVRMGERLPFSFOSWRLR L/RRLKLCRWQGPGRN*Q*QKPDGGA RASQTDGGGERRGVOTGSQAERTDTSRE TYSFPGIQREIVRVSKGKTGRQWQSQR QIQREKRVGR
93	13994	A	98	115	359	LNFFFFYLLNFMLLPHRYALKVSYFKKS LDRKLELLWNKYVNVNTLSSSSLTYS/ DYTCKECI*ILSKLHSRLISETLFHRK
94	13995	A	99	1	490	CVDPRVRTIFRKDKVGGLELLNLCTYYK ATVT*TWYWHKD/RTDQWDRKSLIN PCIYGLQIFFNYYFSQ*CODSSMEGNS LFNKWC/CRPLTLYTRIGSKWIKYLM*E LKLYRLSLHDPEFGNGFLEITSEVEITK EEIGKLD/LAKLKTFC
95	13996	A	100	195	3	SRCCQRHLVQWNRTERPE/YGRLIFFNK GVKTN*WGNLNFKNWYDN*ISTCKRM NLVPLYLSPYT
96	13997	A	101	1	371	FSLIKISMMLLNKMKEM*NLQFINN/HRR LQIAKARLNKKNKTEGITLDPFKIYYKA VVWYHKKRRHIDHNRLENSINRHICS QLILTKVPGANTKDHPFNEWSWEN/VCT KMKPDP/YLSSYTK
97	13998	A	102	6	370	KKGTIPNYF*RE*TDRSKPN*NYATKEN YI/FIS*KKIL*KLANKIQOHKKKPD NSLFYKIQFGSILETFITINQISKPKKEK NHIIISTDAENA/FDKIQH
98	13999	A	103	298	24	KCWISYLLFFRDEVSIGCCPGCAQTFR LK*SFCLSPKCDYRRREPLVGLDQ/L FLESNSVGLKKNVP*WFSNSSGSKG NHDAFCGIS
99	14000	A	104	2	352	GTIADFTQCCQADKACCLLKLDELPL QNGRLRS AKHRLKASLQKSGKRTFRW T*AGL IHRFPFAEFAEVSNTLFTLTVH TECCHGDLECADHRADLAKS ICENHDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
100	14001	A	105	139	361	ISSKL KHTEAF*MPCKARY\LEFGSLNQICALPE KTPVSDRKTCKCTESLVNRRPFCFSALEV DETYVPKELNAETFTTHAK
101	14002	A	106	3	350	ELEMIMLSEEVMLKAKTRQKLGGL/QPV S*VVNAKEKFLKEIKSATPVNTQMI\KN SLIAD/MEVVWIDDQTSNVLPSQSLIQ S/R\ALTLFSSMKAERGEEAREEKLEGS RGWFTFRKER
102	14003	A	107	225	1	QGIMMDTVEYVGKGEVPRVCWWCKLVAL L*KTWKLRLKLLK*\YDPAVPLLDIHP KEIKSIYORDSCISMFTA
103	14004	A	108	390	2	LGYSGVAPLEAEVCRFSLDKLRAGRTT TLFKADRGHLSLQRFLLTFDSLCP/AP RGQVTRGRQASLSCSGLHPGVGASWPRCL PTQASAWAGAPAAASLPPCSLISDCCAS NE*GSGVSGVESEPTGHN
104	14005	A	109	304	33	KVWGKVVWQKQNTQIVQWDRFTESPQID N*SLTKIQWRKDSLENK*\GANWTAPF SS/RSNLNKLDTAVTKIKSKWVTDLNV KHKTIKLL
105	14006	A	110	135	1	KQAILWPGAVAH/WSCNPFSTLGGPGGQ IT*GOEFKSLTNMVKP
106	14007	A	111	140	338	IMSTILYIGSICCYCYWYLD*\TLRLWTL ALVAQAGVQWRELGSGLPLP/PCLSLS SWDYRPP
107	14008	A	112	26	361	RSFFWVFFFEKKSLLLGPGGKGPPLN* LEPLAPGPKGFSGLNPLENGWPGPPC RGDFGFF*KKTPFFFGPGGVKTPNPG TF/BPKPKGVGFFGETPGPGGENLYQ WK
108	14009	A	113	11	330	ASIMLHIFLFLSYFLEKGPYVAQAGLN LLGSTGPLSASRAAGTGAHCTQL*TY LLLPKHGKAVFF\QETLLLRSTHFFPLK HVYPTTYELLVMDRDSLSRPR
109	14010	A	114	350	2	GCCFCLLFGSPPTVFGSLYSIRLVAFVR AVFPVWKAVP*PPVKM*FFHFLYFLPL KQ/VSLMHPGWS*LAQSQVSRFFPRSLP SNWYDYGAPPLRLTLFFFFFKSQGIEAM VLAL
110	14011	A	115	3	341	RNVIS*\FRDEPAPASQKAGITGVSHRA RPVYSLLLSNVPMVMDQDIYPLVDG YLSLPLVCCV*V*VLLCYPTWPLKRS SCLSLPSSWDYRHEPLKPA/SCCVLLSS G
111	14012	A	116	1	384	PSYPGDLTEIMDEGGVPCNQIFSTDDTF FYWKMPSTPLTTEKSI/GF*ASKNK LTFLEANVAGDFKLKPVPTYHALRNER TLKKYATSTLPVLCKWNNKA*VT/AHVF TTFTEYFKLSVETCCSE
112	14013	A	117	43	347	CAAGFGLL*TFPRT*TRKPRRGTYKPI SLMNNAKILKK/ILANRIQRIKTK\LL LQSDQVGF
113	14014	A	118	351	23	PNK*CWNNWIFTCGMNLEFYFTPTNTRI NAIKAIQLEENKEVNL*LGIGNGF/S RLPKAQMAKETIDKDFIKLKALCSK\N TIKKVKSELEKIPANHIGTSIQNI
114	14015	A	119	123	340	AADSTHSLTKPAPYLEKQNFPPFQMEYC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LIPLAEGPWFNL A*MQPPPTGFKQSSCL SLPSTDW*R/HWSPRLAN
115	14016	A	120	1	371	PSYP*DLTEIMDEGGYFNQOIFSIHDTT FWKMKPSTITFLTKEKIS/GF*ASKNK LTPLE*ANVAGD/FLKKEPTYTHALRNPR TLTKYATSTLP/LCKKNWKA*VT/AHV TTWLTEYFKLSVET
116	14017	A	121	82	367	YSKRNTI VAGD/FTPLSALDSSSRIRI NKTKSNTCTIDPMDVIGIYTVFHTVST TFSSANGPFSKTDHLLGYKTSKTF* T KLK*HQ/CIFSDHN
117	14018	A	122	27	253	MKTENILGENIGEVFGVGKDSLDMSPKA *TIKEKNLKLFFIKVKNFYSKHTI* KI KNQATVWQ/KLLTVHKSDR
118	14019	A	123	3	305	GTRQGCPLSFL*FNTVLEILVR*ISQNK *INKT/SLTADP/MVLHIENPKGSIK* V LELINEFSQVAGYKINM/OKTVAFLYTN N*LSKKEIKKTIQFIASKRT
119	14020	A	124	1	327	QVIFCLGLPKCWDYRHEP/RNPGLRGAD FFSLI*ILWEHMF*VMCILPHPCGDFWA MLNF*EREGMFF/CLRWKSHNVSA/G PQTPRFKRFSRLTLLSSWDHRHAPPHLA K
120	14021	A	125	74	334	IFEFGLVKVITCLSVSSHEVGKLCPPFF FFKNGV*FCCPGLGQYNGS*L/LELLK QSSCLSL*CTQDHRCLPPLANFNLINS SIH
121	14022	A	126	381	60	TVSQVLAHTCSFYLKAKAGGSLEPGSC YPGCSEL*SCHCTPANIT/SQTPSL*KI H*KKIIVKRAIVECVVYVYTIWLLI KFSDSI PFAQIINGPHEFPYMNQC
122	14023	A	127	323	2	RGFLGLSDEVSQQQLFSILSEIENQFN NLGCGGSC/LSI PKCWDYRQPSRLAY A*LIIFELVE\WVWGFPRIVQAGLELL TSSDLPLALASQNAWLGTISHHAEPI
123	14024	A	128	2	354	ENCQINILRFLRLRFRKEEYTKPTASRR K*IVNIRIERNGIEOKTIEKINELKSN LFENINKIDSHSGKMWVGE*CVFVCVC VREQSDRERETRLIKI*NERGIDITADL TEIK*LLILQKLNLY
124	14025	A	129	74	327	GELAMLPRLLINS*PCNPPA/SASLVT GTTDTPLYPAHY\IIIIIIIEMEFHT S\VAQAAMQWCDLGSLEPL/PPGFRFSS CLSL
125	14026	A	130	83	382	YEFHASDGGSRLLSQHFGFRPWKDYLSL EVEGQPGQHSFTPLGLSLSF/CFLME SCSIAQGVVQWPFYLSGLQPLPPRFRF *CLSLPKCNWYHGEPQL
126	14027	A	131	749	2	RQSLALSPRLCSSTISAHNFCLOGSS DSPASASRVAGITVHCHAKLI FVPLVE TRF\THVGO\AGLELLTSSDLPALASQS SGITGMSHHVQARCVIF/CGFTFKNQDM KY*KKKEKNQSTFLEHLQNOQENRHAH TLRHHTAS/LKSSEFLFAIRTSFLIS*K RSGTIGMF*YN/WTIGNGVEDRFVLGPP FGLGVQWYHNSLLQPSQSGLKQSSLSL PSS*DYRHWPTPSFLKFLRRMGLAII LL

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127	14028	A	132	371	1	KKNLNLNLTL*VKINTNWIMDLTIKYKI IT*KKQEKVGNLEQGEFSDLTTPKV*SI KGNTDK*DV*KPFSL*KPM*GNRYQATD *KKMSAKHVSNNKYP\LSRIYKFNDAKKN KPIRKWAKQMN
128	14029	A	133	2	318	NHKTILDKAKAFDKM*HPFTMKILNK* GIEQYAT/DIIKAMCDPTADIIINQEK LKAFFLRSGRRPL/LFH*IW*VLARTVR PKRKNKSGQEWLHMLTPTSLGG
129	14030	A	134	3	362	WSELGSSDFPALASQIAGITDMKHAYO PGTDF/STSVYETLPTQIRL*ALKRRFL L/EPF*IFASI*QFAKCSMSRNFLLPAQ PYVHWHPNEETEAGNFSLWAC/LRE DWIPTD
130	14031	A	135	12	398	KCSTSTVIREIQVTRTEIYHYTPTKMAK IKKPDNACK/WSGGGATKTLIHCW*NN/ SLEIWLFLMKFNI CLCPDEIVPLDLYL REMKTYYHENTYTKVSIAPLFK\QPKSP STGESINCSIIIPMECII
131	14032	A	136	309	1	QSEAPSOQNTKKQTKVGLTS*FOTYH NATVVIKTVWH/W/YIGIDIDQWNSQSP EINFHIHGK/LISNKAATNEWGKNSLF NK*HKDNRIFTCKRMKVDSSQPHI
132	14033	A	137	2	251	QCGKAPRAASVLRMHGRTHPEDPKPYECK Q*GKAPRASHL*MHGRTHNQE/P/HE CKECCGKPFPSAQNLRIQ*RTQAHIRMHS G
133	14034	A	138	396	3	LELLTS*SACGLGPKCWDRREPPHPAK MIL*SKSS\LPFLCSKCLNTI WALLLLL CSLVPLLTLPLKEFYAAH*SPDSLKYPV LQKLSKLEMLVLHETVQRKBOLTSYLYK PIFGFLVGYSFPLFCYSYKTS
134	14035	A	139	3	384	LDFTMKNCSSKELCGRYEKP*T/MEK MFARKHISNK*FIFRI*K*LSKLTKKK*A KDLNRYSLKEDIQANKCM/KKCS*LV IREQKNTNTRY*NGLS*RS/GOTK** QGWGOTPLIHCWEPHI
135	14036	A	140	63	388	FMYLFYY*LER/CLTIACTQVQCWCHSS LQPTQGLKH\PPASASGVATTIMPQ/ FLFFF*KRGPWCVAHARTI/WNLGSP
136	14037	A	141	370	3	GGGHFPALFFRGFGPLGFWPEITFALLE G*GGGFPGP/RGSGPPGQPCFLKXONF PGFV/GAPVVGPPGMLGRGTALNPEAE GSINLKGPPGLQPGGKTKLFPQKKKKKY QHFQKTQLILCF
137	14038	A	142	363	2	REKATEENFATS*DWLMMFKEGSHFHSI KVLGETPSADVETVVSCEPDLAKIMDED GYTKQIFNVGET\PSRTLITRKEKSVFG FKASKLQRIG*LLGVNAAGDFKLQSVL MDYSENHAE
138	14039	A	143	99	375	KNNQNINISPLVRYTLLSPLLLFFTIINS FFFFFSF/CFP*KKSRFEPKVA*PQGN LS*LNPRPKSGKEFSCLSQSTWITGSP PPHWADDF
139	14040	A	144	39	399	LQIITYNYIWIYIWIYIFWLSKIYKELL QINNKETNKGQKT*IDVSNMNMNMG* *LHEKIHIDIVIR*MRIKTIVTYHYMSTR MVIKETENKXW*GYGEKILLYCWNR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, =possible nucleotide insertion)
140	14041	A	145	358	3	FEK/SVWFPL REHTAEDRYEASRSWPRFKEK/SPLRN IIVQGEAATNGEVAVSYPEDLAKNID EGGYTQQIFNADETF*YWKMLPRTFLIA REKS\RLPSRDRLTLLEGANAAGDFKLK FMFIYHSDSC
141	14042	A	146	3	376	AVMGMYKINUVFVPTNTSILQPID*GVI LTFRSY*LINT\FCNTIGAIGSDSSDGS GQSKLKTFWKGFTIPKS\IKNTCDLWEE VKISTLMGVKNVIFPALIDLFERLKTLL EEVTAYMVNIGRRLL
142	14043	A	147	374	161	EFHRVSQDGLDLLTS*STCLSLPKCWDY SKWQRRT* TQ/DLCDSDE*SSIKPIQLC QELMS*MAEMAHQGP
143	14044	A	148	373	2	FFFFFFFCDLLFLFPKQPRSHASFSLPSV VPFPMPSSSLTLFYL FVYNLLR*YL/N SVTQAGVQWHDHGLQPRP/SLSSWDH WCTTPCPAN*IFFL*RVGLAMPRLLLN SWAQAILPLWSPK
144	14045	A	149	3	282	ILKRIHPDQVFFIPAMQGFNI*K*IN TV\NHIIRIKGK\NRMIIISLDTVKAFKQ IQQPFMI*KLGIRGNFLNLIKGTYPNP QLAGHSLGLCL
145	14046	A	150	3	360	DIIT*ESKFGQHHTTGQVQKLOYGIILFI I*EVFFPAGFWAFYHSSSLAPMPELGGH \VPDGI*FPLKRLVP/LINTSVLFASG VSVTGAHSHLIEGNRKQIILALSITITL GIYFTLLQI
146	14047	A	151	349	3	KKSSSGSHLETKSNRLPGSPGPFCKEIR KGLAWQEKSWPFYKPFLLVGGGRVIR GSRMTRHGHLIRSSKTLIKHHVPK*TVQ FNPCLFIFLEMESRS\VAQAGVQCNIG SLQP
147	14048	A	152	500	0	MPSRLCEGSA/ISDAQCNLQNSGAPSEF SSALNSPCG*DYRDTLPLPGYFLKFFVK TRSRYVTPAGL*LLASS\IPPTSA/FSK HWDYRHE
148	14049	A	153	373	2	QAGFTLLTSSDPPASAS\QSAGITGMNH RTWPGNF*PQKSCDSFVTKLMCTCHKNH IYAQSLVT*LGHSYIFF*DSLQSPPRP KQFSCHSLPSSWDHRHTPPCPARTQLHF GYEYFSRHLRRR
149	14050	A	154	332	3	THKFORLTSSKSKLKRKLLIFHQGAQKSN SLNPDIKNKLKRSORNME*EKIPTDHL SRIYRELLKLKAK/INLIKMGKGYFVEG DT*MDKHKIKRCSISPIIREMQKTTIR
150	14051	A	155	337	21	LGLLFFQRCAPKRGGI*RGSLAAVALL NCGELHPV*ASWMLCL\VPVRKLPTEAS VMGDAPPPTKLECPRSTSDCCDGSKNFE SVDSLGLSGVGVGVLDLPVAP
151	14052	A	156	21	491	HPGSRGCEPRSGHCTPANGTKVKTPAS TKTKGNKKK*RTVCLTPWHLL/RVWC DDGDSSSLL
152	14053	A	157	3	394	REDLLSPGFQSCCEL*LCHCI PAWVT/S ETLSQKXKK
153	14054	A	158	36	354	LSKAPTQLLGLKQNGVNCSEPRLLH HCTPAMATE*DSVSKKKKGFNI\PNPL SSLSFATISGQGFWEHLKNFGRALQGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
154	14055	A	159	78	340	GFOPILCPRPGRTHMSLKSPPRRP VVFHKAQRGILLAEIYPSGSGAGHSIEPK TITLFFLGKVLCCPGWSAVA*S*STV ASN\FGPK*LLCLSPSSSDSRVAFPHM ANFK
155	14056	A	160	2	362	HLSPILSIPQNRHCHHGPPFVSCWAHLPD GVVAGQGGSSLP/M*GRPGRGAPSPRR GGWGGGLTPHLPSSRGGWPGRGTP\PS Q*GRPGRGAPSPPRGWPGGLTPPPP SQTGRLAGRR
156	14057	A	161	293	2	PHLAIRPPTTVDKSAIYWKMPSPRTYKV RQKMPGFKSSKRLTLFLGAKAAANF KKKMLID\HSKNTKALKNYAKSILPVL CKWA\HKA*MSPHL
157	14058	A	162	2	136	LIVPILAMAFRLTERKILGYQLRTG PNWVTPPTGATYRLLS/P*Q*+LEIK P\LEPVCTITLYITDPTLALIALVL* TPLPIPNPVGNIILGLFILATCSLAVY SIL*SNRNGIPKTYRTKNSRLTYTTHRP ORLDAAYWCYVQTPIA
158	14059	A	163	1	464	RQGL/DSVTQAGVQGRNLS\LOPL/PP GLK*SSRFVSNSWDYRCAPPHANFPN LFFVQRC/FITMLPKL*TRS\GPD
159	14060	A	164	1	353	FNYSLSLGNKSETPQKKKKKKXGRGG ENPGTPTFGGAKGGNGPIKILKTGPK GGNPFCKKKPK*PHRGGP/HGNPVYRG GPGKNFVPPGGGGSGK*KSPIKPPGG KKGDFP
160	14061	A	165	45	389	FFVCTFCRERSLLCCRSWSGTGLK*PS CLSLPKFSDYRHKWP*CSARNFLPACPLA CLPPSLPSFFPPS/SPSSSPPROGVTVIQ VRVQWRDYGSLQP*PPKTRSFITLAFQD LGPO
161	14062	A	166	330	2	WDYRCAPPHVPLYLM/STFNIFFL*RG VTMLSRVSSDPPISASQVARIIDVSHW AQL*RSV/CYVFETGSGSLTQAGVQRYN HGSVQPHSRLS*SSHPSLMNRYFFPC
162	14063	A	167	2	396	YSNVLGITYPKELKTLVHWFICQ*NTFC IMPTITALPLAVES*CSSVGE*IGKWTY IPTMKYYSVMKRAISSHEKSTWRLKCI LPSESRCDRLQTV
163	14064	A	168	486	2	LIFGKIYKINSSKTDNKRKGTQIGLG MKTGDIMTY/QOTSKEYAHEFNNLEEM DQLFKKHRRP/RIHQVERGHNLGTGMTIN EFEFINVKTQKNQSGWDDFIGKPYQMF BEFLSENKTGELIL*S*YVSLTNSPYEA SITY*PKPDRO*KKQSCGPISFM
164	14065	A	169	200	3	GRVDLPPTQESRPPGPPSPDGVAQRP SIVRNCGLILTRGSPGPD\PSPLSS*AGL CGSPPPSPFS
165	14066	A	170	2	327	PGGICCGELR*HHCTPTCATERDSV/WN KIIHYIIMLASPNELILPLNLICLEIL* AGPLTAICISMFMATLFTIAGMSKQFK CPSTNEWIRKNWYIHIMEYVLHFMMK
166	14067	A	171	2	343	PGWSQTPDPR*STCLGLPKCWYDR/AA TVPGFLFLTALC
167	14068	A	172	367	3	FIRDVOFISALRYLLTPERMA/MIKKSK NNRYRCGGCK/RG/TLHWC*KCLVQP

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						L**SVWRFLKELPLNSVIFLLGTYPK/D KEVIYEKDCSILVFIAVQFAIA/RNIHP TYCPINE*IKKMWYIY
168	14069	A	173	102	345	YQLQNIPIRWVYSKLNLSFAFVLL*RDR VFLCLHGWSSLL/QLKRSFHLFLASSWD YRQVTPFRAN*LLFRD/RGLALLPR
169	14070	A	174	22	401	STRLSQLPBCNDYRCSSPATLTFPHS IPFLSQLQVQVHRRYFHLPELGNLPL LSKNVS*TY*KSFLS/NPGLRVLPCEVL FCFVGTQPHSVQARVQWNGHSLQPQPPS LK*SIHLSLSPS*DCR
170	14071	A	175	2	388	SDLQLKAGRTTALFKAVRGHGLTLQRFL LSF/V*LCAPRGGAAYRGQASLSCGGL HPGRAYRLSCLPKQAWMVGAPTASLS SCSLISDCCASNHRDSVGVGFPEPCAGC NLTEHRLFSPSGAVVSC
171	14072	A	176	334	1	KLELEIN*FNKVAVYKINTQNLQHCYTL IRTTQKGSCLKTILTIAPKRKYLG/I/O /LTKEVKDLHSESYTLLEIK*DINK*K DIPCS*MGMVFFGVCLFVFCFEMAFRS
172	14073	A	177	339	2	KNSPYNFPGKNGPGL*SLKSRIF/CWG STFAHIGELFFFKMGKKFPAI/RPFFFF EDRVLLCRPGCSGVVRSWLIASST/CLG WDRCTPPCLANFL*RGQLTMLPRLLSN SGLQ
173	14074	A	178	3	303	DLRRAACLLPFCWDYRHVPPRPADNSG FLHLII*VCLPLLCHAQLVIFFIETG FCHVAWAGLKFLGSSSPILTLA/PSKCWD YR
174	14075	A	179	342	1	INKLNIPTMAIFSTLIYRENTIPIKIPA GFVEMDKLILKLVWKFKAHGIGKTLKK NRVMSKAYYNATVSKTIYWNEDRNTNG WN*IDNLKINPCVCGQLIFNKDAKTNEE R
175	14076	A	180	2	323	STSVBPTGSHAFL*PQNVVDAETNS*HI NNVNLRLKIIKLEENTENKCHDLGLAT DYI/SVTPKA*ATTITDKLELTKIKNF CTSDDIT*KVKRQLIGENSCKSEFM
176	14077	A	181	326	3	RKRKKKREREREKKDEERKLYIGKDIK KRRKDTM/DWEKILQGVORQRCI*KI* RGVTOELKANPIRGGNNLNKVHRI*M ANGIMKRCPS*VIREI*IPTIMRYH
177	14078	A	182	5	326	TKTTEKAAN*IRRSRRKTKFKPETIKNR KTTTKINESKSCFYKKTINKTDKLLVKLI RKKTKTKIITKDEKNHTI*DCTEVKGM TECYEQVYANKEDNS\EKMDNFLE
178	14079	A	183	3	378	TVLCSFIVNGLDFPG*IHTIYSVFECY WNCVHNFILFRFSAIY*YLLIFVY*S*I MHLCLICY*LLL/CSCIFFWIFYMYLFS FWL/CPLYFYFYILCPFIFF/CIFICLL FFVYLLFFIFFIFFIFL
179	14080	A	184	365	3	MQLCKINKSISVQAGVQWVHNFGSMQGP PW/LHHFFPASASLVTGTTWARHOGGVIF /IFFFLMRRSL/DVSDQAGAQWHDGGS LOPLLPQFK*FA/CPCWDDRRAPQCPAN FVFLA/RHGFTILAR
180	14081	A	185	51	293	PVYVQASVLTNSFYQAS/I*KKSNIYRP ISLNMIDAKILNKQTQIKLNKVNDSRQT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
181	14082	A	186	326	3	GEDQIPKYCTVSDGRMMRDYFPLFSS TKIQWILNLGKKREFGFKKKKKIKCPN KRHRLANGIK*DPPTGCLQDICFRSKD AQRLOIKGWKKIFQKTGI*/R/GVAVLTS DNIEFKIKTVTRDRVANYI1KGSIHQ
182	14083	A	187	17	330	KDNEM*IKRTNRCYTSFTMAKINLKN NIKC*QG*GTTGT/L/LYC*WGHIVQF FSKTV*OFLMRSNKYLRYNPAILLGIY SN*VKI/C*KTYMRMFI VFLTKDWKQP NYSS
183	14084	A	188	124	357	SLWGGDLGGCGEKKRGENPGGPKPGK KKKKGGNLGARG/VFKKRGPKCKPGK KOEKGG*GAGI*GGCGNGVKKK
184	14085	A	189	333	124	RLRQENRLNF/GSRGCRFPSSRACFGW ATE*DSVSKTNKKWYSIARDCHAENS IVSFLSKRGCVFLP
185	14086	A	190	1	327	KSWLTGDNIPSSQSLTKKKGVNPSFKSM KADRGKAAAEKSEASRSWFMREKERSH LHN/IK*VQGKAASYPELASIIDBGY TKQ*IFNEDY/NWKKM*FRSFLTREKL
186	14087	A	191	53	400	VNLTGLPFHLFTTFVONALSNPTMYTHML TSLGPLHMSLQTGFPKPSYLKQPSPH SVFVGF/IPGMOR*FSIHKSVNVYHVI RMNDISHMIISKDT*KAFDKIQHIGSLF PALSL
187	14088	A	192	65	321	RARTEIYLHTLLGVVAGETRTGPGYTDC M*MPPTAPTTLVKTWI*PKSLSIGERIN KL/WILICTYMEYSAIKSVLTLTWTWV NPH
188	14089	A	193	127	241	IIKNDSSRICNLTEKLPLRKINS/WFGA VAHACNPSTLGG*GGESRITYNESRNKG EQTONNK
189	14090	A	194	1	337	DLPASASQSAIG*ESIRN*NLVVKRT LKCSQKDPKEDLNK/WKDVCSWLGRIS LTKVSLPKLIYKFAKIPKLYYD*KKN RFGVAQAYNSSTLGGRGQI
190	14091	A	195	2	333	NFNSLFFVEIEKLILKFLNLCQ\VARR ILQRKAVQGRILTLPFNFTDYKATVIKTA WH*HKDTMDQRNRTSTKINTYKGART I*WRKNSLFNK*CWQD/WITTCRRKVD P
191	14092	A	196	299	2	PHFORDVQPSPPSICRIFSPSSIPGQ SWFNIIQKSNVYHYHVIINTQHRSSSSS SSSSSSSSSY*LMKF/LNKIGIEGNF LILKAIHGKPTVNH
192	14093	A	197	2	199	LALSFLKECTGATAYCSLELLGSNDPF TLASKVF/GITGNSH*AQPQVFLLLYY FIFFFSSSVL
193	14094	A	198	226	2	KKFFFFNPNLKNFPLGRVFF/CSPG*K FAPLGFFLVSFLRQKVPHLGSPGKTF FFFFGDRVWTCPCNSAVA
194	14095	A	199	338	93	POHNGSCL*SQLFERLRAEDPLNLRVQG CNEL*LYLCTPSWVNPVSEKKSIOEKNA NLDFREY/RDKRRENTCV*NSIERSE
195	14096	A	200	1	361	PRSHLSQLRVLRSQ/TKKQKRTIGKQPR AIG/MGKKF*GKTLKVPFTRGVNQKF LKLKSLPRKKKTEITL*TLGKHFPRWE KFFATYPSSTRE*ISKICRLNHFTEKKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ITPTFORAKEL
196	14097	A	201	2	358	ENKTTMRVH*IPTRMAEN*VLAVOTL/L QPMWEYKRV*PLWKTNSLAVTLNINLP CNPITILLVGIYPRERKTYVYVTVACTQMF LTVLFTVAPNWKQSQGPSTGE*KNK*WH IHIMGHYS
197	14098	A	202	110	357	IWVFINCHFLPEKTSFFPGFPQCLDIS *KTLFVHVSVLFFFKDRVLLCHPGWSAVA Q**FTAASD/FOESSCFSPLGSDWYKRM
198	14099	A	203	2	374	ILKLHAFMAETPGACKTFCDLRQVIF IFIYLF/MRLSLTVAGQGVQWRNLGSL QPPPPGFKRF*GRCLFYPKDGLVCPGLA GS*TGIGKGIKIRTLSPDLCLSDGFCGSK PKS/ASASQGHVG
199	14100	A	204	375	3	LSSILIRGSFNLSLTITTEHLL*LLPS W\PLAII*FISPLAETNRTFPDHTGES ELVSGFNIEYAGPFAILFIAEYTNII INILTTTIFLGTTYDALSHELYTTTFVT KTIPLTSPALMNS
200	14101	A	205	393	3	SARLGLPKCWDYR/ASTVPLG\SLMLL LKSYSVMKKCE*LVKPLKAKL*DSCE L*VGNLIMPSTYDQENDRVDSLTWCL VLLLLLLLLLLFWRQSFALVARAGRW RDLSSL*PLPPGFRQFSCT
201	14102	A	206	2	377	FRVLQGRWSLQKFLFPFVQLCPAPKGG VYM*QR/SLSGCGLRPVRSWLLCLP TQASAMVNAPPARLLPPRSISDCYTS EQGSVSMGAEPGVGYDLLVCLLRPLE KSHIWRVSCFSRY
202	14103	A	207	327	1	ILTGNFKOTRMLTYHSVNPRLAKNYAKS TLFVNYKWNKA*MTAHLFIWPTGCFK PTVEPYCSKKK\IPKVLILLIDNAPGH PRALMKMPEEISIVFMPANPASIL
203	14104	A	208	310	2	FCWAFPMGFFPLGEGWGLILGGSFFFLK EGFPVGVQPGPKRWGLKG*PPGAIHWKG F/IFFFADRVSLCHPCWSAVAQSLTAN PASQVQAILLPQPDYRIR
204	14105	A	209	374	3	GVRDP/LEEVCVF*DLKLARRT/SLF FKAVRGHLSLQRFLLPFVWLCPAPRG VCRGTQASLSCSGLHPVRASWPLCLPTQ ASAMVGAAPSASLPCCSSISDCCASNER GSVGMGHSETDVG
205	14106	A	210	3	196	LENLKF/LDKFLETYNLTRLNQEETEL NRPMTSSKI*SVIKNLARAMAHYNPST LGGKGRRIA
206	14107	A	211	34	339	ITKSKRINVMSCELYFNINIDNFFFFET VFRSVI\KLKCYGAPMVHCTLNLPGSTN LSTASQVSGAINRGYPGQF/IGLEK*F LVKTGPFCHVA*AGLEPLGSG
207	14108	A	212	200	312	HYGQHFVFLCSLF*MSHSVT/QAG/VQ WP/SLALQTPPPGFKQFCFCLVSSWDY
208	14109	A	213	300	124	NHIFFFYQIHRVCVCVCVCVCCLVCV YRYIYCVSPW/RN*SL*KECLSLVLLT PTC
209	14110	A	214	1	357	QVDHTSDRKANLNM*FKIKVIQTMFSDY NFTENENNRKTKLTIQKLNST/L*I SNETNEKFPKIRYFENVINENTYQDL WDEVSIQAQINPSTLEAGRLLEPRS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
210	14111	A	215	360	1	LRSAWTFTE LTIETVCSE\KRTFFRILFDNLGHP RALMEM\KEMNVMPAKTTSIMPLI\S SFNSYYLRIRIHRFUVVQAQSWLQCPT AISDIQIGPVMGLLIPSAFVLCWLSI QQVS KLKH
211	14112	A	216	3	347	SSRSADGLFFYQCK*QTLYW*HLWYKT QKEKKTKOMKEKKQRIKAR\GDKLPEC EAVCGKPKNPANPVQRILVGHLDAGKSF PWQAKMGSHHNLTTGATLINEQWLLTTG KNLL
212	14113	A	217	75	347	PFIFRTARGKVTGWEYPAKG/CGGTF LGNRLFPNPGPSGPPKKQWEGALCA PG*KVCTLKF*FI\SLAIPNGSKNFFT LFEGBSPIL
213	14114	A	218	3	397	GGQGVSGTGHGGH\WHKMER*RLPFPK KKKKKKKKKKKKKKKKKKGPPKKKPR GGQNLKGGGKEKPPQKGVKKKTLSGRI IKKDKREKHTRGELWKKTFIW/EGSEKIG EKPPKI*DHEGKKKVLRGK
214	14115	A	219	3	401	DSWATLHGNIMK*SAVL*ALGLV\FGF TVSGPTGIVLSN*LDIELHDTYVVAH PHYVLSIGAVFAIIGLH*IPLFSGYT LDOTYAKIHFTIIFIGNVLTFFPOHFLD LSGMPRRYSDDPYDAYTT*NL
215	14116	A	220	162	3	KPAQRNL*SNPEKEDINILKRNQ/WPG TVAHACNPSTLGGGQKQIRSGV*EQP
216	14117	A	221	374	2	WCDREERERATEREREREREROTDRQ TDRRREA/EGWAAWAIN*GRAPGTSLE AALECSCTPRPPQAPPEQGPFFRTTAR GQPRPKLLOPEADPSQTRPHGYPWELRV LPQSGPEVRPRE
217	14118	A	222	3	264	DHMRPKVRGCSL*SCHTFAWAT\SES LSQKKKKKKKKKKKKIGEKI*GAFFKVAP PFFFFKKMNLKSPVGIAGVARNRWIL KHRG
218	14119	A	223	2	410	ATSPITIEELIT*HDAHALINILLM*FLGL HALFAVLTITLTNTNI*BAEETQT*TI LPALILVLRLPSLR\LIYSDEVNDPS ITIESMGHQW*TYEY\TDSSGLNLCY ILPPLFLEPGDLRLDGGDQVALPT
219	14120	A	224	399	3	GVGKPGFPWAKKNALFPYSGYPK*VGN LLLVKLLLLKKNPGENSLAETGTWGLP PKARAPLKPW/DSPKRNKPGAFKKKK KRQPTWEKIFANHASDKRLTSRIYKEL QQ*SKQPIFLIP\IYHNLHPKG
220	14121	A	225	360	71	NRTTWVPKTPPLLYHINTKK*HTGNC KHKTKRAKRRKTKKAKK/EKEKNHPHQ RPQRRK/EEQPKPKGKKRGGKKKPFK EYSYL*K\YHNTNLQ
221	14122	A	226	3	386	PSTHVSINLAWGIFL*ADAVIIGPHSKI KDALARFLPQGTPTPLIPILAIETISL LIQPIALSVRLTANITAGHLLMHLIGST TLTVSTINLSSTLIIFTILILLTL*IA VALIQAY/VCPPLVGAY
222	14123	A	227	3	372	YSLDSPSLTRFFTHFMLPFIISAALAA RLFLFHETGSNNPLGITSHSDKSTFPHY YTIRDALGLLLFLLSLMTLTFSPDLLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DDPNYTGSRNAPVVKQPRPHI\KPE*YFLFA/YTILDPFYKL
223	14124	A	228	2	263	PRVRSRWEDCLRFGA*EQ/LCAP*RDCHF FKKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKGGPFKKKPR GQNLKGGKKKKKFFPKRGE
224	14125	A	229	314	1	LKTTILFYQVSLCCPG*SQTPGLKQSSC LSLPKCDHRHRKPPCAQSFYFTTTERA LRVIY*FI*QSQ/LRSVAQGVRCGPG SLHPPPPRFKQLCSLSSW
225	14126	A	230	86	405	VSYMSIQDHENGHWSGYFLVUGQCLRV GIVGGSTFSSNSHSYIYFSPYLFPIFF EMGLSVTAQGVQWHKGLLQPPPG/LT *SSHLSPFRSDWHRPVSPPWA
226	14127	A	231	386	98	FFPQRR*FPFGNFPFFFPFPPKLQ\FSQK SPIGDFPPPPFPNPGPGFPFFPPFPFGK GSPFFPPL*FGPPGGFF*RAPPPFFFFF EFFFFFELLY
227	14128	A	232	2	362	TKVLVPIPVYEDLVQ*AG*SYSMVSYN LTRLQTLNLNVFPNIALALTLRLLYLHE TCSNNPRLITCHSDEVTHPYTYTKDAL G*L/LPFLSLMTLTLFSPDLLRDPDNYT LANPLNTPG
228	14129	A	233	5	365	KNVTPPNSSQHDLTIDYKNLYLMA*EY TFFSN/AHGTYTYTKDHNLSKRNLNKF* RLKF*RLKLSNGVLWPKWNQNTNQ*QK DNRKLSGHLKTKNTLNNP*IKEEVSWE ILKMYLREG
229	14130	A	234	3	367	NRIVPHDIPYFSLCVCLFFFDVRS\T LSL*GWSAGAGSLTAAPTSCVOALICL SLLSTWNYRRNPLRPAYL/SYFKSKSFT L/LPKGIL
230	14131	A	235	107	2	QBAYE*DKERSRRTYMEK/SIQPKFPN NRVKKWTKEINR/HFSKEDTQTKRHKM KC*SLICTSLVID*QRNAN*TPNEIRL IP
231	14132	A	236	349	0	NNL*IFLIFLFTSVFSLISLYFYIYFI RSLPICGLFTYFFSFYIFLKYMLTLAI YYSF*\VFSLIQVILFALIFI
232	14133	A	237	3	317	TRMHISDKTYNTNKRIFRIHLMRQTT QLKIGKRYEQLYKSI*FEWTINTYKEVK QLNSKRKPTNTVIRK*SKDLYKHFSSE DITQTRY\LKKC*ASLIIKEM
233	14134	A	238	346	1	AAQMPAYGEVEEATAGRKLGGSGSD QTMANDORFPMASAILS*IPDVVSTE VHARLSFDKYMSARA*RLLELSKEYG LKSGRIVI\KLSSTWEGLOAKELDEQR GGC
234	14135	A	239	1	279	LLFLFLPSLLLFPSPSSCLPSPSPS/SP PSP/S/PPPSLLHPPPSLLPHLPSLL DPPPTSHLLPSID*LDIPNAPT\NSSNP SCPCRPRSTYFK
235	14136	A	240	98	2	RRPRPRVLNS*\VKLSAHSLSLKPQWDY RREPP
236	14137	A	241	342	1	DTASLQPMDCGAYSTFNVYYL/RNIFH EAIAAIDSDSPDGTGHSKLKTF*KGFTI LDAIKNICDSW/EEGKISTLTGVKKKL ILTMDDFEGFKTIVGGVTADVETARE

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237	14138	A	242	3	339	LEL RKDSRKRRKRNKEKRGRKEGRKKFIRM TVHFSKKTVMK/ARRQ*NPVFRMLEE* KN\FPPRILYSEIIFGSEQIKKFSGD GNPKGSFPELPFLRIPMEVFNLEAYLR KS
238	14139	A	243	216	3	NSTGTOTQSQKFMLSLVKKLISFIYL*D GVLLFAQDGVKWRDLGSLQPPPP/GPTL FKQFSCSLPSS*GSRI
239	14140	A	244	408	2	VLTS*SNIAST\WGLYO/TOLR/KILA YSSI/THIG/WNNPVLQYNHNIITILNLT IYIILTLNA/FLVLNPNSSIGTILLSRT *NEIT*LPSLIPSTLLSLGGLPPLTGFL PKWAIIEFTKINLSLIPTIATITLLN LY
240	14141	A	245	3	243	IIMLKAGQMTVPFPNEDVWMAYKHTDRYS TSLVNMEN\QIKTTMGYYAPIIVAKLL N/SNTRYW*RG/CSRVHCRKRCR
241	14142	A	246	2	337	FLIMDLQKYINPKIKEPQEENKHTVSP MHNIAKILANKILVQI*FPKKNVSKF G/FIP*/SQGCFNINQCYSLDERKYM ISKNIKAEFNKIQHSSFMKIKNRKKLP EL
242	14143	A	247	347	1	HYTPTRMTKTQNTDNKICW*GGNG/GT LLHCW*ECKMQAL/WL*TVVLQFTKLN LLLPYNPITFFGIYPNEGRTHVHTKTCT LIFIIAALFIARTOKQ/PRCSSVDEMI NKLWYIQ
243	14144	A	248	319	2	KKTIILFTICTERVFLCCFGWSQTPRLKQ SSSGLPKC*DYRRESS\PGNLNVL*CL KFHLRVAMLFYFV*IVIFFLRQSL /DSVTRAGVQWYNLSSQLPPPGFK
244	14145	A	249	329	3	KFPFFHTGEAKNYAVPVNKRIRKKQHI HIIYNYGGHQKAECKEIAHVHCWWEYK MMQ/SL*KTAW*FLKK*TMELPYDPVIL LLRTYSKELKAGTRTDVCTSMCSFLFL
245	14146	A	250	316	3	KTHRTIMGTNHTPNKIDST*LNKLNLR AITTKLL/KNNRVSLHDLRIGHGLDMT PRAQAKKIKR*IDEFIETKNFCASQ NIKRV/NRQHE*DTMFANHIS
246	14147	A	251	152	364	QLTLSNHNQIKYK*TRHS\NHHHHH HHHHHHHQ*KRLP*SYKSKSQEHYTY GMDTGPKNLRTIFL
247	14148	A	252	230	1	PCWICEFTVSNFCWVLETGSCYVAHA RVQKCDNRL*PQTPGLKRYSCLSFRSG WD*RH/VPIANF*TLPRGVL
248	14149	A	253	3	345	DVGLAGLELLTSGBPALASQIAGITGV SHHSWPLLFFFFPF/CFEGGFFFPFL V*SQGDGLSGRPWPYFKGISRLRFPN EGKIGPQPLADMFCDKTLWSTVVP WFH
249	14150	A	254	194	1	GRVDTKWANTHERFSKCS/TTVD*WFK SWYLCTMEYYSTINKKELSFVTTWMHL EDIMLSEVS
250	14151	A	255	327	3	VKTAEFVNKWKQNSTKLWNSQAQIDKKK IVNQINDLRQTEIWMGDRIMNLESRIQM QCDWNTSDFCVTPQ\YNETER*WKKVKR HLEGREENLT*IVKLQDFEASQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to last amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
251	14152	A	256	314	3	KNFPLSLINFLKQSFAPNGQGGVQRVDLGSPOPLDSRVSRRIRLCPKTKQKKRFP*QTILKLSKV/E/MTERVLTAREKHLVTYK/GKPIRLTMDPSAETLQARRE
252	14153	A	257	2	308	RWWW\EEEEEEVUCGGEV*FFFFCFFFPFCFVVFYFLFPFCFFFIFFYFLFFLFLFPIFFFFFVFFIFFFFDFCFFFFFFIFFFFFFFVFFVFF
253	14154	A	258	52	186	CFGKLGWDDCLRSWGQCS*ACHCTPAAWT\NETLSLKKRRRG
254	14155	A	259	1	269	LKRSSHLSLFRSNWYRCMPGAFN*TFPVETGSHHIAQAHKL\PPASA/FPKWCWYRSHSLCPALDSPPTNINSATIITILQ GKCWHYC
255	14156	A	260	387	3	PLLQVAKINPKRILDLNVKPKFKICLQENTGENCWDFSGKDFLDMTFKMQSTK*QISKLIKINYFSSKTQ/SFCTTDHENFLEDIVKRIKIQSHKLEKRVNHIPIKRLISRIYQELFRTOHEKPHTIK
256	14157	A	261	62	72	LRIITKFSSESLKKAEMG*KLGLFHQAVNKCNSLTVNEVNAKKRFLKMKMSATPVKTHMIRK\DMKVLVWIDQISHNISLSQSLIQKRVLILFSSMKPARGEEAV*KNY
257	14158	A	262	2	193	GGRGCSLRSCHCTPAWVTRAKLSLKKKKKNSKP/RELGNKQFMGP*LRKGPTCYKRSPLIF
258	14159	A	263	3	330	QLKKRYEELYANKLGNPDEMDKFLCITLQKLTQHKN*KFFDKSRKSKMNRPIITNRLIQ*PKELPKRKTLPDGFGBELYHKHFFFKLTLPKLHFF/AKIEEFPFNS
259	14160	A	264	326	43	TQTEAGESL\DPGGRGCN*LGSCPCPTPAAWATGMKLPFKKKKKITSLPRLFLSYTCSSQNFL\LNDDTIHPVAQAKNLGDLGSSPTDPIQ
260	14161	A	265	311	1	PFEPF/SEPLERKEKFKGRKKRGTKRGPFPPFPFSSLPGLFP/SPORA*FLFPRFREFLKFFFPFVLPKPGLGKFFFPFPPFWDGVSLCRPGMSAVARSRLTV
261	14162	A	266	5	323	DSTIAQKNTVSTEFGEVGTLLHC/NVQPLV*KTVWVFLK/DVK/LELRYPALIAHLGI/YPKKNKT*TCQVNTALFIMTKMK*PKD/PINNEWVT/KLWYMTMEY*STIN
262	14163	A	267	3	293	GSLOPLAPRFK*FSCLSLL/SAGEWHEPWRSLQRSCHCTPSSGLYRAGLHLKNNNNNKSEVSRICTIGIFLFIY/CIYETESHSTV*AGVHWLDF
263	14164	A	268	3	332	HLSIINLVNQNSPLKAYTLFVNI*KKKWENY\CCLQEIHFAKNTYKLVKELKKFQANEKEKHADKTGFSKTVK\KNGHYIMI KRSVQENIYIYMFLLADPDIC
264	14165	A	269	3	326	KVLERHDVLKLTQ/DICNLNM/PYTKMESIVNNLPKKKTPLGLHSFTGEFYQTFKNEMILTSYNFSQKFEAEELNSPYEASILL\IPKLDKDIIRKEN*R/PNAKILNKIL
265	14166	A	270	1	318	PYPAKLSLSLKSGETGTF\LDKQMLKEFVTTRPALQELKGAINVLI*/LERKDHYQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
266	14167	A	271	1	318	QMCKH LKLLTSGNLPASASQTAGITGINHRAQP HLSFSL*LNWNET/CVPG
267	14168	A	272	108	322	DSHVIFLLCGNLTVFVCLFLRNLG/DSI THPGVQWHHNSL*P*TPGLK*SYHLSL SSIWNRYRTPLRLAFL
268	14169	A	273	341	3	GFFFFFPPFQGFLLAQVR/VPGNFR SLOPLPGVVKQFSCNLNLPN/WGFSKLG FFKKGCHFFP*Y*IFFMGVKKPKDKFSI FTNPPFFFFFETESVVGAGV*HDLGS TRP
269	14170	A	274	41	328	FWLLTPQGETERERERESETEREREREA GEAERGRETGIDSLIYSKLYSKTILHK ZLEYVATYFKALFYNWEL*TA/K/TRI IEKPSVRHCCQORS
270	14171	A	275	3	322	EAQELLVPGSGGCSRLSHHCTSRNAT KAKLRFKKKKKKKCPGRYLGNIVLG/PN LIAKCDKYHIVKLIF/CFSSAYTASIQK LIQVSRVTHRNKKKTROVVYILD
271	14172	A	276	175	313	STLISYFRDRVLCCVPGWSAVGQSQFTA A*NFN/VK*SSLSGSPSSW
272	14173	A	277	254	3	RPRRQFGIEGSLFNQTKNIYKSTANVI LYVDRLNAFSLISGTQGCPLSRLPFNI VL*LPVNIIRQ/EKVI*GMQIVKEELNL SL
273	14174	A	278	186	1	PETMQARRQ*SEIFKVLKKN/LQHRIL YPEKLSFQSEREIKTF/QLKKFITSRP ALQRLKE
274	14175	A	279	288	3	GRLRGKKGNPEGENSKFFKPLPGLG AKTQPVFKKKKKKKTRNPKK/WAKDP NRYLTKEAI*MASRHKRCSTSCVIREL *IKTTMRYDYVLI
275	14176	A	280	3	329	LKESRLSLSCSWDHFRALPMLSLGLVW NSCPQ/CDPSASASLSIGITGMSHHHTL *WLF/C*ETGSHPVTOAGMQWYDPSPLH PTKKGVYL/RRFWRGLGSPSAW
276	14177	A	281	233	3	ITTKDEEHHFTMKRSTHQGGITITNIC VPYNGSK*MK*KLTKLMGENR*/HSII IAGDNFTTFSIMDRAIRKSAKG
277	14178	A	282	32	309	LPDITPRDLHSPGTMDFIQETGCSKCWR GGGTPVCC*WECKL/VIQSLSRVTWRF LKKLIGQVRLMFPVISALMDVEVGSGP EARRSPAW
278	14179	A	283	1	302	CKRNNKAWMTHLFTAWLSEYFFPVTET YCS*KTIPETIL/LDDNAPGQPGVLVE MHKDMNVAFRPANTASILQPMNQQGIST FNSYYLNTFPKAIIVAE
279	14180	A	284	155	1	PRRFFFFF*DRVLLCHG*STAT*SL TTKASQVVRQFSCLEPPSSWDY
280	14181	A	285	131	15	DRSNPGRFLWTSNSSLVERPREIRPSSQ APPVNDPI*T
281	14182	A	286	1	359	FFFFFVVFVFCFSFFFFFKKGGAPGGG GPPPPKKTPLFSPQKNFTLQKPPPGK FKGGLPPNFGPG/RNGGLPKGDPHP PDFTPRWLFPKPP*KRGEFFPPPGFP KNLFLKKVP
282	14183	A	287	52	419	LEERAGTSWPKKENKKQHCFMKKKKKKK KKKKKKKKKKKKFKKGAQIFS*GGV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NL/H/SFGFVLKTTGGGGRHSPPPFPSP PSSFLFPSSSLPSLFLSLPLPSFLPSS PFLSS/CPFPFSS
283	14184	A	288	236	325	LNIRTPGSLXAVAHACNPSTLGGRRRTT
284	14185	A	289	218	409	KVKGNKADLIRSAAGS*N/VKGVLC HQY LEKSFCLTEFHSCLPQLVHPVDLGLLQ PMPGPIARF
285	14186	A	290	3	426	HEETSGPRLECSGMITAHCSLDLPKLK* SSHLSLGS/RHVPPCLAFLY
286	14187	A	291	382	1	ANFYVTLVQVQGFPTWLSRRPA*CDPP TWASQAGITGVSHHAWPMKMTITLGVY SPGESEVFSIFKFYFLETGSSFLPQAGA **CNHSSLYP*TPGLKQSFHLSLLTSV YRYLPPCPLCPVLV
287	14188	A	292	3	309	HEVVFYFTLNQOLEMIKLSKGGVLKAKMG \ISQIVNAKEKFLKIKSVIPVNTMIK QNSLIA\ETQEVSLVWIEDQTSNHIPLS *YLQSKFLTFLNSPKADM
288	14189	A	293	2	415	ARDQYKSTKK*AKDLYRHFKNEAI/HM ASNYK/KRCSIS*VIRKIEKSMSTSCY THLQN/ALKLKSDFKFC*OKCTAMGIL SWWECNLVQSLWTH\QNLLMLNTHKPY* SAI/PTSGLYPTMYRNIQASLRMFWA WROG
289	14190	A	294	335	108	IPTPK*PLSSPPIHTPYTIIKPF/RPPF P*HPPHIHPPPPPLTP\PLPHTLPTPT PTNLPHIIPPLYSIPPSSPKIS
290	14191	A	295	266	2	GFPRKVFSPFIIGPKLGFNSVFS/LFT FFNGLCLCKFFQFFPSAFLPLGFSFPF FFFFFFFFFF*DRAVLCHPGWSAVVRSWLT ATLV
291	14192	A	296	347	1	DSLQP*TRGLN*FPHLSFLTRWEYRCAP QCPANFC/VPL*RWGFAMLPFLVSSDLF ALASQAGITGVSHCAWLVLLSLFYI HFSKASETPWACNQSQTPEYPATYNFK IYSC
292	14193	A	297	284	2	CRQGFVLCRLVNSCDVLCVRLCV*VL GLQACAT*LGAEGVSI EFSCHFHKRGCL CRHRS/HSMFSAMC*PHTHTHTHTHT THTSPFMQLV
293	14194	A	298	1	96	GTRCLGAIITLFAAVALCTOKDLTKIV DFST*SQLGLILVTIGINQPHLSFLHIC THALFKAILSMCYITIIHILNDQDSQT IRRLNTMHINSTS\LTIDLSL*L/GKF FLN/GYY*QKDLTKIVDFST
294	14195	A	299	3	134	HEGRD*PGNHGDTLSLLKIQKLAGSGGV CL\KRLKLMCENHLN
295	14196	A	300	2	333	GVGREGGREGGEEESGWNGGIRERRRS KREEEGKEYRDEVDRKERGEEGRERER GRGWEEQKQAS*C/EGRVK
296	14197	A	301	354	1	TENELLRIYKNFYQIN/RYKQNSIKK *RK*QAI/TTETIQTVNHKLKCCISLI IRELQTKTR*ILYT*IVEKKLKTNGIYC WECCRELGS
297	14198	A	302	1	282	GTRGMVAGAYNLGLPSSWDYR*CLPFC LANFFVSLVERGETRLTTLVLLS*LYDS PASRSETAGIPLIHTSCIVYSLRNAD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
298	14199	A	303	361	3	IATLCKAQAV LPKWDYRHEPLCLATFFFF*AFPPVPL CMYVPPN/RVYAFFFLSSSF*ICCTFTL YIFPQLMDG*AVSSFLFLQPVGVKFKKK FFLSFFK\KRSSLGMLPRLILNSWAQVI HPPWPRPRA
299	14200	A	304	2	352	ARMVSV*PCDDPPA*ASQSAETGMSSH AQPIIIS*TIAYVSFSLSSLT*ISSVR SFTKMSQLLYFFYFVSL/PSFW
300	14201	A	305	334	1	KNSFFFFKRSLGLLAQI*/VQMGDFKT LQPLPGGVKQISRLNLLKKWDY*RGPSG LGKFW/IFL*KQGFQQLQVVLNFFFP/ CFETESRSVAQAGVQWHDLCSLQAPPP SSC
301	14202	A	306	270	2	DWCAGGGGGVPRRQVIFVLVETGFWR VQAGFQLASSYLPALA/FPKCLDFRH *PFSALKALFF*DGVSLLLPRLCNG ASSPRA
302	14203	A	307	306	2	HIFQCVCVVCVCCVCVVCVVCVVCV KLVISQT*LSPLCSGP*/A/CTTFSVCV VCVCCVVCV/CVVCVCVVCVSDLTNLS TLCSP*/A/HFFSVCSVCSC
303	14204	A	308	117	332	SPPVLLRCSLSLVQNGKTRFLK*LK MEL*FHSAPILLGIYPKGGKFLYQXDT/ CHSIFITALFIIAK
304	14205	A	309	1	351	GTRKTN*KNWDLRSRHSKEDIRNGO* V*/HMKRCSASLIIRIM*ISITV\RYNL TCIIM
305	14206	A	310	1	352	PSPPNPSFPLPSRPPPPPPPPPPPP PRSP*YTPAPPY/PSPILTPSP/PS DPPEPRSSRP
306	14207	A	311	1	405	FKPSP*PLTGALLGLMTSGLAM*FHLH SIT\LLILC\LLTNT/LTIYQ*WRDVT ERTYQGHHTPDQKGLRGIILFITSEV FFGAGY*AFYHSSLAPTQOLGHNPPPT GMTPLNPLEVLLNTSVILAS*VSI
307	14208	A	312	3	176	HEILGSNF/CGETQVSIHCPG*S*TR EQSSHLNLPKCWLHRA*TTVPLTTFH LGKPKHKVR
308	14209	A	313	298	327	SLTSLRL*KIRK*KK*KKCKQCKE GAPTHCWQCHQVPLNKS\W*LPKVK *KLSYDPAIPLV
309	14210	A	314	344	3	HSTSLVIREM*TKTNTVPTTTHKALI *KNRS*\WLGCKTGSLLHSW*KC*WQ SLWNTFGQFFKLI*ELTIPLLDLYLRE MKTVDHTKTCI*MFIVALFIIAQNVKMS LV
310	14211	A	315	18	321	WALFVYCLEKKEFGQPPRLACFFFNDR SLCLPGWRAVMGWSWT/VRPKLLAFN*S SHLSLSSWDYRLIPCSAKDSICEKNR VSTVDGADKKVRRGKEGD
311	14212	A	316	289	52	ETSCDVPKGLHFGKRNTHIMPEKAK GMR*YFH\KEDK*MAHIHVRC*TSLVI MKMQIKSSTPYHFIPRLTKPLKSANTK CW*TCIWIYLSMMKILSHALCPFFWH DVCISLSTEKNAPTGHITRRFS
312	14213	A	317	57	324	YCVTFFFGQKQSFVLSRLNCMGFFWVN CSLSLSLTWNYGLVPGTQPPFEFLVOR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GFHYVAQVGLKLLTSGDLLP*GSKGAGF TGLTHC
313	14214	A	318	65	341	QWLLKSRSYCYFFFL*DRSWAVAQA*VQW R/NPPPPGFKQF/SCVSLSSWDYRCLP PHLADFWEISRDQPDQHSSTSLKKKK KREI PNLPLGL
314	14215	A	319	2	182	ARGDYRHPPYTH*LETGSCFVIQAGL ELLDSSHPPALTSQCWDCICEPQSWAP CVSI
315	14216	A	320	345	3	MPFRQAHF/VFFIEMGFHHVARAGLELL GSINPPTSAQSQSSNDHR*SQSAWITGVSHHAQLGTITTSYHILLFLKKGRAHAC*SQ HDP*TCILHVNLCSSLLLAISRPTTTLN PRA
316	14217	A	321	122	466	QSFSTYC*KNWTT/CFLKSIDSYLVFY TKIDSKWIDLVNPKPTIKLLGNMGEN LCHMLSKDSDVTQKA*STEQINKFN SHGGTRLRSQPLKRAEVGRVRLSPGGRS YSDL
317	14218	A	322	3	345	HEDAVSAFCNLHLPSSNCSPASRVAE MTPVA/PCPANFFFFFLEREFGCCPG /CK*K*VFQKPKGKKKRIEGKKGVWG PKLKERERKKRKRKRKRKEVRTE MNNG
318	14219	A	323	206	446	GNLHQCYPYKWLHLAKYCEKQDSIC*IL KECYKPLLEKSHLIAQVENEKPADW/ PLLRGEYVWND
319	14220	A	324	62	327	VERLLRDLRENFCRNPDSSEAPWCFTLR PGMRAAFICYIRRCTDDVRPOGEAQAWG LQSRAGSLPEGRGEVSA*W/SARTRHR
320	14221	A	325	441	1	RKKK*TLQGL/EPFLEHVASPHRDHRV WPRQGLFSEGNKATMTVLYPEE/S SKKLGSR*GSE/CTAVRITLVGYVA YTGAPVSTSERPSAIIYHRMNKH*HQHR RHLLGFSEQEPVQGVPELQSSGQPKPEF QPSPSNPAPRA
321	14222	A	326	2	358	ARARTLRIMVNLNYSKSTLPVLCCKGNK VVWTAHLFTASFAEYFKPAVETTCLEKI FFKILQLIGDACHFPRPMDMHKEVNVF VPAKTSIQQPM*\ISPFKSY*EITFQA GCCGSC
322	14223	A	327	1	430	ARENMPGHLHRCITIEQDNRTHMLPKLN TQMIKIV*YWKDHYVDTE/YNNIESTE VNLICYGELIFSRSAKIIQWNGKRIVLN KWCWDD/WNL/SCSKM*MDSYLTCT/K ITPWIIINPTGRAKTRMLLP/EKTGVSF CDFG
323	14224	A	328	146	374	KCLMLTKPYINMRLT*PYEIR*/CGDTF P*SYIA*TGTAVRTWGLTFVIPAWEAE AGGSRGQEMETILANTEKPL
324	14225	A	329	2	322	ARASRTFIVRKTOCLASDKLTLVRG*C SCDFQLKSMILIDYSENPRALK/NMLYR NNKAWMTLGLFTAWSTAKPTVETYSQ *AKTTLKIWL
325	14226	A	330	350	47	ENGFLIAGAGLELLTSGDPPASAFQSA GTTVSHRARPAH*KKK/CLKT/RVFL CPGWS*TPGLK*SSCFGLSHMNYRHE PPRPAQFLIDFVLYRHYRES

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN: 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
326	14227	A	331	753	458	FFFVE*GVL\HVAQAGLKLTSRDLPTS AS*VAETSTTHHA*LHLNFKEYFCKE QILLCCPGWSRTPALKRYSHLCLPNSWD YRHEHCNEPEEISLI
327	14228	A	332	256	3	TLVLMQSCSLSSWDYRHKPF/*LSNI FNLPMLSGHNPIINGGISVSLDRVVL FLEF/LCFETGSHSVAQAGVQWHDGSL HSC
328	14229	A	333	25	358	TPDLR*STCLSLPFCWDYGHVPPHANI FT*QKLFPSIDGQYANLVWFEGGTFHT *A*RNHHYSXLRKDQTIIFLYLF/LR WSL/NSVAQAGVQ/WHNLGSLQSLPPEF K
329	14230	A	334	3	329	HEDVVSFFWPGWSQT*PDLR*SACLGLPK CWDYRREPPHLLALNAFLT*NIFNL*W/C LSGSNPIIRISICIRFLKGG*LLFIFIF VWFITQSLTHSVTAQAMQWHDLSQ
330	14231	A	335	26	330	SQLLGRPRQENHLNTGGECSL/CKITL VCFWLGHL*PVWFRCL/LVLE/CVVSIG FNFCSVLV/CWFLLCFFCAFMCLFY* WFIWCHFLFFFLFYFFVMFLFF
331	14232	A	336	3	348	DEVFS/YH*HMLKC*GDYSLFHGES DLDITQILTHPSTTAMYFVHYCOS* IL YGTIDT*PPVIHRNPINIRTPYPCLOAS TAINLQLSHMNCNSKATPHSLGHQHTYP PLTV
332	14233	A	337	2	329	AAAAAARVIGIAWAYHLIGKLEPFFF MALLFLR*GL/NSVTLARVWVNHGSM* A*PPGLRCMSLCPA/NFLYFLVE/IGFA TLPRLOAICLGSSDLPTSTSGSAETGV S
333	14234	A	338	60	354	NGKECKLIYLSIYLSIYLSIYLSIYHL C*YL/SCLSI*LSN*LAVVYLSVCLSVS VCL/VASCL*ISIYLSIHLSPYSIDRTL AHHCVPPTCSLPHATH
334	14235	A	339	1	351	RDADVMLLQILVTFQALALGVQTEGMAG VTHDRVLYVMWVR*PQCL/HRV*SNGT PAVGTSASRPGCLKSSHPSLPSSWDYR CBPFCPVE/CFV
335	14236	A	340	190	358	FGSLVFF/CFLETDSRFAP*AEWQGP NFG*LNPPPPGLRGFFGLSLPGTDGYP V
336	14237	A	341	306	119	LRWENHLSGN*GCSEF*FRCTPFWMT E*DSVSKQKQNNLKLKPGSS/CVVF LPETLPT
337	14238	A	342	1	122	GTRGCGEPRSRHCTLA/W*QSKTPSKKK KKKKKKKTKGPPFF
338	14239	A	343	92	316	VCWDIPHRKSRITCILFYPLVILFPEFK ICSSFSF*KGCM/WLGAHAHCNPTLGG QSGWIT*GHE/FKTSLA
339	14240	A	344	83	329	ATAPAPCYFLILCYCMNCVCMHTSVCT /CVILCMCMGLCHIL*TCVA/CTCLGMR FLLPAHI IICVKRFLCMCGSGNSGSLCL
340	14241	A	345	127	357	YGVLSRGRVLPFCWGF*SRITSGF/SSPEA NSWPPCLANILYLVETGFCHVAQAGLEL LDSSHPTTSASQSAEITSMN/HRA
341	14242	A	346	312	1	LMNLNRSVGLLTRGVKCHKAFRTISL LTGALK*QSKSDGLISLKVVDLNNND

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						IYRSLLRQSEEDTS/KWKDTPCS*TGTF NIVKMSILTKAIVRFNAS
342	14243	A	347	350	243	FHHVGGDGLNLLTL*ST/PCLGSLPKCWD YRCEPRLAY
343	14244	A	348	165	338	HTLDPSASHEGPTFLFSL/PVEQCLK*LT LKVATIVLPCFCF*DRVLTCHPGWSAVM QSO
344	14245	A	349	328	2	SVCPHGSINLSPAETTGACH/RRLA*NI DSRV*AKTFKGK*INCSYNNNNNNNN NNNKFLLLRLAGDRHPDQLCPPRRCH FNGATPAGPPSCSLRRSHSSAVCSC
345	14246	A	350	3	338	HEIEELITFHDRLALINILICSLVLVAL FLTTLTKLTNTNLIHIAKEIDTVRTILPA IILILIA/LPFLRLIYITDEGNDPSL/TI KSIGHQNY*TYEYTDYGGILFNSYTLPP
346	14247	A	351	124	382	NTFKS*NSNKTNAIRT*AKUTQHQFTG EDIQIANHKMKRCLIPLGR/SLNQEIS PRVRINKIRPGMVAHTCNPTLGGWGRQ IT
347	14248	A	352	3	368	RDRASLFCPGWS*HPELK*SSCLGLPKC WDYRR/AATAPGLLCL
348	14249	A	353	390	161	FSRDRISPRWSGWSF/DLRLSP/CLSLP KCWDYR/R*ATMPGTFFHFNLNQDARN QIITCPNLTKNYIYMTSSFFILVHS
349	14250	A	354	123	345	LAPQHFASLRLAR/PAGFPDCRPLAPP RPS*FSPAPLPFGADRSVPLSPSPVP* LPPPAGAPPR/PPPPRDSPPR
350	14251	A	355	37	393	TKHFVSTCYVPEFAGTINQRKRNRISVL ANVKDQIILLRVTAITEGYRNYHVLV LVFVCFSPPKQGL/DSAPQAGVWHNH NSL*P*TPGLKSSHLDLQSSWYRRVF /RMSSVF
351	14252	A	356	2	335	ARETSKDLTLLGAMAGGDF/KLKPVL LYHSENRLPKNYAMST/LPVL/KWNKA *MT*HVFTWLAEYFKPTVQTYCLN/K FSILLINNPLSHPRALMDRFKETIGVLM PA
352	14253	A	357	199	377	VGSSCFLKVCQ/C*AVCVGVCVCVCV CVCLRCV/CVCL/CV/CVGVFFFLVLCG CGCVVCV
353	14254	A	358	1	335	GTRITCMYHVPPRSANF*LVLERWGLPM LPRLVANSPPQITILLQPTVLNPERT SALY/YRPLDLLSPTSLSPPRSPSLTS SLSIPAPPRSHLAPPPPPPPPPPPRPS A
354	14255	A	359	3	369	KPSP*PLTGALSALLNTSGLA/W*FGFH SITLLILGLLNTLTITQ*WRDVREST YQGHHTFPVQGLRGYIILFITSEVFFF AGFF*AFYHSSLAPTPQL*GHLPLIVII LLNSL*FPTLY
355	14256	A	361	337	121	LWSQLGLRLQEDCLSPSPSGGNKP*CH CTPANVTE*DSVSKGKVYIHNKKSL KKK\NSCNMQQFGGT
356	14257	A	362	256	375	EKKTTVQYPTYGINV*KNLEAKTKPGP DGFIDKLYNTERGETTSPHILF*PKE VAVLLNSFSK\AASITLTTPKPKNDIMRK ENYSPISSTINWQCSFFLEQIFPLSFKL NCPGLIIFH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
357	14258	A	363	170	1	SOLLRLRSQGAHAWLIVFVSVDTGS HHIGQAGKLKLS*ATHPPCPPKILARA
358	14259	A	364	330	3	RIMSASASQSAVSDMSHDVRLIDI*HE P*FYQALYSFRQ*ITSSPSYR*SYLLSY KWQDEARC/AFVTAQWAEAGGMLEPSRL VLDS*PRDLPTSASQAGITDMSHHSC
359	14260	A	365	1	341	SOYGLDFHDLSDLPMTASQAGISGVSH RAWPASQ*FYVSREIVCSYRL*GYTPSL LVLESGSSSVTQAGAQWNNHSLILYPHTH GLK*SSCLSIITR/WDYRHESP
360	14261	A	366	2	338	ARMVIS*PRDLPTMASQAGITGVSHR AWPATGKFYVSRGVICFII*KDTHLFF/ CFLETGSSSVTQAGAQWNNHSL*PQTP GLK*SSCLSIKFC/WDYRHESP
361	14262	A	367	2	337	ARAGILRF*QRKCKSRIPGWNVGYI LKLAGITHTDPAIPFLVLYSEMTTHY *KTSMRNCITTLFIMAIN*FKKS*SEE E/IGKFWYPT*LLYNNENEHLQHTTW IN
362	14263	A	368	59	348	SAPGIQENMPAGGGGSHL*SQHGRPR RVDHLRSQGVDP*LDQR/GETPSKKKKK
363	14264	A	369	350	3	GWSQTPDLRWSTHLSL*PKCK*DYRGGFHA QL*TLMYKYLFEHLLSVLLGICEPEWVC /DHMAILLCLISLGTVLSSKALHHTYFS PVTCKCSNFISLSLTVTPHCFLNACYF PLFSRA
364	14265	A	370	908	30	ECSGTILAHCRLLPLPGSCHSPASAS*VA GTTGVCHRARLIFLYPLVETGFHRLGLN LTS*ST/SASASQSAEITSVGHNAQL/C LELELK*STCLNLPKCWDYPA*ATVPSQ FGSVFLRIF*PMFISNIGQLFSCSAFVN P*HQNAGLIE*VRKYFLFLFKLKEFA\ RTGINFR*MSGRTDW*NHPVRGISLLKG F*LVIC*CSY*L*VYPYFLF*EVSLLSP RLECNVHSESAGITGGSHHAQLVYPYF FFVCDSVLVGFVLEICHFIWLFNLVLY LCLMYLLITLTIKAVKQ
365	14266	A	371	164	1	SCRVESYGIKRTICLSSASWNYRHAP PRPANA*PPABMG/PLVHQASLSDC
366	14267	A	372	3	383	MVSTFEDAVNIVDMTN/E*EYSLNLV DKAVAGLERIDSNFETSSVCKMLPNSI ICYKEIFHERKNQMQKSLLYPNKLP QSIQHSAITTLISQSLTIWQS/PPPTK /RFOLTEGSD
367	14268	A	373	1	349	TLLGNHIVNIVTAFAPVVIWIVPI IIGGSGN*LIPLIIGAPVMAFARINKLR LRLLPST\ILL\LAYALLEGARTG* V*PALTRNY*NPEAYGHLMSFSLHGTG SSISR
368	14269	A	374	443	2	SSGSRSECRFLPLLFPNVLEILAGAIRQ /EKE/IKGIHIGKVVSILKTEVINPKFI KVA*YKIN\QKSVCLYTNNEQLEKFKF IPFKIASIKRIKYLEINH*GKDLYNENLK TLKEMKENKWINIPCSWIRRLNNVNIS ILSKVTYKF
369	14270	A	375	3	201	LWIKKLDIPIIPS*LPFNTELDRLILK LILWFRGPR/ITONSFKPKIVGGLISLD FKTYKATVLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USNN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion
370	14271	A	376	11	324	DKFLEHPLLVLQAVAGKSGPLHCLSTL PTSLF1*DRVLLCSPAMSAVAQTWFTAT ASMAQ*SSNHSFSD*/R/PHTTGHFFCR DKVL/TMLPRLYSNSWTOAI
371	14272	A	377	85	364	YQHNYSFCFLSQYVYRLF*FF*FFKKK GQF*RLNFCQGNMG/SMEP*PP*IQPF FCLNPLN/SDVRGPPRGANF*1FLKK GQVFPFSLSKIP
372	14273	A	378	1	382	GTSQTSYSTIFAGTLITLSSH*EFT*V GLEINMLAIPVLHOKYTP*YTHAAIM HPLTDSGA/SVLLIEILLYSNLSGE*S SIIELQLISIFLSMMLVIPNKGAAAYS IHALCLDRPOLLHILLI
373	14274	A	379	24	323	IPGLKRSSRLGLLCKMDYR*DNFQHMCL KNFNNAWAAYYFVCKI CCAVDPHGCSIKV SFFLSF/CFFFTKSRTVPQAEVQGGDLG *LEPLPGLMPFSGLSL
374	14275	A	380	2	317	AGWFOFDLR*SPCLSLPKC*DFRG*FP CQKFLFCPIKIF*TRLK/CYLNLT*QSL PLMHFKKNVIYFILYKAALFFFLRRSL /HSVAQAGVQWHDG/S/LQTPSPGFK
375	14276	A	381	1	323	VKRQPTWEKIFA/TLYPSGKGLITRIY KGLKQLEGKN/KSNLILKWAKEDQTA NRYMKRCSTSLIIREI/MQIKTTIRYHL TPVKMAFIR*/GNNEC*GYSEKRTLI
376	14277	A	382	2	248	TQPLLLRCLPPRSIYRFNSIPIKIQVNF F*EKEKSLLKFIQNLKP*ITKTLRK KKVDGKTFPDPITMYIKATVIKTSWYO
377	14278	A	383	178	1	HNPLLAISFCFF*FFFLRQGL/NSFAQ AIVKWYDHLQ*PLGLKRFSLHLLS SWDH
378	14279	A	384	312	26	FLRGV*FFFLRSL/DSVAQAGVQWPS FSGLAQPPGMPFSPCSLL/SFFFFFL VG/MGPTMLARKVIS*PFGPPASASME VEITGMSHCLANWF
379	14280	A	385	1	849	FFFFKQTKFKLSKYNIKK/SAFY ISNVLKMKFKIPST*L*FEVNLTKKLK HLTFYSYEHYTN*YTHKNNIHTS*TG FNS*TFVLHMKICRYNATSIKIPVYPI DIF/EKAYLKFIWVKTP*AKAIKTRK GI/LPDFEIHYKTVVTKTVHNLKNRDI GQWSRRKREQKYSVFTAN*F*IQVTF FKGNNSIFNK*CLENFMSTCR/KKK*DP HLTPYVKINSK*ISHLNVRPKTLKLL/H QKIE*XPHNIGLGSKF*DLT*ISQDTKG RTSQSDHF
380	14281	A	386	3	318	LREMONALESLSNRTEQVEBTTSELKDK AFE*TLQNKDK/KKRI*KNE*RLQEVWD CVK*PDLRIIGVPEEKGSKYLENMFEE IIEONFPGGLARDLDIQIQAQR
381	14282	A	387	1	382	FTPTRTAVVKR/SNDWCWRCGSGIGTLR HCSWECKMAQLLN*TV/WTFPRKIRQPS DVCCDMVIGLPYDPAVLLLGICPREMKT YVHTADMSVITSVSLVII/ADSENNLNV PSADEWINEMWYITVDY
382	14283	A	388	1	341	HKLENLENIVKFL*TH/TLPRLNQEKIQ TLNRSITSSKISKILKNTPTREKKKNV PQKGFPRFFPRA/KQGVPLGNPFO

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/015,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KFERGSLNLYFYKPLGFRIPKLGKRNPRGKKK
383	14284	A	389	168	1	KKFFFFSFFF*GDRVLLCHPGWNAVMQT RLTAAS\TPGLKQSSHFTLPSTAGYTG
384	14285	A	390	337	1	TGTFPLNPLEV\PLINTSVLASGVSI T*AHHSVIESIGNLI IQALLITILLGLYF TLVQASE*FESPFITSDGIYGST*LVAT GFHGLRVIIIGSTFLTITCSIROLPHFT
385	14286	A	391	1	235	LNFSYESSMYFALFTTVF\WVWLFN*KF FMN*LYHLCYVL*YFLLV\FVCLLTWFM VFCFFFFFFFFFFF
386	14287	A	392	1	258	SCORLPANHLNKBELVSRKIYIYF*KSQ DSTIRKQTDKK*AQELNRRFSTXDLQMG NKHMKRCSTPLAI/REMQIKTMLRYHICI FIG
387	14288	A	393	2	317	LAYCNLCPLGSSDPPTSSSRVAGNYRG\ HHDSVF*RAEDINMHEIQFISFLFNRD EVSLCCTGWS*TPGLKRASCLDLPKCNW NHEFLCLAFFFGSFWQCQI
388	14289	A	394	91	408	LGAEFDVAYLTSGRITGPGVFPPLTG FY SKDHLIAYETANIS*TA*ALSITLIATS LTSAYSTRILLITLTOGEPFLTNINE DNPPTLMP\KRLAAGSLFAGFL
389	14290	A	395	3	165	RNKKLKNRKHAKG*EKGTLHCACWCK LVQPLWKA\W*VLR*/LKTLPDPDAIP
390	14291	A	396	661	1	LCPLSSFYRKCALLGEWVCLFVFGTRV SLCCPRWLQTPGLKSSHLSLPLSNDYR HLPRLAIGAVFLFVLMRTCLR*FADP ISLSFE*QQRN*LHILISLL*MVDCILT OPTKWIFL*PKNS*LKQCKLPKITEL /PKNRIQIYPTD*MSSIPHLSFYLVCL FVCLF*MESCFVT/TMAAVQWHDLS/L QPLPGGKRFKSCLSLLRSWDYRRSPC
391	14292	A	397	320	1	PDSKQQIFNVDETVFC/WKKMPSRTFLA REEKSMPLKASKDRILLVQANPAGGF KLKPVLTTH/SENPAIKNYAKS\TVL* KWNSKVWMTGHLFTALNVLSPPRAL
392	14293	A	398	1	158	CIGPMWENRLLILGGRGCSSEL*SCHCTPA WAT\SKTLSQKEKK*NMKVMIQC
393	14294	A	399	264	1	LINEFSQVAGYKINKQSLVFLYTRY Y SKLSEK*IKKAIPTTIPAKKKEIKLYGI NLTRDVKDLYNENYKILKKIEDT\KKWA DTPC
394	14295	A	400	3	343	HEQKRQSKVREVELSQGLNMDRKRWSQ DFNPGCRTVALSPYHHTRLALNCPGRGW FVGNNF*KKKIFFFKEWDRVLLCHLG WSAVPSWLTAAALISW\VK*SFRLGLLS SW
395	14296	A	401	1	345	GTRKNTDNTKCR*VCEETGVFIHCWNGY KMVYPLGLWHLFLKKVSIHLPYOTSAL LSLMIEKLFTT/CHTKTCTQM/FHVVLV PIVKWKQPKCLPVGELLNLWYIS IHT IYSAI
396	14297	A	402	102	355	DRVIRLANFCIFGRDVSPPCCPSWARTF GLKRSTSLSLPKCWDHT*ATAPG/LRAI LLYFYDYRCLSPDLVNFACHEFSVELVA FF
397	14298	A	403	156	3	NNKNGFP*SMLFQPSNLGVSI*NI\PLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						*QKWFSSFFFEERVSLFHPGWSAVV*SWL TACSLDLPAQVILPPLSLPNSSC
398	14299	A	404	1	364	GTRSEVITYRLLLTPTWVI*HMRTRLLQ ACGAR*MMML\MIILGLVTCRLTIYQ* WRDVTRESTYQGHHTTPVQKGLRYGIML /FITS*VVFLSCVI\WVFF
399	14300	A	405	3	365	HEQTSHNIPLSQSPT*SKILMLLNSMKA BGEAEAAEEKLEASRGWFMRFKKRSHVH S\KVQGEAANADVETATXPEDLVRTID EDGDTNKOIF\NVNKTAFCKWMFSTRS TAREEKQCLP
400	14301	A	406	3	356	HERSDQLVAN/RKLDLKKSKFLLEGYK LQKLTKQEIQTNRPTTRI/EISKKKKK KKKKKKKKNSPGGF*GIPPTFKGQPKK IFKKFFKNLGGKTLPI*YAG/IKLL PKKK/DPSKKK
401	14302	A	407	116	362	YKYSLTPOKLYNHSTYTKNNHKNQNNRH STTTT\TKQPPPPGFKRYSCLSFPLS*DY RCTPSCPVNLF/CVFLVETGFHHVG
402	14303	A	408	3	360	HEVRLWDFAFERNEGGGNEEKVDMLNY RMWFHLIF*AEYCISICRLHAYYSCLGP VLLLLFVLIIILLFCLL/SFFDYF/VEMF FIFFFSFFLLSFLSFFSLF/CFIPLYF FIF/CFPLYFFFF
403	14304	A	409	388	1	ALLKFFFPKVLKKPP*GSFFP*GF*LLS /LIFPPYFGRETLEFF*KNVPLCPDPW SSMARSVPAGSVFPVK/ESLSLSLLSV PPQVQVNGELTFFFFFS*RGQLPLLP RMVWNSWAQAILPLWPHAS
404	14305	A	410	1	386	VFNAEESAY/YWEIMPQRKFI/EEKQA P*FRQERIS*YCANAVVTIRTTHICKP ANPQALKKKKKKKHQLTVFWLYTKKS* T RTILFLDWFCQCFVVKRYLYASKTLPL KVLILLDNAPGHLKPHFN
405	14306	A	411	2	417	AHHITARTDVDAKLYFTVITLIDIFT GDEFS*LATLR*INMK*SGAVL*ALRL IFLFTVRGLTGIALPDL*LDIVHDITYY VGAHPHYLSVGAVFALCGGID*WELF /SCYTLDRPYAKIHFTIIFIG/VDLAFL P
406	14307	A	412	295	397	WQWPTVAHACNPRTILGS*GGRV/TLRS GVRDOP
407	14308	A	413	437	3	PGFGSLIGNLIPASGNGRKSXSCVVCV CVSVCFKSC*SLCEHLFTCLCPQICVR LQLMV/CPQNCVVCPESGFLDESVCV RLCVCAMMAVWVGSGSG*VCGGC/MC ICVGFLLDSELCLVCV/LLGQSKDCDGL RCRLPAWCV
408	14309	A	414	2	392	HLQFIFFWLKILFIHYL/FLWFWFYLTSM ALFYLQ*QKRNCMYEVNRLGFF/SCGE GVSGSPASSSSSPSCSSSTRGGGAVGGG GLGFVCFLLFLWGFVFWFLFCWFLVCVG WVWCVWVFFLLGV/CWCFFP
409	14310	A	415	376	1	GFOASKDR/LLLG/ATAAGDLKLLKPL IYNSKNPRVLKNPAKCTLPVLYLYLR*K NYAMTAHLLKSWFTEDVKSTIQ*KISF EMLLIINNVPGHPTPMEMYKELNFF\M PANTSIP*PMDQGIIVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
410	14311	A	416	409	2	FFPIKKKKFAGALVFFFFFRKIFFFFPK GEGKRGVLVSLNLLPLC* KDFPSPPPPG EGVLWPPPPGPIFFFFFLKKGFCFCQ GFYNPSLYLIPLSPFKIWG*TRGF/LP PPALFFYFFFF*DRVSLCHPGWNA
411	14312	A	417	425	3	RELLAFWQNFKLPRQGFPPFP/GEGGEK KR*SLPKTPKGGPPPG/SPNGRLPSGG QLPPPRGG/SPQGPPLPKPGQGWGPPFP P*RSFP/CPFHRIQVQVSSSTPGLVFP RGLPNDGMLGKTKKKKISSKAARDLEL VTRTG
412	14313	A	418	1	346	LLPDRNLNTFFD/PAGGGDLYLRLH *IPGHGEGYMLMPLPGCIILHIVITYSG KKEPFGYIGMV*AMISIGLGFIV*AHN IFTV*IDVYTRAYFTSATIIAIPQGVK VES
413	14314	A	419	2	382	LFSTNHTDITGLYLLFGA*AGVLGAALS LLIRAEGLQPNLGLNDHIYNVIGTAHA FVINFFIVIPII\GGSGN*LLPLIIGA PDMATARINNISRLLPFSLLLLASAI VEV*SRTG*IIYSSL
414	14315	A	420	261	378	KKNFFFF*KLNF*KFLLIFFPPKKKIF FKKKKKFFYKIFF/I*KNIFFSPQKNI *PFLFFFI*YDFFFFFFFPPPPPPPP FFFFFFFFFFFFFFFFFFFFFFFFFTLN SLYFSGRVGGRV
415	14316	A	421	124	428	KPAATHACATIFMCLDQEAITSN*H*AT TQTTEVSL\SPKLDYFSIIFIPVALFVT WSIIIEFSL*YINSDPNINQFFKYLLIFL ITILILVTANNLFLQFLIG
416	14317	A	422	8	355	PVFSYNHSTLLTFSLSLSPFFFFFFFAPGK KGEKNGKPGPFRRGGFPFKKIKKPPPPP/ GGPKKPPGGGFPQKPHFPKGGGWPDSKT LPFGGKPNPGGPKPPLV*NPPSQGP/ HGPSGGG
417	14318	A	423	356	3	KPLGIDLTKKVKLSKKNYKTLMKKIED DSN*KDNSCL*IR/MTLPAKAIYRENTI SVNIPMRFLPDAMADAN
418	14319	A	424	2	338	PSVRLGGHWRSGITPLNVE/VGLLNT IRLLASGVISITGAHRLIECNHQITQA LLITILGLGLY/LTLLOAS*YFQAPFTIS DGIYG*TFGSGTGQGLHVIIGSTFLTI CF
419	14320	A	425	55	342	GPPTPWSLC*GDLQR*P/RAVFFFLLKKK KKKKKGNPIRN*RDISS*FLKNLETAVER NFWTFYSYFKSKKLIQSDHPLKNVKKI LQNDKRYLKLWDG
420	14321	A	426	2	367	DRRRCFTYHKDIGALYLLGA*AGVCT AVSLLIRAEGLQPN\LGNDHIYNVIV SAHAFVIMFF\MEYPIINGGFGN*LVPL ISGAPDMESGINNISFWLLPPYVLLLL ASAIVEAGSRT
421	14322	A	427	359	74	ICADYTRKPPYMGAPIEFSACATCVL*LT STQRECVCVCVCVCVCVSM*VALIDP SN/CIFLSAYVCVCVCVCVCVCVSI* VALLDSDNSYH
422	14323	A	428	52	361	NYPQLSEI***VS*LHY/LFSLFFYFFF *LVSRFVARLECSGAWH\IAHCSLDLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
423	14324	A	429	105	361	GSS/DSSPASASLVACTGCMCHQNCQIIF LFKKYFVGRVQWLTSVIPATWE
424	14325	A	430	1	379	SRLFFFFFEKTNFGFVRGVGK/WAFF GLMEPFAFRVK*FSGLTHTPTWYRNP HCPVNLEF*VKTCFNLVDKAGPKLLT*K DFP
425	14326	A	431	1	390	HAYHTVKESP*PLTGALSALLMTGGLAM **RLHSITLLILCLLTNTL\SIYQ*WRD VSRETTYQHHTPPVQKGL*YNIULPIT SEGVSFFAGIF*AFYHSSSLAPTPQLGSHW PTTGITPLNALEGL
426	14327	A	432	1	392	KKVKKWNILFMIGRLNNVMSVLHVI YKFRACLRL/TFHFRHKKKNLTA*KHK KALIPKTLKNGKSGGITLSDYK*YK TTITTTIRFWKF/DINKYNKITTHEIY FHIYQMYFFKIAKTFQGIK
427	14328	A	433	382	1	TRTRGRTQWD*T*LRPT/WTKKKKKKKK GKKRKKKKGVFFFFYFLGF*FLLWVFFF FFFLGFFFFFWFFFFFWFFFWGIF FFFLLIYNFFCKF*FFFFFPGFNF FFWFFFLDFFVFFPRV
428	14329	A	434	375	1	RGKGFQNGQKRRVSPPPKKGFFPPAA PKNIKGGKK*TPPKGGVS\PPPKKR KSPPHKK/IGNFFPPRGKGGPKPKK PGPFFFKMPDPFFFFFLFFFFFA HKDGLLAREQTQAEVK
429	14330	A	435	1	459	KYSQILPDKTAKATK*SKDCLLKWFN KWTSTHKSLLD/SPPTKINSK*ITGLNL KCRITLLENNIENLDRLOFNDLTT LPEAQSKTELISY/DFIQTFCSANATV K*MKRQATEWEKIF
430	14331	A	436	14	382	PTRPPTRPSTRTLGFTMLAKIGSNARPY /DYPSGASHSAGITCVKHCAARVHDF NGVHRPLLW*EFIVRISFIDPFLETN PGFITKGLQGHNLGSLQVSPGLTLFS CLSLQKSGFYG/HLAKYLVKE/CFGLPS KRGF*GGYPGGAQSPP
431	14332	A	437	3	192	MARNTSQKDTRIDNNKCLWLVLKRRKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK TNVMSPOLHRLIIILSLMIYKSTTE* VEKQTCYIILM
432	14333	A	438	1	364	TPGLK*SPCLGLPKCWDYRR/AAAVFGL *DILAIFFHHILSECLFLVLFHCFNA NLFLRWSS
433	14334	A	439	336	2	DRIALGTVDLFGFGRTPR\AHPIYLVKVS LADRDAT*NLWQIPIVAS*YIPLGF/WS KAMPSCVDIYSSFEKKKTVEFDRGQGP TPEIQVLGKAEVGPPEPRGSKPSWRIM AKPKFYKRFL
434	14335	A	440	1	333	GMIPKMGNAGP/SG/PRKPGFVLG*KG KVKAWLNFKPPFRAFNPKKILLPLGFS GILGPGKGNLSRPGPPQAFPLGFCQV LGP/SGPGVGFPPKPGIGWSNNPCLTLQ KWK
434	14335	A	440	1	333	HKLENLENIYKFL*TH/TLPRLAQSKIG TLARSITSSKIKSLVNTPTTRKK/BSK PLVPKGTITFSQLCKLRVPVFMKPFQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KYGERGLFLNGFYEPGLTLIPKFGKNFGG
435	14336	A	441	320	1	WGNNWLSLP*EKKGRPFLL\SHPKINSK WIKDLNVKGKI*KPLEGQIG*YLMIFGV EKGLFKGGPKYTLTKRY*NRELLFTRK YFSLTEKSPAEICHIKKLAKKK
436	14337	A	442	8	391	ERILRHQVGIIPGM/QGVRI*ESVDE I/QHV/NQLPKITHITTSVSGKARDKF NTS*FKLQKTEKERNFLHWKISCTSP AASILLEGKESFP\PFPSGTAKD/CLL* P/LGSGWLEALGTABERRTRKK
437	14338	A	443	363	2	HHVGQKLELLTSGDPPSNLASQSAETG MSYRAQLSIUTPSAVFLV*KLSHARCL ML*QSIII/HVLHPHQVKKAPHVS/PEN SQPLHNVEPEDNIF*EHQKRTVPPIHTA RKLQDLPECLV
438	14339	A	444	1	900	DSSAGIT/GICHHAQII/LFVVFVETGF HHVGQAGLELLTSGDPPASASHTGGDYR HEPPLLASLSPFNKELCTWPERRRKP I F SLPKLDPNKRKFSPP*LF/IGS*TLIW SLFCFRNVCTQLADPTKSIAYQSSLMKPF GQKSCIFGSEKFPDKVYLFSSDRKACE QVLVVVVVVEY*I*DMACFO*ALGFYCLSIWN/YELPEKFEVLACLSLPSRNNDL ILSLKKKSQNSFFVCFVFFFKTKSNFVP QAEGQGPLFG*LKLPPLGPRNISCNLNLP GSC\QTGAUVP PPPVNFGLKKNRVSP
439	14340	A	445	3	346	QIGKVKLNK*VPHEPSKNKL\FLEASS LILCNNNEPFLSRIVTWDEWILYDNH* QPAQLD*EAPKPNLHQKKKKKKGLAP FWGAFSRGNPFYFNFQQLHF\KFSSQ KRG
440	14341	A	446	2	246	FRCGKTRALMHCWNBGKMLRQLRKVWV LLAAMLNMLPREPAPLLSIPSRK/S TTAKTCA*MCIAITVCITVKKKHRLG
441	14342	A	447	38	393	VTLRHQGLSL/VTGQEVQVYVYNSL*P* TPGLKQSSCLSPKSYCHG*LPVVVVVF KWM\GFTMLPGLIINSWPO/CNPPAUDA QIAGIRGFHS/VGQAGVQWHDLSLQPL PPGFKQFSHLS
442	14343	A	448	54	540	RIFFEHAGFLQSSHQPKHLLHPLSGG VSSDGO\FRKFGISRLGNSGIYKAAPFL HDCKFRQSEDSPCPSNERLYLREWAHP RSTI*YKQPLDLIMKYGEKIGIYFAWL GYYTQMLLLAAVVGACFLYGYLNDQDCT WSTEVCHPDIGGMIIMSAQRDL
443	14344	A	449	2	310	FFFLRQSL/DSVAWAGVQWRDLGSLQFP PPGFK*FSCLSLPSSNRYRAPANF FLYF*YRQGVITLTMVLIS*PRDLPS ASOSAGITGVSHHAWAKISL
444	14345	A	450	2	466	KQKIFVSDETA PYWKMPSTFHS*REG TASKLHTAG*ILLPNAAGDLKLKPVFG DDSGNLRALKNYAESPLPVLYKWNKAW MTAHLFTAWFTEYFKPSLRS\FKISWK I*LFMDNGPHHPRALMECKE/NAVFMP ANITSILQPMQGVILI
445	14346	A	451	670	212	SSSSP*GS*YQNRNTIPSPKKQTKK\ KNNHYKIFPTDAEILSNLANAQSSI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KRFTRHQLGLFIVLVGLWUNQTPTNAT CYTNRLKRRNNHTLINAELVYKIQPSV I*KLFLRLGAF
446	14347	A	452	407	219	PLTSLRWENHLGPGVQCCEP*LCLCTP AWMT*YPIPSQNKTKQ\HTRKQNH KNCVKQ
447	14348	A	453	2	395	WFLWFRERSHLH/RVQNEAASADVEAA SYFEDLAKIIDAG\AKQIVSVEETAFHW KKVPSRTFITREKTTALKG/RC*LSLV DNAAGHF*VEA\MLIYHSDNPTL\KN/ YAE STLPLYKWNNAWMTACLFST
448	14349	A	454	424	38	BETEPL/HRPISSEVELVIRNLP/KH KSPRPDGFIAEFYKMQE*LVPILLKLC QKIKEGGLLENSFYEASISLIQ\NSGRD TV/RKENFRPIFPMNIFAKILNKILANC IQQHINKLIHHYQVLFPSSLHRS
449	14350	A	455	2	309	PRVRSQTPGHKRSTCLGLPKWCYDRHEP LHPATASFLVAAPGM/FADPP/CNMHL NE*MNE*MNGDDASEILSFEMRSHSVTQ TGGQWCHSSSPQPPQPPGPK
450	14351	A	456	3	441	DAWGLVLDREIRFFIFFFFLGLNGGYF RGPGRPGGEGPMMETSVSPVKILRGP GQGGKARKPHPLGGPRGNHKTGG*KR AYPTGENPVLTEPKFTGPGGNGPETPV IGKAGAGKPLNPG\MGGSRNPKWACPC* TSGKKGK
451	14352	A	457	1	234	PTKPNHLGLDGRGCRPSSSCTPAWAT ERDWVSKKTKG/KK*KORTK*MS*VE QGGSGGKIFTLASNSPLPFF
452	14353	A	458	42	470	KRIPOLKKSPLPLNKPGEHWGKINFP PRERPKNFF*KKKTLTKTPPKQLFRKKS PFKKPHFLLYSKATKKQKRGKKRAPP KKKKKKENPKVIFRTEITVASPVLWSA VKPIIHIFPFRKKKPHA/KPPPP
453	14354	A	459	2	393	DRPIEQWNRKRPINLYIDGMTPFSK TTAFE/WK*NLCKYVWNAWIC\NRKN PYLTSSSRKINLR*IIDIKVK/PAIKLP EQNIRCSL*VLGVGRDFLENNNYTRKK\ IGKLDFIKISQLGMVADTSNPI
454	14355	A	460	338	33	GDERIKESFFFFISSLCFVP/AVL*QQI RLLI FTNRLFLFIY/CLFLEMGSHTV QTGVQWCHSTLQPRPLGLQSSHLSLL SSWDYRHLPVVLKWTACAV
455	14356	A	461	77	435	AKEVEASLSTLARPISQQQQQQQONER KNKN*PRIAKAI\LS*KGEITLP/ELQ CYRAMITKTAWY*HKNRHIDQWNRREN ETNPHTYSELIFDKGPKSI\SLFNK*CW EYWIFICTR
456	14357	A	462	157	3	NGRVDLKIQLKARCGGACLGSQL/ROEN HLNPGEKGCSSE*LHHTCPD*VTGQ
457	14358	A	463	363	3	PSVAQAGVQWCHSSSLQPPPLRHP ASA/SQ*LGQLQQATALYIHKYILPFCN VLISFIFPFFLEMRSHSV/SQARVQWH DGSPPPPFELKRFNSWAEALAVSRDRAT ALOPRRO
458	14359	A	464	3	396	LKFAIEKVKKIIFKKQLQLR*MKKTIINR YLKEN/LNQLLEIKGTLRELQNAVESFN NRL*QIEEGISKLEDAF*WTESGKIRK

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						INK*TK*TDYIKEPNLRITIDVPGGEKA KSLKNLFVIEENFPGLAR
459	14360	A	465	399	1	PPGVLLNGPPFFFFFLILGPGWVGQPL KTPLVFFPNQYHIFPPFKISRIE/LPTR PPFQVPLCP*PPSPWGLKVFILLFS FFFL*DRVSLCHPGWNAVMSQLTAASN TW/VK*SSHLSS*DYRCVLS
460	14361	A	466	279	1	TNINFRVRVSTAGPLNKKKEKENV KRRQATGWKIVAKDTSKGLLSKIYEE LKLKLNKNTK*/ILCLKWSKGFNRYFA KEYIQMANK
461	14362	A	467	2	436	RGELPQLDKYLKKTATALLNGEEL/E/A CPLRSRTROGCSLSP*KKFFPKSHI ESLLFPNIIILEVLYSAVROENIKKVEI GKEENKMVLTDDGNHLCKNSERIRN/YS KVAGYKVVV*T*ITFLYTSREQVEFEIK KTLNMRNF
462	14363	A	468	2	420	RTTALF*AVROGLSLQRLLSFCCLC PAARGEAYIG/ROASMSRCGLQAVQAC LLCLPQKQWAMGAPPSASLLPCLSLID RCASSQDSVGVGSPSAGVGYNLVVRGL LSRSEKR/NIRLGVTRFSRCV/LSPLSL TRR
463	14364	A	469	1	416	FSP*PLTGALSALLKTCGLAM*FHFHSI TLGILCLTNTLTITQ*WRDVTRESTYQ GHHT*QAVQKG/LRYGIILFITSEGSFF AGLV*AFYDSRLPPTLQLRGHPSTGIT PLN/VLQVAVLGEPLVLLAS*VSIT*ADH
464	14365	A	470	211	398	IFFFFKMGGLSITLCNRRKRHPQKLE* STCLGLPKWWEYRCPP/VPGQKNFRP *KTKESPPLVSGGASSASNIK*/IALPP FLEKKKFKQGFDPFFFLFFTONPGQG NFFPGKI*YCPPIFFFLRRSFTLVQAQ GVQWHDLSGLQPPFGKRF
465	14366	A	471	62	424	TLKRCWKKRWVHLWKTIVNLLIKIN/ RTLANT*PCNPALPLGVSLREMITVH KKPCP*MTVALNWTNKGHLKSLTC KNINKWLSLYTMKYIATKRKELNHNH SCRNYSSDMS
466	14367	A	472	427	20	LGRLRFVEQENKPYYPPLADSPSPBP MSLYKNSPIYPGKGLPFPSSNNKIPPLN FLKMSNL*/FALLGNKDFHLLLLGGP IGIMGNMATTSMQFYSRVPIFF/CFFE TGSHSVAQAGVQNCNLSLQSLPPLK
467	14368	A	473	424	98	NWLYYYYYYHLLF*ROGL/BSAAQAGV QWHHCSLQPRRRRLKQLPQLA/TSW NYRHKPPRLSPYVQAQGL*LLGSDLPD SVSQSAGIIGNEPLHLASL*PLFAFP
468	14369	A	474	415	75	NHFLKFFPQTQANGPGSKNFFFLKTRF CFFPPGKRPWAYYKSLQPPNSGGQI/S APT*IKGAPKGGPPTRVKFFFFFLF/L RNSLSVAQAGVQWHDLSLQAPPFGFM PFS
469	14370	A	475	3	413	PVQKGLRYGI/ILCITSEV/LFFAGFF* AFYHSSLAPTPOLGHWPPSTITPLDPL EGPLLITSVLLASGVSI*AHHS LIEN/ NRDQIIQALLITILLGLYLTLLQA*EYF ESPFTISDGMVSSFFVATGFHGLHYI

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470	14371	A	476	1	440	ITLTDRLELSY*NRLL*LAYTITFIV* IPLYGLHL*LA*PKHVEAD IAGS IVLAA VLLKLGPGVIRLTLLINPLTKHIAVPL LVLSL*GIITSSICLRHKDLKSLIAYS SISHIALVVTAILQTP*SPFGAVILLI AHLGTTSS
471	14372	A	477	2	397	LFVYNIHDVGLAYLLFGA*TGVLGTGLS LLIRAEGLHGMNLGNDHIYVNVITAH FVILIFIRIPIIIGGPG*NVLPPLIGA TDMAPRINNISL*LLPPYLLLLASAI AEDGAGTGGTDYFPPLTGNYS
472	14373	A	478	442	44	SSSSFFTPPRGKFFFKTKRKKFFS/SP GNKGFFSPLSP*KFFFFNPPFFFGGFF PNFPPPKKNFFFKNSPGFFFPPLKKKI FFFFPPLNFPAPKVFVKSPDPFFPPFF FFFFFFFFFFLRHGWGREGI
473	14374	A	479	1	439	PTRSPTRFVLDRERPPFFFFFKKGGP SVPPAGGGGANLG*GNPPPL/GVKKFFG PKPKKIGE*RPWPPPGQPECSFFLKKN GLPHGGQGR*N\PPPRP
474	14375	A	480	420	0	YSPSPFPK/YRAPGKKFF*KKPRKEK* KKKILGFFPPLSLKFFFPKAPKFFGG VGPNCPPKKRFFSKNSPGGFIKPLKLG KNFFFPAPVKFGPRGFPKGPSPFFFPF
475	14376	A	481	371	2	NKI*NKFSKLNKSSSSSSSSSSSSSS SSSSSSSSSPVVK*IKKCSTSLTSSS SSSSSSSSSPT*IAKINKIDS PKCWQC RETGLTV/LVQPLMWQFLKLMSQII*D SAMWLSMIARK
476	14377	A	482	3	335	HASGKDRHTDQRNRIKNPETDT*LYSTF *QKC/RLI*WRKDSLVNWK*SNWA/SP MKKIKLDLSSSSSSSSSSSSSV*NV KLLGNVNGNLQVRLRVHTVDVKAQHI
477	14378	A	483	1	418	GVR*FSLNPPSRWGPKEGPNLA/LNFF FFVFVFLVETRFHPVQAGLELLGSRAP PASA/FPK
478	14379	A	484	1	356	FCANAVRSIMIKTLVIDKATKF/RANKGN YKYHLVPFNCKTGR*DSGNPLNWFYQC FVPEIRKYLARVGLPFNVFLILDNAPGH PEPHEFNTEGFRVVLTPDMLIQPLEQ GVRLTLTA*YQCFVPEIRKYLARVGLPF NVFLILDNAPGHPEPHEFNTEGFRVVL TPDMLIQPLEQGVRLTLTA
479	14380	A	485	166	406	FTFWGSVSSAEGGGGVSSSLPRVTVR PDETVDVTIHLKKE*CRGPAVAHACNPS TLGGRGRI/TLRSGVQDQPSQHG
480	14381	A	486	107	429	FWVTQTFGFFWLNPPGGLELWPPPCPG NFGGNFKKGGFPLWPGVQTPGPRGIT PPGPPRGK*RGGP/SPGPGFLGPKPKG GGP
481	14382	A	487	399	2	GSAPAPLPKNGWGRGPGPGPKGVFFKL PKGGFPAGAEI FLGEFFPQKKGGLFP FVPLKTBEGGTL/NSFPKGRVFLVFKP KAGPKKKKKKNYKPLNNTDTKFFNN MLANRI*QCIEVMQYDTRG
482	14383	A	488	419	2	PPPPPPREKKGELVFNKILFGKSGFP RNPKDS*PKRVGIFEGPKPKKKK* FGPWGKPGDG*RNKPFK/DFPFFFFFF

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						*DGVLLCRPGWIAQSRPGLQEWNSIS KKRSGPCVLGISSSEKVPDAWADAWADAW
483	14384		489	629	0	SSSSR*SLLCRCFKN*GEKIRNPIEKWA KVMHRLFTKRCINI*KDVRSTSLMVRT *ITTTLRHYHFSPIRLSKT*KLNRTLYG* DCGETGIFHCWWECKMF*VL*RE/VWQ YLKLK/LHIPVDTA
484	14385	A	490	2	351	KNRPMDPM*GY*VNDEGDTTYQQGNE ELRS/WCWDNRLAKVKLDLYFFPHIT EINSKI*DLNKNPPIHVLEENM/I* F*HVGIGKHYLTI*VKI*NP*K*TWLH ENKMYCL
485	14386	A	491	42	507	NLAK*IQ*ICTIMHHDQVSFIPGIQGW LNLKLSINIIYTNRL*DKTHITISIDA EKAPDK*YLEMKGK/KPLSQLGIEGN/ YLKLTIGIHI
486	14387	A	492	18	417	REGKKSRVHFNIGKQVRMSTKH*KTOL /SHSNAHSNAQISKSQPHGLHDPFKKK KKKKKKKKKKKRGKKKKKKRGKKKKK KKKRGGGPP*KGVREALFCFFWKKKFF VGGGGGKTPLGCLQADTFLWGA
487	14388	A	493	413	82	FFSSPPPLFFPPPHLFPFPPNFFFFF PPPPPPP/PPP*KTGPPPPPLFPFPPP LFFSPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP
488	14389	A	494	1	413	PTRPPTRPPTRPPTRPVLDREHSFNLP KKKKKKKKKKKKKKKKGGGPLKKKPG GAKKKG/EKKKKKF*KKGKKKPPGKF GKKKKIWGGEKRAKTPQKKTP*GKKKI LKGEQKKQNPGRGGKKFFSGEKKKKK
489	14390	A	495	274	1	IYRIDCAYMKKVERSITSLSFHRIKLE N/QLNPK*/RRRREIKIGAEINEENRK *IEKINETKSYF\WKISKPLAKLIKEKT QITNTRNRAY
490	14391	A	496	336	1	VFOYTYNKLVSVMFYCFPL*RWGLTVLL RLVNSNG/PSD/LPSSAS*VAGTIDAH HQLCFTTLLSOLLEPFLGLSFIISLL* FFFLNTESHVVQGV*WHNLGSLQPLP
491	14392	A	497	445	382	PKVLFFFTLRGPPFPFPPPNKVFPPPP PQNPFPFPPPSWGGAPK/PPPPK SFFPPKPPVPSFPPPEKKKFFPPPP FAPPPVF*PPPP
492	14393	A	498	430	2	SPFPKPTRM*VKKFGK*KKGGGGGGG PPLSPPLWGSKPVPV*VVKGR/PLPG* GKPPFLKQFPFPRGGGPRCPPLFGGL GQKNGFTPEVLL*PKFSPFSLVD RIYCLLMLEYKSVMMILLFASCLNLYT FPIV
493	14394	A	499	363	3	KKLVTPARVLGDIIENRFLQMPQOREN FLCQVMTKPPPTTFVKTGTGKWLISL KRFCPAKKKT/IKILVNRVNRQPEWEK IPANYASDKGLISSLYKDLQVYKRN PITK*VKGM
494	14395	A	500	145	435	VFMCISSFLFIPWYETITWVPVTCRR T*MFIALFVIARNWN*SRCPSTGNW/L KLWYIHTME
495	14396	A	501	162	1	FYNYYTIFLYFIFILRRNL/DSVVHT GV*WRHLSGLQLPFPKPKFPFPLSLP

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496	14397	A	502	343	2	TKKFRWGPKEFLKEPFGV/SPDFPII/NFGNPGVPVGKDFKFPNFKKKKWSGRAPFVVPITPFGG*WGRFP*PPAFGVPRGDDGSPPPGAPKEGPLSKKKKKENKEKERKESARL
497	14398	A	503	23	405	KGRNLYLWEKKKKKMLVWGIQGGPPRIKPF*KVIFKTPPGPFPFFEGCPPLAFEFFKTDAFLPF*NHPKSKIKWALAPPKKKIFLNPKKPPDPFFFPFHFKNFPRAFFKNF\AFSPRGASPSPPP
498	14399	A	504	418	247	PPKWF\FPKPPRGFFFPFKGKKFFFPDGF*FGPPQGF*RPDPLEFFFFFFFFFF
499	14400	A	505	26	426	GCTGLLHS*MYAKVVCCTDHPIT*VLSPAFISIRISYSPTHQILIF*IFLFLVETESCHIAQAGLK/LPASSSLPVWASQSA
500	14401	A	506	337	2	IPNLKESA/CPNLPKMGWFKD*PPFPSQISLIFKYPKFLKFEI*KKKPLKGLFWVW*RKAPVGF*G\EMALGEKFFFFFFFPPFFPPRRSFAPVAQAGVQWRDLGS
501	14402	A	507	454	2	TSKTGQGRKGSPPPI*WAAQKRSSPPRRGSRAEALLTSQTGMWPGRDTPHFPDDGRPGAPLFPDGAAGQRRSSLPRRG/VPGRGAP\QSQMGCOLGRGAPHPFDVGAVGRCPFPFRWGSQVEALPTSQMGQPDRTGTHIPDGAAGQRR
502	14403	A	508	390	13	RIPPPKSRWKGKGF*VS*NRPPI*KNFLPPPP*K/YGDPGRGPPPIKFLPLKKKGAPPICPGCFEIPAPRESPLAPPKS*NSRGNPPPPPFKKKNPLFWGGKTKKLIFFFFEAGSCVA
503	14404	A	509	2	282	WQFLTKNLIFPVEVIMLCIYPNESKT*ITYTKTY*ILLAALFIMAKTWQGVLLKV\TDKVVHIMTEY
504	14405	A	510	400	250	LLSVTOAGVQWHDRLQPTFLRLKHPPTSAS*VAGTIGAYVHAWI\IFF\IFIYCRDAVLLYNLWFFPKGLLKCWDWCEP/RMSGLFVFNLDLGRSEVS*ILSSWDYRCVPPCLDNFFF
505	14406	A	511	99	242	VTKEKEGHFIRIK*LIHQEDTTTINIGVPNNRNLKCMQKLTCLKKEI
506	14407	A	512	139	374	SLWGRKIRFFFFGADPHFVPOAGGA\WGNHG*LQPTPVGLKKSLLTTPISWYRLGTPPPANFKIFCKNGVKPCCPACF
507	14408	A	513	23	401	STCLRLFKCWYRRSEPLFALCMFLF*MKGKYYVMGFI\LFFFLFLHKI*LLQENFVYVCLKKNKTKLKA*TKKQKNETG*NILVDNLVLS*KWKCLLNGFILFYF/NFLRQSL/NSVAQAGVQW
508	14409	A	514	7	386	FFVFSTHITLLFLFLFFFLFPKPPGFFLAGKNTTPAPPEKPPPP\PPKKRGGPPFFFGPPQKPPNSPRGGRGPPPPPPRPMKEKGGPPPPREIPPPPPFF*PPKTPPPPPGGGGGGKTPPKR
509	14410	A	515	370	2	FVFVQVLPE*NSFLFSPF*KGCL*RDLPKRRFPFPPNNKLWPSLF*GFLKNS*KFNFSLSLEVPPFF\CPKFPFPWI*APFRFFFFFFPP*RG*IFFF*DGVLCHP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
510	14411	A	516	1	163	GWSAVVQFWLT NTRKLSGGGGTQLS*/LLGRPRQKNHL NLGGGGCSEPRS\HCIPAWMT*DPVSK
511	14412	A	517	1	390	RIVRVYVKHLC/Y*GSVNPREKIDNFDL TFNLRLNQEEIETLSTPISSSIETVI KSPPT\KQKSPGPE
512	14413	A	518	47	312	EYTGILRLLYIE/LFTTQH*KOKALNOA K*LAKGLNKHFTKRCGMNDPKHMKSSA SLAIRKM*IKTMMRCHYLT*MAKIENK TESTRP
513	14414	A	519	320	1	QNPINKQ*KKNKKYRLV*HKKPPPTT QPHSQNHQ\PN*PQKHT*TKNHTTP PPP*SPPPSLSPSPPPSPSSSHPP LLSPSPPPSPSPSPSPPPPTSP
514	14415	A	520	1	368	LKTQGEANNLLKMKADLNRYLIQK/VY RVNKHTRKCPTE\RELQIKTRYIYISIR *RVYKKKRDNTKC*GRETTGLVIHYS *EYKVV/P\WETV*QFLTKL/E*SY/P* DPAITLLGIYSKELK
515	14416	A	521	2	264	GKTIPLVFAETKCILKLV*KR*KAK *ILPNKKAGGLKFPDFKTYKAASHKH QVGGWLKELRSTLQAQQTWPRELRST SPS
516	14417	A	522	1	408	LEKMTSLAI/RVMSCKTMMKCHYIPR KAKI*NNDNKICW*CRETGLIYCC*E CT/LVQPL*KTV*QFLIKVNM\DPAFVL IFIPKK*KHMFTHKKNCKHTFRAALFVM ANTRI\PNIFQFVWLNKLSYKHIVDY
517	14418	A	523	320	3	TYIYIKTCPRMFT/AVMLTITKKQOPK YPTDE*NV\YIHSNAYSEMKNREVL HATTWNPKNIMLNKASSRKRPHIT*LN IYEMSRIIQMVLCNCLLPSMF
518	14419	A	524	426	9	AELPASPTGTCTCPPLGSGRDQVP\GA VGGTHPGSGGLAGSP*GGLGMAGCKS* ALPROEVTEAWRQFKGERRQASSTGGP GAPSAAGPGAKPLTAWGQRHQPAAPSA GPAEPLPTQNCWCPASNPGSRTRLSLHT
519	14420	A	525	13	461	ICITWRKMILLPYTKLNSRWIADLVKRG TTIMFLEVSVREHLHDSQKKIF*DAKL MNQKE*LDILDSINIKSFVH*KAPLRN KGLQSAIHIEYKGLVSRIEYELLQ\TY KETL\KAKKKIDNFIK\WAKNLNRHPT GCPSIYKHVK
520	14421	A	526	288	570	ATGSLCPCGWSVAIHGHNSAL*LLTP GLKHFPASASQVAGTAGMSDCTQLCKIN FFVVFVL/RQSLAVTQAEVQ
521	14422	A	527	3	438	AVSHDCTGLGCP*QREILYORKKGTG SPLPPSPGIGGKPLPFWGPKTWPPPG IPFFLSPPPSPSGGGGRPLETAGSF SQNPWNLRDGA PPPGGGFGP/CPFFGP PGGLG/PPGAPPPPLNFPKKKGGGGG LFPPQAKG
522	14423	A	528	2	616	FFFDTEWSVAQSGVQWRDLGSLQAPP GTFPSCLSLQSTWDYRRPPRPPANPFL YF*RRGFTVLARMVIS*PRHLPALAS QSAGITDVSHRALQVCFITTL*LSK/H QFKAGVTL/PHLQCLHEIGLDCVLHKKH /WSVHSP/HKTNVC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
523	14424	A	529	57	485	RHSSLGNKSETQSQMKKKKKREKKKGKEI SFDPAISLSI*PKENKSLYQKD/TCICM FITALFIIAKTONQPKCPSTDE*INRKR \IYIYIYIYIYIMKHSPKKNEM/SP AATWMELEAIIISETMQQKAKYCLFSC I
524	14425	A	530	399	3	FFFFFFFWENPPPEPK/WRGGGKKKAP PFKFFKYKK*LFFF*GGGGHQQKKKKK KSSSFFFFFFFVFVFVFVFVFVFVFVF FFFFFFFVFVFVFVFVFVFVFVFVF F*FKGFLGTTTHASAHASAHAS
525	14426	A	531	491	4	SKWKIDLNLRK/TTKFVEET*VKIFMN LGLGNDFLSMTPKA/LKIDKSDFMKIKN /FCSKD/TIKEVKRQHTVEWVKIFTSYI FDKGSSTRTCKEL/RKQQNKPIQKCSK VLNRFREDIQLSNKMLKGCSTSLNH
526	14427	A	532	184	509	PQWFAHSLPALGSSSGTGP*VVRQIPD SKDKESSQ/WSHETSDRPKPADHRRRSR PSLATSP\PRLEPHPSLEPHSGLPILSS LPWGAVALAPTHFSALAWP*RPLPCNSQ GEKFFFWGPF\ERESH SATQAGVLGHD LGSLKPPWGSKGFPSPSYSGG/WNQIN HLSP
527	14428	A	533	401	3	VIREMQIKPLHIQ/PGLW*SKSVKRY*Q GCGQS/NVLIHY/WLKT*MGPFWKI/W QFLIKLPYGTVILLSGIYLWRMEKKP KFCTQIFIAAFFIIQ*PKSENNPNIHQP KNQ*DVIMYIHTMEYLAIRMNIIH
528	14429	A	534	419	93	SLAIRQM*IKIPPRYTRVAR\IEKSHNT KIWKRHGATGILLHCWECMA*S*KIW *FLIKSNINLPFWILL*CTVPREMT CLYKD/CM*MFNAVSFIEQNGKQPKCL
529	14430	A	535	414	2	NFLARGYINCQPOFFFFPRXHLKWGVP LSNFPFKL*KGGFQEGPKKVKKNFFPF FLFFFFFF*KKPPCPSRLKAK/WKIFGFL KPPPPGLKKFSFLTPIKNGDKRGGPDRR GNFFFFFFVLVFLVKTEFHVYVGGAGLK
530	14431	A	536	32	435	DRATALQLG*KSETSSYKKKKKKKKKKK DGGAPLKKNPGGAKKPGKKKNFSPKR GGKKNPKNFKNFKTNFGGKNGAKPPQK KKT/ANGKKKNLKGKRGKNPKTLGAKK FPPRG*KKKKPPAARPGKASS
531	14432	A	537	348	1	EYIKSTHQMGKNYPLKNTVSSGQVOWLS PVISAQFAIAKSSQPKCPSLNEWIKKL WCV/WCVVCVVCVCMMEYHSAIKRNE LMAFANT*MRLETIIISEVTQEWTKHR MFSL
532	14433	A	538	523	66	TDQTSNHNPLSQSLTQSEVPTLFSVKA E*CCEA/AEHKFEASRGWPTRLKERSRL RNMSV/GEAAGSPEDPATV/INGGRTQ PQIFSVABATLNKKKTPCRPFIGREKSM PGRFRKDSLTLCRDFKTHLCLVFHYWN AKHVQVYILLKVTAKI
533	14434	A	539	413	2	RDKV*PCCRSWSQTPELK*STRLCCLK *DTR/R*APAPQFLLVHRHVSIFSG PLSCRSNFD/HDSIKFSFPTIQYAHG NKPQL*TPDILFLKSSSTFQACTQV WHNLSLQLLPFGFKRSDAWADAWADAW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
534	14435	A	540	385	2	MASKHIRT/CAROLAIREVOIKTTQYHV IPTRMKVKT/DNECWGHC*NTLINCW WDCKMQLLWKK/SVWHSSRGKMYVLPL CTPAIPLGIYTELKTCSHK/T/CT*T FIAALLVIAEKWK/KCPSAEW
535	14436	A	541	44	398	RPPFFFFFKRPLWKKQGFPPPA*RGE IPSAKK\PLPGVSGPGNPPGP/KP/PQ NPPPLGGSPGKPPPLDIPFGGPIKGR KWGGPPLAGGATTGN/PPPGNFWKGGK APFFFSQKF
536	14437	A	542	370	10	FLRTFVSLFPRRVEGKVQSQLLAAPPS WQVITPPLQSP*LRQKDPFSPGG*GCS EPCSCPLPAWMTEDPSVSKS*KKKRKK EKN**KKKKSPTINTGKIRPRIH
537	14438	A	543	1	370	FLLRHLLCHPGFCSVATYCSRDGSS D/PLPQAPLPDQ*PRLOA/WHRLAPPH SANFF**RQGFVTLARMVSIQPCDPFH WASOGATATKADDYQK
538	14439	A	544	50	395	IPGLTRQWLDFPCASSTPTTYP/P*VQP STPQNSPSPKTHNQKGLPMPLSPTPKP STAWKKAILEHTSSSSSSSSSTCRNR NGYTYTVPEHRPARGHTASQTRKQVLAA THKP
539	14440	A	545	1	370	LCSVTAGVQRKLNLSVQPPPPFRQKVS CLSLFFF*KRVTLPRLRGRGPII FNGSPTLRG*GDDPPV*ASKELRTKGGPH QQGLINLF/CLGATGPTYGAQGGFKSPG LRRWAPLGPRA
540	14441	A	546	178	365	YKKTDAKTKRMDK*DSIRKLSFSTVKET INKGNR\QPTWEKIFASHTSDMGIIISQ ICKELKO
541	14442	A	547	11	236	KGTTKLVLKSDFKSYFAVIVIKTVRN/ WHKYK/HIDQWNRIONPEINPHIYQMI FKKRAKNQKWKDGLHKR*WNSDFQET CQEQTEKGRSSQEKMM
542	14443	A	548	355	3	IKKKNLGRKRCFFQEETWP*TPKKRP LBNPGGVFFNPGFPPFKAKIPEGPPFG V/SFF*RGGFQYPPPLFFFFFF*DG SLCHPGCSAVAQSRLTASSASQVHALL RHDDEGR
543	14444	A	549	1	373	CFILICRHTSHMWRIFQTTAINQINQ*K ESQVVSQ/LYI*KLHLLEYVO*HFV*K YTO*LLENADTK*AHAVGKMLVLDLKL AALSILFNL*KNK*NLXWPCNVAHACN PSTLGGGGGWLTS
544	14445	A	550	446	2	NIDKAPTVLGKMSVTFPTSRSPPLGPPK CWGHRREPPRPAYFGI*ILFLTPP*NEL NNSPQHLGKISGIFSDPSLSVFFSSFF FAPPKKFMLCF*PFFFFFF*DRVSLCH PGWGAVERSWLTAAPISQ\IR*SFHLSL LSWDHRA
545	14446	A	551	342	26	WAPP1FFFFFFPKRSQKFPFFPGENNSR GF*IFG/RGGFFKKEGLSQFFFFFFLKVV FFSPGGEPOGYFPPPKASFLKRIFFPP PPIKKGDPGRGSPPRGNNPPF
546	14447	A	552	3	167	QPHLQDCL*QONPVAVG*AFSSHPRDSL NNPW\WPGAVAHACNPSTLGGRGRII TLTALSSH*PFT*VGLINMLAPIVPL
547	14448	A	553	3	413	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^possible nucleotide insertion)
						TKKINFRTEAAIKVFLQTASTILLI AILFNILSQ*TTNTTNOYSSLIITIM AIAIKLGIAQFHF*VPEVTQGTPLTSGL LLLT*QKL\APISPIYOISPLSKKK SSPPPOARGETFF*KNFGEETSQHNKN EVFPFPPP*KFPPSPKAFI/RGGGGPK RDPKPKKFPKKTPRVYKPKDKKKKFF FPFVFKGPPRIFFKSPPLFFFFFFF FFFFFFFPPPPFRRMGCDRHWGKFIL RDGF
548	14449	A	554	441	1	NTSSMYVCIVFLIRQSL/DSVTQAGV QWRDLSSLQPLPP/GSNDHRHLAQ*YL FNVLLELVFVYERGTTMVPI*DCNVN CRVFGTRSLSVYCVMGIFYRC/HIESML CDRCFIFFDIGSHSVTQAGVHWCNIGL\ MKPLPG*RNFSGLN
549	14450	A	555	3	455	RRMRGKNRWNPGGTGCSEPRSHCTLAW ATEHDSVSKKKKKIRSSLGKKT*FYHNI LKAMG/CITGIHKGPEGAMQREGHFTPP QGPKAPQRGQTYDDP
550	14451	A	556	1	299	PVMWNSPEASSGWLIGFKIKRECICNIKV QGETASASVEAGVSPEDLAKITDEDEGY IKQOIFNVDKTT/Y*KKISSRTFIVRE KSMGFKASEDRML*FLGANAASN*LK PILICHSKIPTMTFSRAKS
551	14452	A	557	3	391	TRFPFPLGGFSKFFRPLRVFPPLL/RE RKFFPLPPVFGGPPALOPFWGLFFFN PSKGRPPGFFWGF/CFKFLFPKFL GFFFSFRGFFFFFETVSLQCP*SAVV Q
552	14453	A	558	337	1	IPFLLLVGLFFFFIRKKRGVFSRWR GGGNSFGLLETPPLGIDPPFSGLTPPKSW ELRAPPPPIKF*KFPLKKNQF*WVSPG GLEISALLVPPA/SASQ
553	14454	A	559	117	419	IYKELKQLCKRRKSNLYLKKAKNPINRHF SEEIOMANROMKRC*TTPIIIEMLIK TTLRYPASPVKMAFI*DR**MF/WQRC GEKGT/H/CWWECKSVQL*RAVWRFLK KLKILLP
554	14455	A	560	347	1	IPFPLQNGEKIFMLI*GAEKAFYKIFP FPPIK/TLNKVIGKNFPHIIRAL*EKP PAYIFHGEAESFPVRSGRTRCLPLLLLF HPVLEVLVRAICPLK/E/IKGTQIGKEE
555	14456	A	561	2	375	ASGSKKKKYPPFLRGSSPLPGNPLFFL EGGEGKFP*P/RNMGPPPKFPQKQGN PFFFFFLKGPKGGFPPQGEKGVGFP PGEKSQRP*GEKGVPPP*RKKPPPPF FFFFFFSETVLLLPKLECS
556	14457	A	562	391	2	ISDSGVHPLGLPKRILLQCLSYHWVP*P KCFC/PHLCFLMTLQPP*GLPSVCAPS KQEEHGCFFISVARQEC*PLFPKNLDT* HFVGNLFLKFFFFFF*DGVS LGHPGWSAI LHNCNCLPGSSNSL
557	14458	A	563	384	3	SLFLPLTCNGTISAHYNLHLHSSDCP ASASLVAGTGMNCLDSSIDPSSAS *VAIDLK*GARGNCPVS/LEKSGPE EMRGREGSASWDRPLGRPGVAKRICRR HCCPVQCPQVSMFSPGSPSN
558	14459	A	564	522	120	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515.1 26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
559	14460	A	565	73	264	KDRHIDQWNRIESPQIKSMTHLWSDF FLQGY* *KDRHIDQWNRIESPQI\NL*L YIYGHILFFYKQTE/IQWRKKTLSKWF WDNWFIFKCKQ
560	14461	A	566	413	1	EKKKKVPSQVLTPKQVQLNFFRFSEEQ *LSLVPVSSLPLQSLSGKNQGP*ARRVA LCFGKSPGSQIWF/RLP/EDIVTTVQA SYSKKRLFLSLDLDFQYVQLQRREGAVNSA NLSLAPW
561	14462	A	567	397	1	FLGQDLTVAWARVQWCSHGLKPRFLGL KGSSRSATG/SASPYLVPMFLSNLFWHV YLL*LYKTMIGI*MEM*FTPSCPMYSVV RDV*IFPSFETACPVACAGLQWRLSLG PPPPPPGPKFSCLSLLTSWD
562	14463	A	568	437	1	KFSEDPAKLIGEDGYSKQVNLNAN/ETA LYWKMMLSSSTFLARKETSMPLQGTQ* LLLGANAAGDFOLKSMMLTCHFNPRALK NYATSPPLVHLKWNKAMWMTVHMTALL TEYFKPTIKITYYNTNTGSLTTPHASAH ASAHAS
563	14464	A	569	234	1	FFPPFFFKASSPPGQTSRSSRGVF/PPFF PPPKKGFFPKIPVGGSSPPFF*EKTYFR FFPPFLAPPGVFFR
564	14465	A	570	2	396	FS*AFYHFGALTPQLGSDWSPAGITQV KSLQVPVNT\SGLLASGERIT*ADHN IQNNNRRIQALLITVLLGLYFTLLQAS ENFKIPFTISDGIYGSTFFCAGLHGLH VIIGSALLTICFIPQLTFDC
565	14466	A	571	3	403	HASGLPSSWDYRRPFRPANFFVFLVEM GFHHLNKAIKSFACNEIQPLSAVSAG LVGCV*VCKCLFPVL*Q*LPQF*/S/HS IANWMREWPLRLSLF*LIC*GERMSGFA TQSRDDPSLGLFLYQVLSLAKFR
566	14467	A	572	100	371	YKSNDFVYVGIHLPLTT\FFFFFPPKK KFPFVFQGGQGGNLS*LNPLFLGLKGF SCLKLKPSWNNRGAPPFPFPFGFFSKNG VSPCNG
567	14468	A	573	371	1	REGARES/TWSSSHTPVQKGLRYGIILF ITSSEVFFAGFF*AFYHSSLAPTPQLGG HWPTGTGTLPLNPLEVPLNTSVLLASGV SIT*AHHSILIEN
568	14469	A	574	333	103	SLQQLPPGLN*SSHLSLLSSWIYRHKFP CPANVRVFFVFCRDGVLVLAQGLRA/S ASQASGIGTGVSHLQVNLPLLYFSRAG D
569	14470	A	575	1	206	FCIKKITIGFIPGK*GWFNISQPV*SLTN RIKEKIHISMATAPISIIITEKVFQDKIQ HPLILQKPFQK*EYKFLNLIKIGICEIN /PIENIIYNGEILKQGCLLSPFLFNVL EDIVIQSVKIKEGINIETQELR*SLTNR IKEKIHISMATAPISIIITEKVFQDKIQ PLILQKPFQK
570	14471	A	576	157	255	YISPTPPPPDLFP*NYLNPRLTSPAP NFQIY
571	14472	A	577	365	3	PPHPSPVFF*KSPPPPPPPLFFPPPPPL FRGGPLYSP/SPPLFFSRRGKDTNPP PYSGLSVAGQTPPPPPRTPPLVSPPPP PPFFP*RGGPKNKKAKQTTTFKSPPT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
572	14473	A	578	2	323	NKPKHKNDRI VGSWEPEKDVSHRELLLSFLYPFFFSHI SS*ETLIDFALTSSTDIWALWHAENQTV VKYINFE/WWWT*PCHITSFQAISC*E DERPGAVSHACPNPTLGRGQIIT
573	14474	A	579	369	1	AHLKGTLCGFFDFPTINLEFRGGITSCP NPLNNWE*/R/RPPDPGKIGFAFFFFF FKVETGFHRVDLLVLIS*PCDLPASASQ SAGITGVSHRARPTPG*FKKKIMTF/CL *KWSHVVQAIG
574	14475	A	580	394	125	AAGEGQGRGWRNRPGRGERASDREERER VR/ERGEERERGEERAPQ*SERWR/E/R SRERERVELWSDSDRALEREALLR
575	14476	A	581	416	1	KGQDLYGEV*KVLLKVKIQVLNKKKMS CS/KINILISFIRIALKFFF/ELDEI/ CSFV* *NKC*RIAKEVLKKQ*CLGGHL /TSPHIRRSYNTTFSQIWCCYRTKQID *WIRTQNPEDLRI*GDLIYDLRCCSSS RA
576	14477	A	582	3	403	NCFSQFNVIIMEIPAKFFIDINKLILKC FCKGRSILKKR*EDS/QRRNLFVITV WYWQRECHIDQWDRINNPENLHKYSKL ILDKGAKAIR*TKES/I/YSK* C* NWKFCM*EK/IDPKLNPLYK
577	14478	A	583	402	121	QSLIHSKALTFLFNSMKAEAAEGKVEAS RGWFMRF*ERNHLHNIKQVEATSAGVE AAASSPDQ*GKTTDE/GGYTTQIQINVD ETAFVWKTMS
578	14479	A	584	255	517	IYIEGFIFRGRVLL/CIHPS*SVVLQS* LTAALNFWAQS/LPSSNDYRCTPPCLA FFFFPCRKGSTLCPRLVGNPNLPKFFP LGTPCF
579	14480	A	585	1	414	SSHSCCSKA*SSMGFSPAPYKLVLEPLC LPIDWDVNLCHPGWSAVQSLSTAATS Q/VHPSS/CLSLRNSN/EYRVYP
580	14481	A	586	392	43	CNDYRCEPPLA/ETGSSSYTSAGLEL LASSNPMWCHPKWDYSHETMSAQNF FLKGIS*F*LCCSHFIHNLHLWLGKVIH TYTHAHTGLEKYYKQCLDVKCIYSLLD GAIK
581	14482	A	587	1	394	GTR/YGINLFITSEVFFPAGIF*APYHS SLAPTPLQGGHWPPTGITPIEPLGPLL NTSPLLASGLVLT*AHPSLIENNRNOGI QALLITIVLGLYFTLLQASEDFEDPFTI CDGIY*TFVVVTGLHGLHV
582	14483	A	588	190	3	DGINLKIPGGIFPFLKARSHSVTEAGMR W/P/NYGSQPRPPGLK*SSHLSLSSN DHRHAPFSC
583	14484	A	589	157	387	TKKRGVRGGVVIKILGINLTKEIRDLY SENYKSLKEIKER/DTNKWNIPCF* T ERVNTVMSILPKAIYRFNVIP
584	14485	A	590	891	0	PPPPPPFFLPALIFFPPPPPPQ/PKTPKK KKNPPPPPPPP/PPPPSHIP*QFLSPPPQ HHHFIRHPPQPPPHFPYNYNPKFFFF* NINVPPPP*K*YFF*TKFFFFIPNIEF F*TKKKIFLSPPKFPPLLTNLSPLIL IKNLLSKPPPOI
585	14486	A	591	1	496	GTRAYQIVKPTF*PLTGALSALLMTSGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PMKVHFHSITLLIRLLNTLTIYQWR DVSRESTYQGHHTPPGQKGLPYGIMLFI TSKGFFPARFL*AFYH\SSLTPTPQLGG HWPPGTMTPLNTLKDPLLNTCVLLASG/ VSIT*AHSLIENNRNRIEALLMTIV
586	14487	A	592	175	2	PPFFFFLLRHSLLTAQAGVQWCDLCSLQ PPSPGFKRPSRLSLP/H*PGMVANFCIF SK
587	14488	A	593	107	733	AAAAASKVLM*REGQLPGAT\GTGGVQA *APGSVA/AEGASVEGPGDTPAHQG LSPTRSHGQGGAGRAS/SSQSGPGGRG DGASRVNSGAL/SPGGKDGASASVPRG PYAEAEKGGWALRGVAAKPGPPSRAG QAPSGS/YTGPNAPAPWPIPGQGGRL RQDAG*VSSWTCSTEGAHTAHAPGHS KGKGSPOQHPGQGIPT
588	14489	A	594	10	435	FKWLLKSHATCFWTR*SYCDNVCVPSL WAHLGLIRTEIPEFFLSKFLCTSIIPH TYRQLRLIQGST*EA*EDKLRQK*AL GAAQFTLPQMDVFCVFCF/CLFEMES HSVT*ARVQWCDLGSLLPLGFKQFSC LGL
589	14490	A	595	437	3	DEPKKWTIPCSWIERTNI/VLKMALP KAIYRINA/VPICKLPSFFTEVGTFSQN *KTLIKFRWQ\KRA*IAKATQSRKNK ASSIT/PDVASNYKTTVTKTARHWYNNR HVDQWNTIENTEIKLHYSQ*ILSKAGT SKQWGEKHV
590	14491	A	596	2	498	FFPFLGKTKPPTLFFFFFFFPPIFFFK IFFGLPKKQNP/K/PFFKRPSPFKNF FFFSPPPPFNPLFSKAPPPIFFFFKKI FFFPFPPLFKSPKXPL*ILGFFSPSP FFFPFPFFPSLF*GGVSLCHPSWNPVL SRPSSKLASAFRMPPEV/SPFPSP
591	14492	A	597	1	311	RKVSSESRWRSLERGRSLETQRMERP RCQRFRENSCVAPRHCKGPGGKGLQALF *VFAQLGEPGQGLDPSGAEATVPEV QGE/PKALLPTCA\PCGEGSGPFTPR HCKGTGEGSGPFTQGRETSKAQQRG LLSCRGCLCLSVSDS
592	14493	A	598	302	2	FLRFHHKFKTKALNRHFSKDTLLYSS NHMGCSMSLVIRD/MLLKIT/MKYQFI PTRMA/IKKTDYQWQK/CEKI*TFIH CW*\NEKMPQPSWKAVQFLRK
593	14494	A	599	3	386	HTWPPPPSPPTAPARTQPPSLQSLPA PQPGKKKKALRNEK*NGSKG/RQGR PPPLRGPNGRTRSPAGICKGGGFCPV SKAQGAPRPGRETVPVPGFGRPPPLR GPGPPGLWTSRHCLPR
594	14495	A	600	374	53	EGFFFFFKRWVGGQRLFWSPHFFPPGV KIFPPPPPPGWWGLRGLPPPPNFFFL KKKGFSPPFCVFSQLPPAGVPPPPPP/ TGLDLRG*PPGPPPPPPPPPP
595	14496	A	601	393	1	VSPFKGCVSENKIPPPHNYFAKTFVHV KLFGVAPLFLQILF*GPFLTSIRGLIL/ WIPYSPGYTLTLLIAPRHFLRTIIPV RSVLPKTYLGLSGMPRYSYDPAIT* NIGAFRIARESVGKRLLD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, ∅=possible nucleotide insertion)
596	14497	A	602	1	155	PCFVT*SGQWRNHDLSLOLSPGPK*FS /CSBWDCHADPHLASPCIFRSTRP
597	14498	A	603	170	455	KPNASLKRVLILCIGLQSSRQQKNPT/VKKWAKDAILFSTEDL*TVNRYIKKYL TSLVIKKYHFIPTRLKMKKTEHSKCWE SCGEIETLTCSW
598	14499	A	604	3	449	TLLSNLEAAKKKKDALNETRES*TKLK ELPGVCNETMMALWEECKCLKQTCMKI YARVCISGSLGVRLQLEELNQSSPFYF WMNGDRIDSLLENDROQTHMLDVMDHFF SRAFSIIDELF\QDRFTREPODTYHYL PFSLPHRRP
599	14500	A	605	169	435	KYENTKINRR/VAPN*ISLSPKKKKKK KKKKKKKKKKKKKKSSSSKASPSSSR GG
600	14501	A	606	453	29	TSPPPPPFGENFF*KKPP*K/HFFPPFQF RFFPPPPFLKIFFPPPSLFFFWGVFPHF PPPPKKVFFPKSPRGFFFPPLKKGKFF SPPLKFFPPPGFLLSPPPFFFPFFFPFF FFFSPFFFPFFFPVKNFYLLCYFYKN
601	14502	A	607	170	408	NEYDHSIIKERRRDVCVFFFFFSR*S FTVVTQAGLSLQPLPGYKRFSLCLSL CSWDY/RVVPQGSANFFVFLVEMG
602	14503	A	608	2	448	SLHPVITYSEGISKRSQSPCWR**KTVKKK KKNPNQPKKKKK/RPNPLGGGKKPF *PEKKPGPGKKILKEGKKICPFPPOKK NFKILKKKKGAPLKKNP*GAQNPFGMK KINFPF*REVKKNPIGIFKKKPLFWGGP IGANPPENL
603	14504	A	609	441	28	GTYLKGKSAK*KGPPGWGARGFPA RDPPOGG/PGGGSLSPGNLPPGPGC *TLFFKKPKLTGGGPPPLIPALRCVR P*NSLYPQGGGAQTPPGPPPPGKRAP CFQKKKKPRRKEKKK
604	14505	A	610	445	1	LWLKNTGGGGGSPFLFPPLGEPKRD/G FPRGRGFGPPPPPKNPFFFLKQNNPG GGAQGPFGPWGG*GGEFPLP\SPGFH *PRFGPPPPRGTGREPPFQKKKKIANC FLSDKSLLEEAAGQVVGSPLEPTVA PKPNRKGAK
605	14506	A	611	253	437	KKKQVQDMFSENFKML/NEIKATLNKWK DISYS*VRLCVVKMAILPT/IGSYRLN IIPIKI
606	14507	A	612	186	2	KKKQVQDMFSENFKML/NEIKENLNKWK DISYS*VRLCVVKMAIL\PAKQSYRLN IIPIKIQA
607	14508	A	613	37	453	KTPPPGFENFFLKRPQKNFFPPGNWGVF FPPSPLKFFFP*TFIFFGVVWFNFPFP KKKFFFKNSPGVFF/SPPP*KKKIFPSP PRYFWPP/HGFFFGGPP
608	14509	A	614	1234	0	KKPPNTN**WAKDLNRHFIKDSSIKDD QYY*SLQCKLISQYNFTCTRAIIKKT NNNKSW*GCGETGNLIH/WIECKMVO
609	14510	A	615	327	188	FFSSLLTISIPKPNHVTSLRLNK*AM LGSSHL*QLQLRLRLREDHLSPGVSGCS KI*SH\THCTPVWVTE*DGKGLGADGS HGVQTQVO
610	14511	A	616	103	446	KKKKKKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LOGGALKKNPGGAQKNRGEKKKKFFFF*G G\KKKT*GGFWKKNPFLGGGNFAPPPPK KKKPLEKKKNT*GGRGEKPSPLCGKEK FSHKKK
611	14512	A	617	3	429	GLLSIIYKELLQINKISNLVGKTKRDK/ NKQFLKKEIHLRAK\YMKRYSTSLVTIE M*LKTRYYPFLPNKI KHDNNIHC*GYK EVGILHILLEA*IGKPFWKAITVTVLNA PVFCL*FCFEMEFSHCCPSLKCRAFTSF IGAS
612	14513	A	618	427	6	WGSGPPPPPIFFFFPPPPVYFFPPFFLQ ALPSRVFFFLPFPKKNFPP*GPPFP PPPPPPFCVAPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPFLVENCVPFINSITSIDIEQKISI SC
613	14514	A	619	68	434	YSKD*PINTKKKKKKKKKKRGGAEKK KPGGGKNGKKKKKNFF*KGGGKKNPRG NFGKKTLLGGGKKGEKPPQKKSLGKK KI*RGKGGKK*NP/CGGKFSGGFF* KKFPFGGGGY
614	14515	A	620	454	90	NFTPEKFGPPQGNL*KAPPPPPP*RG PPFFFP*QKRGFKSPQKPPQCKTIFR PHPPKGGPGQPPPPGGKIFFFLEF\KK KGGFPG*PRRFFFGPGKPPRPPKKAG IQQETPRPGP
615	14516	A	621	432	2	PEAFSLSLHHPAFGERFLKKTPEEKFL TAKKYRVFLPPPLKIFFFP/LRALIFL GRFAQIFPPQKKGFFPKIPRGVFFCPE* KKKNFFFLSG*IFAPPGIFFRGAPPPFF FFFFFLDRVWLCPGWSAVARSRTS
616	14517	A	622	422	2	GGGPFLLPPRGGGLPPPK*KA/VGGGKK PPPPAPL*NNPPPKKIGGGGGKNPP PLACFPFGFLLPPPPSPWGGEEKFFFF FLSGGPPPPQKKKKKKKKKKKKKKKK KNKKNQTKKKKKKKRAARDPPVADRV
617	14518	A	623	176	401	KFSMFILWKAYYFLVCVVCVVCVVCV VCVINYLFISSQ/RLCLFLGEGKICIS LTVLRGRSRVCV*SQDLPLVC
618	14519	A	624	1	355	HSSGLDNLTAHSHLCCGV/CLCFVLV VCVVCVVCVVCVVCVVCV/CLVPGQV PK*SKNSSTSCLLFHFTSARTICP/CC/ CVVFCFCFFA/CYQTC\ILTSC/LAIC TASGVCL*ANKYSM
619	14520	A	625	2	400	HTRLIFCRDGVLLCCPGWLTPEKSL PSFGFLSLFFFFLERDPGSHG/VGGG PNLG*WKFWPLG*KQFSFLTLWRGNT/ RGPPPPPPGLVFWF*KTGFCFVAQAGL EORPFGDQPVWASQAGITGV
620	14521	A	626	307	3	VFFRLPLETQGGFLACFCPPPPCRFFFS FFPGSINSPPFP/L*KLNFWAFPPPPFF FFFFSILFDIVLLCHPGWNAV*S** P*TPGLN*SSHLTPSGRV
621	14522	A	627	1	391	NPPLPGAKEGGPPRAROSNPPYPYNET PFFF*NPKIFPGGGGHVIPSFPFG*GR KFLPREGGVPL/RNFP
622	14523	A	628	191	375	LILIFKTIIFNLLINFE*SGGATQAGG QGRNLG*LQPPPPWLRFSCLNLLSSW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
623	14524	A	629	3	382	DYKGRWF HHCQIRLFILLITASEVLFPCVLFVFFET GFCSTVEAGVQ/CN/HLQPLSPG/PPTS AA*VAWTADVHHHAWLFVCLLI*DGSSWS VTQAGVO*RDPSVQPFPTGLK*ASC\P AFQKCLDYR
624	14525	A	630	396	2	CRINVLKKKKLEMSNLSEEGMLKANTG QKLSLLAPQOVVNAKESLLKEIRSA PLNTQMIRMNQLSADMEDIL/VVWIR/DP TNFNIPLSQSTIQSNA/L/TLFNFMKP* RGEEAA*EKFDAISG*FTTFKERS
625	14526	A	631	47	392	LHSFFFLFLGKKIPTFGGGGGGGKPPF* NPDPGP*RNFFFLPP*KTWFMGAPPPR KIFGGLKKKGFLGPNL/SIGTPPPRGT PPPLPRGGCYGGGPPPPFFIFFFRTFK NFSN
626	14527	A	632	39	382	LFSSPPFFKNFFFFGRFFFWGGVAPIF PPPKKIFFSQPF/LQVFFSP*KKKFF FFPP*IFAPPKTFPSIPPPFFFFFFFFFF FFFFFF
627	14528	A	633	2	213	LDPKPKHSRISLQKI/HNGVCLQS*LL GWLQRQEDCLSEGS*GCSEL*FYHCTPAW ATK*DPVSKKKKGLK
628	14529	A	634	2	206	QENGMNPGGRACS*PRLRYCTSSWATER DSVSKNE/TNKITLGLREI*HFVGGPNG KKGLLTKTVKGLT
629	14530	A	635	205	2	KRSLGLLAQI*/VQWGDFTKLQPLPPGV KQISRLNLLKKWDY*RGPSGLGKFW/IF L*KGQFPQFFRVFN
630	14531	A	636	3	399	QVQGT*PASCPLDSLSEDEDLQLAMASM TPPKKKKKKKKKKKKRGAP*KKTRGG PKK/TRGKKK
631	14532	A	637	122	373	VSNILLTQSLLEFFFFFLKGSSELVQPG QGGLDLG*TKFPKRLKEFSCLTLRISG NYGLAPP/HPG*FCFPIKKGVPCCPGW F
632	14533	A	638	390	3	LLVLFLPDGWSPPAPFHEQKLEVS PKANAAMLVQPAK*AHPTFFY*FSPFR FFFAFMG*SS\YFVPMNLKLSLKGPI NDMREVFVFIIRLLILFFGDRVLLCGP GWSSVQ*L*LIAASA
633	14534	A	639	392	42	PSGPGKPGGKTLRKPPFQACRRQGY PLFPPKPLKNKPAQPNRNLGPICPPPK P/QGPLRI SPQNSQSGSL*GPNKNCFP A*TWGPPGAP*RGPPKGPFFFEKVME AMGLA
634	14535	A	640	390	1	LSFSEEGMSTAEGQXGLPLCQ/TSQVI NAKETFLKEIKSVIPVNIQMIK*NSFI ADKEKILVV*I*QDTSN/IPL/SQCLI QSNVLTLSFKKAERGEEAAEEKFINFS *RLRKAASADRAAESYPEDL
635	14536	A	641	368	3	KKGGVGVPPFFSPPGFLGEGSFLFPKI KVQKITL/SWPPPPPPGGKKKTFFFKKK KNFELTGFFFFP*KKGPSFFFF*CPV* KFNQGGGFKIIFFFFF/RDRLSLCCPGW SAVU*SQFTPRV
636	14537	A	642	134	413	QKDQRNRIESLE/IR/DHTNLTIDKSG VTGPQYKDSLFLNKWCNDN*RE/ITQNL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleo- tide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						SLDPAHTTTNNVLKWTCLKARP/VRTL VENMGENLRD
637	14538	A	643	2	436	GRVESINLPLGCRFLFKRRDNKCGQ\G* RAGGSLIHCV*EC/EVVQPLWKRIQQFL IKLNIHLPRDSTILLDLIDLGHPKTSAL LFIIYTHNCCFIHHP*LEQPKCPSTDVW MHKWPPIHSMHYSAIKSAVWDFKGI LL
638	14539	A	644	446	75	LDLLTS* SACLGLPKCWDRSEPPRAF NF*/STTK*SLWSSHQDYICRFLLSYT ATQKPSLTITTY*SHLKT*NAQMPRLYL QSLILGSI*FKSNLDR*FQCAAXENH* *SDLYCQIMLSPFM
639	14540	A	645	318	1	KGVPRKCKNSYVGPSPGPBK*TLFF*I F*DRISLCSPGWNAFVS*LPV\T*TTG VKWWMPLSLNLI*GYKGVPPRPGI*FFFF FFFRDR/SLTMLPRLVTWQVIFQ
640	14541	A	646	3	348	QFSSFFLIYFFLPFVVSFCF/WCFSNL VLPCEIIFLFIYYVSLVLSFPYCLLV LFLSKLSFF/C*YLNITVFICSMTSFF* RIL/CCLNFIKTSFNFL*FGVLESC FFFFFFFWP
641	14542	A	647	2	553	AILIPDKIDLKK\VTGDKR*NVMTIKGS IHQEDVTTINIVASNSR/APKYMKKLK GKEKQISP*K/VVGINTPTFSI/DRAPR QKINQIEIDLNNIIRQIDLKDIYRTFHP TSEYIFPSSAYET/FSKIGHKLKHTSL NKYK*TEIMQSPSD/HGOMKLENNE/N VGKLTNMWKSDDLVSQWLAHA
642	14543	A	648	388	1	GPFR*SPFPKPRGAVPQ/GGGGLKPPG PQENP*FFFKPKITLGPWGVP/RNPPF LGG*KGKIP*/PPGGGSKNPNFSPSPG PKQKQPFPSQKKKKKKKKPKES*C POTSQPVVDGSOINASISS
643	14544	A	649	387	25	PGMRGGFFPFLKNFFPFGP*/MSGGG GGPNGP*PKKGGFPKMPGVFSP*PKKK KIFFSP*PPENLGP*PRDFLKG*PLFPFL QKNPGV*FRAGQGNP*PQKLAKI*PFLPPG GGGGAVRHI
644	14545	A	650	918	2	LGLKGLTIYKILHSTIADHTFFSSSHGT FAMTDHILGHKIHLS*FSKE*EIIPSTS FQ/HHSRNLN*K*INKNVNMKIP\FWR LNKTLNNT*TKB/GLKRHNILS*TKN ITYQILWDAGKAVLRGKFIVLT*IRKE ERSK\TTSFNIRKRNKLIINIRTEINE IENRKSEKILN\TKSWFFPEKKKSIKIK TLARLNKRKRKETQIPKHQ*RRGITTG NMANKIKRNIHQPYTHKLGNDNIGQ FLEKRYLPKLGQGEI*SGWAYIN/SKEM ESIINTLPKRRKAQDLKMFQSSE*YQTFK EKK
645	14546	A	651	282	265	GVFFLKKRPVTF*KKKI*LGPHPQLKGP PGVFQ/HFPI*NFGISGRGDL*FFFFFFF FFFFFFFLRQGVSVAGTGAQWHNQS LQPPQLK*FS
646	14547	A	652	6	223	LYAHKFNLDKMDQFLQRHNTPKLIQEE /HRLTVIK*IKSIVLPLPKQA*GPDGF SGEMYQLLKEEIIYVNF

[illegible]

SEQ ID of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						SEFNKVTVEYKLNQYQ/SQLYLMPKQNT *KV/ILEKHEL* PQITKYFGEILKKDVL NLTYDKYKISLREVKGQEQKNWNVSS
662	14563	A	668	405	566	IHCQNECKTEQILNKTVWVFFTKLNL PGDSAIMLLGIYPKELKMYIHTETCT
663	14564	A	669	218	2	LLMLESIMFVPPFPSPFKWAKL*YI/CH GAHANFLPSPFPSPFPSPFLS*FFFYNRV FLCCPGSAVVRSQLT
664	14565	A	670	2	210	NFGQEESEMNLSCLYHLEKGEQTRP KASRKEIITK*AEI*KVQVSRENK* KWWFFKINKIDKPLARLTAKWRT*ITI VRKEGTITKDPADTKRIMKEY/YKLLY MHSF*NLSENKRYREVIEKINERSGSL KRSIKLTNL
665	14566	A	671	200	3	SLCHLPHVASKATLET/GLVEHMM*DFP CFEETESHCIAGSGVQWNCNLSLQPLPP RFXLPSCLSL
666	14567	A	672	94	374	PKFRPQTTTEQTSQFQINCKKRRKQ KRTYRLGEIQKOSQPMATFELYLD/H*F *LAKETL*LGAVARTCNPTSLGGQAGWI TRSGVQDQPGQ
667	14568	A	673	312	3	WKMGQLPGRPOLPOLSOEKLISLNSPNV FKKKKLLK**NLPKKRPDCFTKRFYQ TFKEIIPF/L/HKLT*EFKKEILLKS F\YRGSVV*AAKLNADINKTTH
668	14569	A	674	34	438	QLT*PD*HFYKYSTQQQRTFFSSTHRVF AKLGHNLVY/KANLNKFKWLQVISMFL DRDRIALKLNKNNK/PSSPLKYLQTHLL NDPRIKEGSKREIIKDFALNDNATY*NL WCL*NGTLRKVYTTKCLFRKEGQPM
669	14570	A	675	3	349	QKDRKSVRPS*NPPLAVEKIP/LKON PERFNGPAFFKIAHGLTSSLVFLANSN YERTHSRIIILSQQLQTGFATKTRKLL ASLANLALPPTINLLGELS I
670	14571	A	676	346	1	KMVLL*NIWVKLLKGLTEVPHGSAIF PFFIPIPPKEMETNVHIIKICTWAFPAF FPMKKKKQSGNNPTDE*IQKKW*TH IIDYSAIKRNELLTHATSCNITLSKRS QTKK
671	14572	A	677	357	6	AAGDSLEKPMFIYCFQKPMPL*IMLKST LLVLYKWNHKAAMTACLETAWFTE/HCK PKLETYFSKRFSLNIT*LMKASGHPR LTEMYEKINNVKPSNTTCTLRPMQDEV ISTFNSY
672	14573	A	678	401	155	YYSVAQAVVQWRDLSSLAQPPGPF*FS C/PASWDYRHKLITSGDLPASASQSGI TGVSHCAQPLSLFVFFLTINQRFVAALS
673	14574	A	679	292	395	Q*KISFEMLLIITNVFGHPTPMEMYKE LNFF*MPANTSIP*PMQGGIVLTFKSY A/RNVFCKAIAV/DSDSFDGFGQSKLET FWKGFTI*DVIKNIDDL/WRGVKIPILT GVWEKIPTLINNFVFKASLEEI
674	14575	A	680	275	3	WFRQASLALNT*SIHIYIHTDMRTHAHT YIFGMKSVTQAGVQWNNHNSLEP*SPGL RRSSHPSLPTSGEHRRTTPR/LADFLHC L*R*GFTML
675	14576	A	681	330	307	GSV*PVNLIIRNCPQVQSGCA/SLHSHQ E/WYMCSPHRYHLVASVIFILALFFP

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						LRRL
676	14577	A	682	390	43	HLPLPIRYICLSISSILCSFTMYLS/IYLSYLSIYLSIYLCQRQCIPLWFLCILL S*LS*ILILNLSFCFVGRTIVLS
677	14578	A	683	396	63	ADPTETQRTISDYVYQQRHTNKLNL*KM DKFLKTYNLPRLN*EEVETLIRFIANLE IALIKSLPIKRSPLVGGSPVGF*HIDK EELTPVLGLQFK IKKEELIANSFVESR
678	14579	A	684	1	396	EETLPLFADDMILYITIKKQRTKTKTKE STKRY*N*A*M\NVFGKVAGYKVNTQKS I N*QYTI*KVKLAS\FSSSPQNNKIGINL TKEIQNVYSENYKTLKEIKDNL*ESIP CSQIRRFNIVKMTVLLKLIYR
679	14580	A	685	283	3	NCVSSNTHLWEPSSQKFLSSVSLTDVCP PMLSAALFAIA\RSYTLPTRSSIDE*IK KMWYIHTMEYSAFCKKRIMSFLMPRME LKIFRVNKIR
680	14581	A	686	53	324	HCFCDRIRAAFCFYILDCFFPFIITHKL I*IFFFFLERESI\FVGVGGGPNFGS LNLPLPRLRRFSCLTLPRGGDYGLGPPC PT/NFCVF
681	14582	A	687	39	208	NIFFCREGFAMLARLVNS*NWPGKVTH IHN/P/STLGLGGRIQTQTOFETSLVDA GA
682	14583	A	688	47	341	SSGRVFLVLCFFETGSHS/VLFRLAYSG GISAYCSCHLLSSGDSPISATR/STTGM CCSAQLGFCVCVCVF/IFVF*VKIGFC HVAQAGLELLDSSNPPTS
683	14584	A	689	229	1	GRVDGRGIACOEKFKARLASQSAGITGVSHRAQFFCFPC/LLFVVFEMGSHSVTQAG VWCAPAGSLQPLPRFK*PSC
684	14585	A	690	339	1	KKGPPGGPTKPEGGERPPROPGGGKEVP PPPPPGGGKEKKRGAPPFFFLKKKKK SKGGG\N*FPFPGGKKGGQKKKRVFP PKKKKKKKKKLSLSLSLSLSLSLLG
685	14586	A	691	372	0	YDYLTKKL\N/LREKTDKFLDTYNLRS LNQOEIENLNTPIITSNKIETVIKSPPT\ KOKSPGPE
686	14587	A	692	117	297	APLLESSASYLHFSN*DLQAH/KHTK RCSTSLAFREM*IKTRRHHTPTKMAT SKRHT
687	14588	A	693	122	322	EQTNSWSDIFFFQRCNSNANGENKCLFN KW*WDNYVAI\AKMKLSLFPYIKTNS K/WIKDLNIRAKT
688	14589	A	694	21	342	RSFHRHLNEYATQOGNSDVHPLLHNS ISTAIWQLQRQERRKEKRLKEVKNKA LKEIFFLRGWVLLCHLGNSPVVGS*FIV TLN\FGLRQSSHLSLSPSSWDYRVP
689	14590	A	695	2	343	KFVPLHSLGLNRSQKQTLSSQRKKKKGGV FVAKAKVQNHNG*QGP*TLRQSSCLS L*GGWVKL/PGGRHWAGFHVKVGLGLE LLTSDAPSSASQKAGITGMSHTAPGPK NLV
690	14591	A	696	336	3	IPPVKSPKFPILLKKKKFSLFCFSGAPP PCYSPPPRAQKGG*KTFSPPPK/QKQPG ALFFSPKPAFFPPPPFKKKKKKKKAKEGH YLMKIGLIOQEKIILNTYASNIGARRRG
691	14592	A	697	374	2	APY*KKVSRTFIAREKSMRPFKASKDR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LTFLLAGAGNFKLKPVLVYHSENTRALKN YAKSTLSVLQYRTTKAMTSHLPTEWTF EFFEP\TVETCYCEKKIPSKILLTDYA PRHPRTLMEMYSC
692	14593	A	698	361	3	PQMCPPPPR*QGIIFL*L*THCFFCTVK ARLFLFPFF/S*RGKGGFFFE*RKFFKY FGWELFQIRFKVFFFCRDVSLCCSGWSA GART*LTAASTSPAQASLLPLTLPSWD YSHVLPLRV
693	14594	A	699	75	362	KDCAYGICSKKQKGFCLTQTGAWQQYEE I*GLET/GFSRSVHSMGQRRYWDYRHAL TEPANFVFLVETRFPLHVQAGIELPP/S SSQSGGTTGVSO
694	14595	A	700	2	277	PFLYTSNMQSEKRI/RETNMFILTSK** NRNVKEI*DLNENSKTFLKEIKEDLN KWKGLSS*TEKLNIIK/PTAI**FNAI LIK/1PMVDFK
695	14596	A	701	1	407	GTRKHFSSKEDROYHKSRLKQKT/TVSY CFTPTKLTTVGKTANSK/CWAGCKVIGT LIHQ*ECMVNLLWT/SVQQL/RNVK LYETAISLLGICTREKTPHLHII\IA KKWQQLRCLSTDWINNM*YIHTMEYYS A
696	14597	A	702	209	3	SLNRRLSFFFY*RGGLALLI/EPGNGAV ARSWLTASN\FELQRSSCLSLRSSWDY RRVPLHRVSLRFSC
697	14598	A	703	308	3	TTGLKRFARVGPCKNDYRCEPPGLATS SVLKAFCPIGVSPPRLSRILSPM*NQ* YRMLTISTKYFFRMVSI SRPCDLPALAS QSAGITGMSHHAELVPLV
698	14599	A	704	603	2	PLPF/GLQVESF/CVSLPSSWDYRIAPP RPAFVSF*RRGFTMLAKM/VLIS*PC DPLASASQSAGISGVSHHAWPKQT*LLD TDKTEGIFLTNHLRI PPMFYQYILIK LESVKETDKRRKS VSSCTLYRCL\ILF IS*AYIKFTFFFF\ETDSRSATQAGVO WHGLSSLQPPPPGFK*FSLCLSSWDY RSMPPRDA
699	14600	A	705	3	366	ARVTVYSGKKEPGYLGMA*AMISIGEL GVIV*AHHIFTVGIDADTRAYFTSATII MAIPTGVKIFS*LATLHGSNMK*SAAVL *ALRFIFLFTVGLGLTGICLSNSSLDIVL H/DTYYVGAHF
700	14601	A	706	358	3	GPHHVQAGLKLTS* SARLRLPKCDY KREPPHLPADRKYFSLPVFARNFVPOG P*\HVWINICLSQVKAATGYEGAGAL RNRLLPH*\RIFWQRPDRVPIKSPWTLRV ISTLCS
701	14602	A	707	358	67	QLSSTIY**KN/RIDQWNKIAQNTSVH RKLISDKVTKPIQWSDSLFNKECWNV* TSICK/LSLDSALTFLTXTNSK*ITEP GSVAHTCNPTTLGG
702	14603	A	708	34	363	RTVEFFFFFFFFFFFFKRTPIFFFGPRGG *IPPEKKIFPPVFRGKFKKPHLDPGG GNFPRKPPFFFLGP*SFPLGLKTLGGGG WIPFPFPNPLFKKIFWAGAGSPFF
703	14604	A	709	1	380	STCKRMLDSYFTPTTKINSKWNKDLTV RGRTIKLIEENIGVNLHDLGFGSGFSDM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TPKAGAKRRIN/WDFPIKYLKPCA*EDSI ERV/N/RRSTEWIKI FANHIQ*GN*NIQ RILKLSKL*ARKWAIEDL
704	14605	A	710	382	30	PSTTGVHHHTRLTVEF/CGRAKISICWLL VNMS*AQSACLSLPKCD*EPOHARFV SFNTRSGIPIITISNTPSLSLSAFSPQCF FLFPHFPASHPETALAEFFLGTFPSLSP GPPTPAS
705	14606	A	711	1	377	LLVIGCMQMKITVRCN*TLNKIATIEKK TAKCC*HYGGLKTLIHOMCKSNMVQPLC KTV*QF*KKLNIQLLYLLK*KKAYIHP NCTQMFIA/ALFSLAPNKKQSA
706	14607	A	712	1	390	LKXIKMLGMAAWACNPNYSGGPGNITA* TW*AYNALTRLEPGRGDHTAALQPGROS TTPF*KKKAVPFRA/RPVKMREREI*KP FSPE\RTYSCAQEQPGRTFGSAQDLEAA GGRGHHRMGAVNQEPHRLLG
707	14608	A	713	2	393	KVRQIINVDATDSTGKMIINWHYV* LYANKFNLAEMDTVVERYKLP,KEIDV MNSLVPKAEIIVVVKILLTKTPDPHIFT NEVYQTFKEYY/PVLYKLFQKIEDERTF LSSFCEAGINLISICRRFF
708	14609	A	714	219	1	PRPGAVAHACNPS*LGQGGRI*TOSSI IKACCLIHDLAIQTQKQMT/WPGAFAHA CNPSTLGGQGGRIITRSGARDQPSQHSKT PSLLKIQKKLASVVAGACNPGYFENYIQ KLLRGPGT
709	14610	A	715	381	126	LIAGGGVCT*SQLFKRLRQEDHLSPGV RGYKEL*SYPCTLAWYTE*DPVF*KKNY /TLNTSPKETNKK*GVRCIKTGKVLIFV AAG
710	14611	A	716	417	1	CYCCWGATNKILLTIDNASGRQIVLMDW YKKNVVFPVNPTRSFVQLMDQGIILNF KSYLRN/TF/HKCIAVINSKSS*ESGQS KLKALWKGFTVLYAIGNICDSGGVKMPT LTEV/WKEVILPLMGDFVRNRTSEKQNY KLS
711	14612	A	717	406	122	MFSRDAVSLCCLGSW*TPCLKLSLSSLSL PKCWDYGRPEPCSAADF*IIIRK/HSC RNIIRNSDAWQR*TLVSYDRNPP*FPS PPNPSPLCPAA
712	14613	A	718	535	1	HNLNKIV*NLHVENYKMLVRDKKT*ISC LWVR/LVKIPVLPKLFYSVIVFPISRL VRYFIEVCTFTLKCIPKEKDLQPNRF* KKKKVHLFPFIKVY\KLQ*YIATVIKT VMY/W/YSKIDKAKWYKTEKAEV*PHEY DQLILAEVQINH\NLFNKCY*SN*TTIG KNMNLNLSFTSYT
713	14614	A	719	255	1	GKIQPNKGLISLIY\NL*KLVRKSNPKE KWAGQNR*LTEKGQIAFRHMKRCSPR FIMKAMHIIITWSYHFSSKRKTRIQRLT
714	14615	A	720	381	0	KPIAVNEYIKETDLPTNNLTLYLKEL/ EREELTCKASRAEVI\KIRAKIIRELT PIRKTDQSWFFLKIHKIGO/PFKLD* LQKKVRREKVFIITKRYENRVITTNFTE /IKRIIREYDH
715	14616	A	721	3	381	IYREWDLTRDGTGYQGHADPGEKG/VC RYGIILFITSGGFFAGFP*PFNHCSLA

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						PTPOLGGPWPPGTGITPLNPLKVPPLDTS VLLASGESIT*AHHS\LIENNRLQQA LLITILLGLYFTLLQA
716	14617	A	722	56	455	KTIINIKPPATIQYQITPLFV*SVLITAE \LVLLSLPGLAVGITILLTDRLNMTTFL DPAGGGDPILYQHLF*FGHPEVYILIL PGFGIISHIVAYYSGKKPEFGYIGNV*A MISIGFLOFIG*AHHIFTGGIA
717	14618	A	723	398	3	HQLPVPWQYKKNKAMITRPLFVDLH*CL VFEVSKYPASKGLPPKVKVIMLDNAP/H PTQNSMSS/DSKGEVILYLPNTMSLI* FLDQGVIRTYR/RHYPOYSMORSIRPMQ EISKENIKVKWNSITDDAIVA
718	14619	A	724	318	14	TFFFLNLNLFFLKFFSPPFPFLTKS LFPFLKLPKVGK*SLSKF/CFPPKFN PKPKKNEFFPPPPFFFFFLRHLN/ VCHPAWSALAPSLTATSAS
719	14620	A	725	2	371	APRCKRPSCLSLFSGRDYRCMPRPVNF F/SIFS RAGGLES*PMPPIPA*A/FPK/ CWDYRHE
720	14621	A	726	430	97	PKNPFWKRA*NGAQKQDVLSLF/SGW AGGSWPGPG*PPLGPKGGPPFSKPPG GVGPFIMPPTPEGGGKLA*PWPPGFNP PVSIFLPRDPRAAGGKGTFFPKKKKKEK
721	14622	A	727	406	1	GGAPPPPPPPFFFKKGVPFF*QEGFFF PGLKN/LPP*PPKVGKGGSPPPGGFF FFFKKKVFFFPGLRTAQIKVPSTLVG QG*KILPPQVSGEGGVKREGPQQLFFF FFFFEMESHFVTQAGLQWRDIGSP
722	14623	A	728	98	368	KPHKNKCPTRVATVADNMENNYW*GYG EMGTL/LHY*WEGNIEQPWE/T/VWQLL EKLNTLPCDPATPLLGIVPKTLESRDS NRFFIFFFSP
723	14624	A	729	19	404	VCVISICLATEILFFLHTRPCVCIYVCV VCVCLAVWGTLVCVVICIESVCVCFHLT GVLC/V*VCVISICLATEILFFLHTRPC VCIYVCVVCVCLAVWGTLVCVVICIESC VCVCLHGV\VCVVICIESVCVCPPT CTVCVCVPRGVLCVVCVQAAWAV SMCLTP/CBC/VCVVCVVCV
724	14625	A	730	432	12	FFHKFNPPAARKGLFFFIYPSKCLTSP KAL*F/FGVGPPFFPPKKGFFPKVPR* CFFRPLIRKKQLPLPPLNLAPPQVI*N /PPPIVFFFFFFFRDRVSLVCGNSAV A*S*L/TAVRTRGLK*SSCLSLPKCWEY KCEP
725	14626	A	731	332	7	NKTRKEFLTRISRF/CFPPFLKIFF FPLRA*FWGGLPQIFPPPKKVF/PKI PKVFFKPPPLRKKIFFFSLPLIGPPRV LLKGPLLFFFW*VFF*DRALLCHFY
726	14627	A	732	70	294	FLRPFVETAINKATILANF*NFL*RWG /FTMPFRLVSKL*DSSDPPTSVSQSGVI TVVSHARLNFFYYQNSRR
727	14628	A	733	1	355	FLLRHILLCHPGFCSVATAYCSRDGSS D/PLPPQAPLPDQ*PRLQA/WHRLAPPH SANFF**RQGETVLARMVISQCPDPH SGPQGA
728	14629	A	734	50	395	IPGLTRQWLLDPCASPSTFPYTP*PVQP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						STPQNSSPSFKTHNQGLPMLPSPTPKP STAWKKAILEHTSSSSSSSSSTCRNR NGTTTYVPEHRPARGHTASQTRKQVLAA THKP
729	14630	A	735	451	0	GPSSSPTNITPTVSNNSFK*SSQVACAT CTCYHAWLIFVFSVEMDF/HPVA*ASQ SAQLCQYFMI FLRQCVSLCPQWSAVAW SKLT/ CLCLPGSSWDHRCALAHANFLY FWWR/HSC
730	14631	A	736	2	477	PSHVSNKRLISKYKELIHLNSKKVSNP I*K*GQSLNRDPSKASPLPP*KCQMVN RYIKRCS*TSLSIKEMQIKTTMRCHLTPV RLAIMKSKDNKPSLWVDC*IRVLHLF/ CK/WICQYVQL/FWLLLSNFLVKQPF\Q LPAPPNSPTLG
731	14632	A	737	3	2344	AAGGPTAQSQAQLAGRALRLARWRAVAV GACRPGAGSPCSVQGGAAESELSPRPOTW IGSLKP*TFGAAAG*AHRCGGGSAALIN* ATPRPAPGLPASPTSSQALPAPLGAWGH SDHQPRAPF*SPQASTAIRKEKKQRAQP GRASVCPASNPFISSRALPVLOHGPPAI SGAGSAVASQAPGSS/GSHAESGSPALA HTP*GS*EPHSLIVESTRKS\ELPSSSQ GRLLLPGLLTPGVAS/PVGTKLPGATAAT AGALHQPLRLSSLQGVGAKNKQTGCC CLQLFTTGLFQAPGALKRFLGRIGPAAAP GEHRRTSPQCTVYGGIRQGWEGFQRL RAYGTALPPHPTPPGSSOP/ROAPCRG SGAGEAAGIRD*TGCGGQPCRRAPCSQASP GRGGWQAQVGCETCRGCAOSS/GGGAQV PGLPRKPYPHS/AR*ENLVVPPFCSPT RAQEPQTQGEZ/GVEGPGQSPCAPGAVR GRGIOLSEPGKLARQG/PASGDGP*EG TGQEPSQAFSSARHPNPFSEARMPTDAIC RNQAQ*LQLTSSQPSMGPLRLKSLPATP QPNYSYWDGNSATLGRITNTRRHCGMSN FGARGDLLGTVPT*QPLMQRRKEKPRVG GEPVQSHTVCG*PAGVSRGWPLRPMPL BRWRPLSASGSGQSRPGLHPFSLA/CGP SSSPHRTCS/GLDPGLPDAGSIKPPSL VGAGQGAGST/GLD/GPLGLSLSPGKSL LPSPSPATGLSGLWAQSAF*SLLTVA* WLNVPVNGPSDTADCTPAQAPTAPAMLE NQANKSDDFFH
732	14633	A	738	37	450	NQKRWPPRSSKPARLFFFL*QKYIRD P*KTYQCCFFSPPPKKKNPPPPKGGG FFF*KKKGGGPP/ QAKKRGGGGPPQK GGAKNP PGGFTFVFKGFFKKRGGP
733	14634	A	739	2	426	QEFVLGSAAGGCGWVGSGRVSSPWGDR XVGGPSNRSRHNKQACPCPPGPSLAAG LPGRRASWAEVWL/PGPP*GLAQLPSP LW/PPSPQEREPLPD
734	14635	A	740	21	392	AQEFKSSLGNMERFLPYOKKKKKRFGG GA/RPLETQPPGGPGGGEKKGKKKTSP P/IRGKPPFL*KKKN/CLAWGGGPA*P QFFGGVGEKKTFFNPGGGGLGKPKPPPT PTRGNQTPQKKKK
735	14636	A	741	1	408	PSSQGG*EAGG*LEPRSSRPAAWI*RD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						/GSPEKGGKKKKKKKKKKKKGGGGGFKK TPGGAKIKGGGKKKFFFKGGGKKNLGG ILEKKLPFGGGKNGEKKPKKKKKGLREKK KF*RGKGGKKAENPGGKKIPQKKK
736	14637	A	742	394	1	RDPLEEA VCFPSDFLQLRAGRTTALFKAV RQGHLSLQRLRLRFVCLCPAPRGGA YRS RQASLNRGGFHPVRAYLLCLLPKQASEM AGAFSPA*LPPCS LIDCCASNQ*DSVG /VGPSEGGGYNLVVRRFLS
737	14638	A	743	384	1	FTGFLYLNNGISFLFLYPPSPVLGNWQP PHGKRVFP*DVNFWQWIFVSL/ISSLK DEPAFSTLYST*QHEFFTYLPP/CF FLIESCSVAQGGVQNCNFGSLQPPPPGY KRFS CVGLPSSWDVRCV
738	14639	A	744	2	410	TPLNPLEVPLNLTSVLLASGVSM*ADH SLTENNRNQITQALVITILLGLVFTLQ ASEYFSPPTISDGIYGSTFFVATGFHG LHVII GSTFLTICFIROLIFHTSKHHF GFEEAV*YWHFVN/VRGLFLVGSIVW
739	14640	A	745	393	1	PPPPFPRGRSGPPPPFSRKGKPKGPPPP GNFFFFFKKRVFP\CPGGFKS*V*GVP PPPPPKIFFKGGTFFPGLWSPLKSKKS QFFWVPKPKGERKKLPFPFFFFFFLRLPCL SLSPRLCSGALSAHRL
740	14641	A	746	2	290	KNLCRENYKYE*KKLKTMKDLCKEYKVV *MKKIKENM*KDKLMNFK\NNIKISTLI KVIYKFNAIPIKIPMTFFAE\LK*ILKC V*NYKRP*IVKAI
741	14642	A	747	59	364	CRFFFFGLGGGGGGGGGGPPPPF*KNP PNPPKKIPNWGFFFRGPGFAPKKKGGPF LGEPPPWGAPLYNPPPPGGGGAFFPI FFPRAGGPKRVG/RPPPPPPPPPPRPK KKKLNH*LECVGTEEPPTRPPTRP
742	14643	A	748	2	371	SSCLDLPKWDYRHELLLAHLMLVIGIF LLLLEFCVLRW/RSCSVQTVG*WSDLT SLQSLLP
743	14644	A	749	339	198	IADEKV*AF*TEHKTNHISLNQ*IS KVLTLFNSMKARRD*EGPEKFASTGW FWRPQEISSLN/IDV*GEAASADGEAA ATCAEDPAKIPDEGGSPK*YIFNVD*AT FIRDLSWIPCTSCCSFSISTCCFTLHVML
744	14645	A	750	249	2	KIFKPPAFPVSFPFFPL*DSSSPEEP*I SGGRVGP1\FPPPKKGFPPKNPPGVFFS PPLRKKILLVPPPLNLGPPKGLKRP
745	14646	A	751	1	288	VVNHTMDEGLVSR1Y*OPLQ\VRKTEN PVQKWTCPNRRFSSEDEQMARHKGQW PASRAIRGTQSKIIMRCHFTHTMARIK KEKEAGGGGCL
746	14647	A	752	494	2	ETGSWFGQRLVQVVMKSSQLP*PPW APVILPPO/LSSG*DRHVPSPRG*LKK KFLL*RWGLTMLPRLNLLNLPSTASQNA AITGVSHCARSAVFLILROGLWVWEB/ GAQW*SALSHLPV*/LSR*WCQP*PLG* DSGSGSPLWRRLAYLFCALWKEVTWCS
747	14648	A	753	1	533	YLSRPLECSGGITAHN/LRPPGLK*SS QLSLQ/SSWDCRPAPPRPAARLIFCFR EEGRRSHYVAQACLKLPGS/SNPPTVA/

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, = possible nucleotide insertion)
						FPKCGVRCPEPHTGLCS/GLSEFGFCL WVGACSRSSSHKNGCGTA/CPAVFLHSV GYASHPSSTSTRTAFTLGWLVFVPRDKG LTVFSQAGSTVGVILG
748	14649	A	754	1	346	ELSKSTLFCALCGNDKAWMTAHRFIAWF TDYLPKPTVENY*EKKRLKVLILLIDNA PGHPKALLEMYTEIHVVMPADTTSTIL* PTHQGVISTLKPCYL*NTFKVQ/CYID SDSS
749	14650	A	755	1	323	EDQTSNRVLLSLNLQSKALMLFNSMEA E/R/SEEAVEEKFESRE*FMRLKERSC LQNIKVGGEASADGEPACDPEDLAI TDEGDCIK*QIFIVDKTAFYSKKMPS
750	14651	A	756	1	344	ARQPGDPARGGGRRRLQPRQASFC TGTLARARHTCEGAGVLRPADKLASLN *HFSQKKKKKKKKKKKKKKKASSSSSS KKKKSSSSSSSSSGSSSSSSSSPPPP PPP
751	14652	A	757	119	317	NRVFFFLRVKKFPWVEGPPFFFL*SLTL LTLVAQAGLQWRNLSSLSKPLPGFKFPS /PSA/LSRWYDR
752	14653	A	758	2	363	CILATVKSAINRIAN*YI*KCSMSIITK RQA/IKRKNKTRRYQLIPVRMTLKKKK RW*RCCEKGRLAHCWFLECK*ROPL*KT R*FLKKLKLPAFITAALLDIYPKQIK SE/CKKH/CAILFALFTIAK
753	14654	A	759	358	1	KADFCFPPTFSRVRKKLFPFPFKKKG* KGP/LDPPGNCVFFPKKKRGFSPLGG GFFYFPFPFPFPMPFKLGEKGLTPPP GPPQKILVFFPPPPPPFFFE/DGVLLCRP GNSAVAQS
754	14655	A	760	316	2	KATRSQDIRRIQVKLEIEPQKPLQKTN KRSYVF*KH*NRNTLTVRMENKREK/N EIDPIQNHKEDITDDTEIQIRKYKH LYAHKKLLEEVDKLLDNTTL
755	14656	A	761	3	321	FPLGLWGSGLGAKFEGQAPLYPPTLSRRV VPLC/DKGRSAVTNTVYSSGSRVVP PPCM* IYRLCIKGRSSDPEQKKKKKKKK KKKKKKAKKKKAPKDDSSSPKT
756	14657	A	762	315	2	KTERW/VFEKYNKMGQS*DLTKKNREN /V/QINKIQNERGGSTGSTEIQRVIRG FCEPL*AQILDNLEKMD*FLQPFHLPRQ NYKKKKII*KKPISKVIELVKNL
757	14658	A	763	226	329	NPTTLEGGGRISKGP/CSRDEVSFC WPGWFQTPDLWRSVRLGLPKWWD/RR* APPPGLNLFRMLSTHGSW/COHPCFKF PTSAFQYIYIYIF/SFLRSSTFVAQAV VQWHDLSGPPPPPPGFKQ
758	14659	A	764	335	1	QSOERPDSPQVMNLTLPRAPSMFLVSQR TELSKSP*VPPAFCLPCVMPHSTLLSQ LKY*IKY*SPTPPFSVFL*RDRLVLF HPGWSTLAGS*LTAAASNWAQVTLT
759	14660	A	765	100	310	HFGRPKRENCLSF*V*DOTLHTHTHTHT HTHTHTHSRSENGMRLTPHIPERVW GIIC
760	14661	A	766	315	3	IFPNPKRIQNPPLFLGFPFKKKEGE KNWAMETPRFSPPLLGKKADTGPPPP IGF*GPKPLIKGRGP*/PP*KNTKIFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
761	14662	A	767	1	309	FFFFF*DRULLCHPG*SAVARW KEPYKLTLEHNEIRVACGHLSSKKRKITW VSDS*ASCPKTRGNFIGPSAGSRAPSE KLEAHFHGCGSVNRVHLT/CK*HKRRPL GVANLEVSOKSGRTSLALD
762	14663	A	769	1	316	GRAPPPPPPPPTFRVHTSSKSESEPER /DGR*EPTRSLEPL/LFFASYFCLEAR QSTSLAPPLSPSGPTVLLCPSPPL PGRPPNPPTKLSREKQTKOTIAR
763	14664	A	770	2	366	ARRIITLTF*ONTIFENTKGRT*SLILA SLIIFIATTN\LLGLLPYSFTPTTOLPI NLTMAIPL*AGAVVIGFRSKKNALGHP LPQGTPTPLKPLPIETIILLIQQIAL AVRLTANITA
764	14665	A	771	2	364	NAPFVIGAWTEYPLSHFIVRCRQRKE/ LNLGLQIGKEBEIFLFDKAML*IESPKES VQKRLDVIYKFSRAVCKINIQKSNIVV YVWNTQFENEVKTI*DPQ/DIKHWGIIIL SQRKKE
765	14666	A	772	3	376	HEPLGKGLKSLFLYATLSLTVYSIL* S*ATNSNYALIGALRAVAQTISYEVTLA IILLSTLLRRGCFNLSTLMTQEHL*LL LPS*PLAII*FICTLAETNRTPFDLAER ESELISC/FNIEYA
766	14667	A	773	3	350	HEFFFFILKMYLGAQYFICLFFFLGF HLK/HKSCSVTQAKVQRRHLGSMQPPPP GFMOFSVARIKDVHHAQLIFYIFRIFI F*F/NFLRHSALVAGDGVQWRDLGTILQ PLPPPG
767	14668	A	774	1	359	GTRYAAMLGALGFILFTARGLTIGVLA NSSLDIVLHDDTDYVGAHFHYVLSIGAVF ALIPGFH*FPLPSGYTLDTQYAKIH\ FTIIFIGANITLLPQHFFGLSGMPRQYS DYPDAYTTW
768	14669	A	775	2	369	ARGSTICLRQTEKLTVIVYSSIRHIGLVV TAILIQTP*SLTGAVILIIHGLTYSL CCLANSNYERTHSRIIILSGLETLLP LITE*LLARLANALPPTINLGELSV LVTTF*ANIT
769	14670	A	776	2	353	ARGTGA*VDS*LTLHGSNNK*CAA\LL \WTLRCKILFTVRGLTGMAITNSTLDIA LHDTYYVVAHFHYVLSIGAGFAIRGPI H*FPLFSGYTLDTQYAKIHFTIIFGVK ITFFPQ
770	14671	A	777	3	353	HEGLHL*LPKRAHVETFMGD*IALDAGLL RLRGYGIHVTLILNPLRKHILHPLVL SI*GIIITSSICLRQTLKSLIAYSSIS HI\SLVETAILIRTP\SFTGADILIIIS HGLTCS
771	14672	A	778	367	2	FCPT/CPNQKFMGVGAVGFPALYPNPFPG LGGLV/TPGAGVLNPAVPG*TPPPPKN PNLGGGPAFFPPLKGLGWKIALTPEAK GSINPNPFPALPGGPNQTFSSKKKRKK LMLVYSIELTSRA
772	14673	A	779	3	432	HEPLHLSSCVCPCVCCVCQ/CLWLQ VGVO*CNYSNWOHEPL*VHTRVYVCVC LCHSVAGAGVO*CNYS/CTAACNSW
773	14674	A	780	213	466	DDILPVWNYISLFFFFENRAFFLPPGW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GAGTQL*LEAASH*GPKGPSRLTLL*W\DNRRGPPC/LDNFIFLQKXNLTLLPRLA LN
774	14675	A	781	304	373	R*VFFFFFLKKEFHFFPQAGGQNEGMG*LHPLPPGAG/R*F*CLTFPHSWDNQEGPP RPNPCFGRGNKVSPCGP
775	14676	A	782	389	1	PEPKN*CRVNSRWVHKRTI/OLLEGNL GASVDLEFGDDFLDTIPKVGKERS / WDFIKIKNVCFKDNVKKRGSPATNMKKI SVKDLNKGILLPKIYEELKLNMTET*R LT*KWSKVLNRLQTLRETRA
776	14677	A	783	1	383	GTSP*PLTGALS*VLLMT*CGLAM**HFHS ITLL*ILGLLANTLT*TPYGRGDVSRQSAY QGHHTPPVQKGLLYRIILFITSEAFFFA GFF*SF*YHSSLSPTPQGGHNSPTGIA PLNSL*VPLLNTWRLL
777	14678	A	784	1	389	GTSTVPTPGVKVFN*LATLHGSNMK*SA AEL*ALGFIPLFTGSGLTGIVLANSLLN IVLHDTYGEAHFHYVLSIGAVFAIIGG FFI*FFLFSGYTLDDQTYAKIHLT\IIFI GVNLTFFFOHFPLGLSGNA
778		A	785	374	1	ELNAYNVMNQLQNLWNAQPLSIMQIFQ ILIKSQIQNTLVVISDGTGLPGDKWN CI*LKILCIKVKVTINRAMPVIDWENTF STYTNDKGLIPKYKELKHS\KQTNNLIK KWAKGLHSHSRA
779	14680	A	786	1	363	GTRLYHANTN*KKLRVAILISEK\TDFT VKKIRNKEGHIYIMIKRSIL*EGITILYV GTPSNRVVNIYRQKLIKLPGEIDESTII LRDPNTLSVIDASTRKKISKNIVESNN TISGLDLID
780	14681	A	787	1	361	GTLPSSERKINF*TVVSLAQKLEMIKLIEE GMLKAE*TKHLRLQ/TSQVNAKEKF LKRIKATP*PNTRKTRIK*DSLADTGV LVACIED*TSHNVLS*SLIQSKAL*LL NCMKPERGE
781	14682	A	788	1	352	GTRNYAKSTKSKLYRWNYKAMMTAYLFT AWCTEYFKPTVETVYCSGL/SLKILLI DNASSH*RALMENYKQIN*VVPMDNRRS LQPVQD*VILTFKSYLRNT*FHKALAA R DNDSSD
782	14683	A	789	365	128	PLDQHG*ETPLLLKIQK*LLARRNGAHLYSQ LGLRLRHENLLHPGGRGC/SHCTPAWVI E*DKLKNQTKTKAPRVSIHSHA
783	14684	A	790	217	257	WSGGVAHPV*IPATQEA*EAEVLSLGG*RD C SELRSCHS\CTPA*VTQAGVQ
784	14685	A	791	2	363	LAILHQTVS*FVHAK*EKFWKELL\KSAT PVAI*MIRNLSLYNLIMETV*VV*KED QTSHLIPLS*SLTQSKALIF*FAMKTRD GKGAWE*KFEATRGWV*MLKEKFCLS/H HIKVQG
785	14686	A	792	2	362	GQKLLG*LLHQTVS*KFVNAKE*EKFWKELL\K SATPVDI*MIRNRTS\LISDMETV*VV* KEDQTS*PLIPIR*SLTQSKAVNLF*FRAMK PVRGKGAVE*KYBASRG*FWQYKEKSC/ RMCNIIKQG
786	14687	A	793	2	360	ARAGSTHAFKNYAKSTLPVLYKNWKKKA* MTAHLFAARVTKYKVS/YCLNKKIPFKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						*VFIDIVPSHPRALIGIYKE/INVMFPA NTTSTLHPTDQEVISTFKCYFKNRFRK AIQLPYSNSY
787	14688	A	794	2	359	AREKLYLSILTPQLRSLVIAFAATELTR YYILFETTLIPSLAISTR*GD\QPERLN AGTYLLFYTLVGSLLPLIALIYTHNTLG SLGILLTLTGQELSNS*ANNLI*LAYT IAFIVKIP
788	14689	A	795	157	365	GIIEBKGYLPEQIFNAKCSGMIASHCSP RLPGSSYSTSA*TD*CVQWYDLSLQ PPPPFRKFLYLSDDSTWYILAPP/RPS **FVFVFMVGFRQTPE
789	14690	A	796	224	372	IFFIFIFILFTFENRQSFALVA\QAGVQ WRNLGSL*PTHPPRVRKRLSL
790	14691	A	797	482	1	NSFFFFFLFPPEAKDHKDFSPSPFFVK KLKGFCA*APP*VQKPVVFLKSF/CLKDY MLSGFSCNVNPSQPF/SPSPFLWVG PLPLPETYSFCF*DHGSNFFLPQGP LFHFFFLRWLLCHCG*STAV*SLTTA TS\VK*FFHLSPSSWVYRCTSC
791	14692	A	798	1	415	NLGGGGCSELRSYVHCSPAWATE*DSISK QTKTL/NKDHTRAGWERA
792	14693	A	799	2	401	VQTGFHHVQAGL*LLTSGNPPASAS/Q SAGITGMSHRARQ
793	14694	A	800	73	307	PMALEHHGCGMCLDFLPTFGKSHCFVLR CAEMETRSFLPSWSAGA*Y\CLQPPPP RFS*LRLPSSRDYRHLLEPCAN
794	14695	A	801	87	401	SLIEIWLKSKSTCHNLVNVVLS*HSLKA IVLARHS/VESLTHVLKMLV*NFVFAP S*RSCLCFFLKISRPFVVAHVCPNSTLRG *GGHITRSRDRDHPHQGEIPS
795	14696	A	802	3	354	LRHYTP\PG*QSETLPFKKKKKKKKKKK KLSFFPPPKFLKKKKGLFKNPFKKKGKI FFNPPPPKKGGFLIVNPPPKKNPPPL GGGGPKKIYF*KTFFFAPPPKEFNPPF FFSPRF
796	14697	A	803	1	830	VETGFLHVQAGLKLTLTSGDLPTLAYOS AGITGVSHCAWLFFFF*CLAVTQTEVA PS*LTIASN\PGKLSSFFTLPHHARLI FKIESRNEVLLFSR\PSQTPNLMQSSCL SLPKCWYRCEPLYPAESLSF\FIKLSC MLKLEVKCNDCVNL*ITLLKNIENI EOWIGRLTCVQKLEKIVICI*VMLKNT QPVGTES*ESRSTNSGAMM*SKDNTF FPVFSVVFVLRQS/LCPVQAGVQVSHL SSLQPLSPRLK*SSCLSLSSWDLRARA
797	14698	A	804	389	3	FIWPFKGADENSFFVFMVTKGKCKPKKG FGRKKNLQPKPIPF*KKKKGAFLMLWK RFQGGFFFFFEMEFS\IAQAGVQWCDL SSLQPLPRPRKRFSCLSLPSWDRHAP FRPANF\CVFSRDEVSFCW
798	14699	A	805	161	21	RGGGCLQSQFR/RRLRHNRLNPGGGGC TEPRSYRCTPAWARE*DSVSK
799	14700	A	806	405	82	FFLRWTL/DTVTRGGIQCWNLGSPQPF/ PPRFRKFSCLSSSSWYRRPPPCPANF LYF*RRGFTMLARVLNLP*PRDPASA SQSAGITGVGHRAWMPFIENRFDL
800	14701	A	807	938	2415	KITFWETFWITTVHPLCKCREATAGIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RRWS*NNW/NITHTTKNLNPLTPTDTKA TFK*IIIGLT*RAKTWOL/LESFOCKENT GENLSDLGVGKDFLRHKKGSIKGEKIA KLDPIQVKNF*SLKDTFKMKKYALGWE KIFARRVSDRGCVSRRYKEL*/L/IELKD NPIRKGGNNLNKHQRI*MANHKMKRCP KS*VIREI*I*TIMRYHCILPRMAVMN/ SD*SHGDKNGGSGTLLH\CR*ECENDQ LLWKTIGQFLSK*M*RCTDSSIPFLII QEK*NCISTKKTCTQTFTAA/MYLLVIA KNWKQLPYPPSSVWI/QQIWCITYTMEYY SAIKRTVDTLNN\QMDLKIIRFNE*S/H NLRRVHCMI
801	14702	A	808	414	1	KPKAKLFVVRQVUNAKEKFLKEAKSAA PLN/RMIRKQTSLTADTEQV*VINIEY* TSHSIPLSQSLIQSRVLT/LSMKAETGE KAAENLEDSRG*FTRLKEKSHLHNKIV QGEAVSADGEEAAGYPEDLAKIIDER
802	14703	A	809	399	1	TGPPPRNQPFNKPAKGNFWLFFFL*F /CNPFFFFFTGAPISLGI/LV*CLML VWGNFSP*PKYCFTFSPFLSIFILFL WLLNLTCLYICYTCFSLYTLV/CPSFLS SIFFLLYP*FWRLLLIHPPFTRP
803	14704	A	810	1	392	ILLAGATEDAEPPGG*TYGPTLFGSYSH PGAVYLTILSLHLAGDSSLIRAINCI\ TTLINIKPVARARLTLFV*PVLDTAM LLILSLPVLADGVITLLDNRNLYSTFPD PAGRGDPILYQHLL*LLRH
804	14705	A	811	66	411	RETRAGAGLSFSPFGWGNFQKIFPLG GPKKNPGPKGNFPPFF*KKFPLVSPG GRGGGNFRSLQGPFPKVPFFCFNPRR GG*/MGAPP
805	14706	A	812	3	392	LSVQFPFFPFLKKTFRKNCPPFCSPNI LGFPLKSGKK*GSFFFFPPPNYSFFWF PSYSF*NQPCLTRGPF*NQKFPRL*KG PILRL*SLPFFGPPPHSF/IFFFDRVS LCHPGYSAVAQS/LLTAASS
806	14707	A	813	690	153	IISIDAKKAFYEIPFSPVISSSSPTDSL YYNLGFLKNFKKGRVYLNIIKIYIEK PTANIIFISGKLKAFSLRSGTRQICPLS PLQFNKVLVLARATWQEKIIRNIHIEK EEVKLSLFVSNILCIENPLKMP*KNSSN **IQRVAGYKINI*KIS\AFLYTKNKL CELSHPIYDIPL
807	14708	A	814	32	376	LFGLARSYITEGGRLENPTIIPHG*REF WELCNKCD\TMRPKPSLHCSRGCRCVTR MDHCHPWNNCVGEDKH*LFQLQCFYTE LITCYALMISFCHYYFPLPKRRTLVRN VYI
808	14709	A	815	2	423	YLYPFFKIFIPFGKGFNFCREVGPICPPF KIKVLSKNSQVGFITAPYKKNNTLPAR VNFSPKDELKRPPLFFPFF*RDGILL CYPWS*TPGLKRSRCLOLLKHWYIC\ PLHPAS*KKHYSRLRL/SLLDADW
809	14710	A	816	404	54	SLAHFFPFPKKGFFPKIRGVL*FPF*K KKFLFS/HPPVNLGPPRPDLKGGPPSSS SSSSSSSSSPGG*MYF*/P**FGPAL VQPMACYCKASCCKVAFPFTSHGLMVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
810	14711	A	817	3	410	PPTTAQS DAEVGGSLEFG\SGGCSSEP*SCHCTPAW VTG*ETVSKKKKKKKKGPPPPFFFKRGP PPREIEKKFGKKPPSKKKKKKKKKRGG PPKKNFVGKGNLRGGKKPPFFFLGGEKK KPRGFFEKKTFWGGKNMATTQK
811	14712	A	818	1	404	IPINSLTSKINKLKRHLKP/HLNQEEI DNLTRTIPT*NIIN*YKQNTGPDGSI KFY*IRK*Q*YTSFQIKNEVELPN SFYEASTPLASPKKKKKKKK
812	14713	A	819	421	2	LPKRRCSFKSPDPGFFAP*GKNIT/ CFPFR*NLADPGVFLKGPPFFPPFFP FRGRVG*SWVPAASPLQGGVLPQ/SS *UGGSPGPPEHARUNFFPPFFFP*F* RQSLTMLPSLVSNWA*TILTQPPKVL GLQ
813	14714	A	820	84	418	ILTCHNARLGEKSQITVMAQSQNNPKLV NICEVFLVFFPWKPIFFGTQVGQVFNL SSL*VRLPGYTHFCLTLPKSWDRPI PS\PIFFCFNKKGVSPGYPGGCNILVP
814	14715	A	821	290	3	FSPFPENLGPNNFLKGPFFPPFFFP FFFFPFFMFCVLIV\PIFFCTNLFLFD CIT*+T*NWFISSKAVCLFLFLQPPAS QKTNNCRKRSFF
815	14716	A	822	416	2	ITKLTEKKTWSGRRKNQYVKYAGASQ YTAVVLRPQSMITLKDSSEKAPHWGEL NVV\HVHHPIWKE*PEV*YIES*AI DGLASWSGPERNKIGRLGAKV*RRDMK TDPLECTQININIFQVCLFGDRVSLCW
816	14717	A	823	409	45	PPPPPLFFFF*KKKAPGGSGQPKF*P PPPPKGKPPFFKKKKKKGGGGPPNPP PPKGGGK/QPFPPOGGNPNKPSPPPK PPRGQKPKPPQKKKKKKKKRLNVG POFQLSESTY
817	14718	A	824	1	408	IPSEHGIL*INTKNNERNCTNIWELS NMLNNA*VNKEN*MKPKITNE/NN ITCONL*DTTKVLRLEYSKCLLOKK KKKKKKKKKGGALKNYLGGOQYGGSE GNFIFPFGGAKKPCGWIFRRRPFW
818	14719	A	825	259	274	YL*YLLLYRRYS*TP/LGYVKKRKL LYQRDTYTMPPIAALPTIAKMSRP*SP VV
819	14720	A	826	422	105	FFFSKIPWGNFFPPPKRIFPPFPFKI FFFPPPPFFFWGGFSFSPDPKKVFPK SPPVFFPPD*KKKFFFP/HPLIFPPP GFFKPPPPFFFPFFFPFFFW
820	14721	A	827	15	402	IKSGLKNTINLGDVLNNGF*YTLPE QATKEKIDN/WDLAKAKNICA*KDTIKE VERQPK*QOTFVNHLFDKGLVSKH/N EL*LINKTNH\HL*WAKD*BRACKE DVHMTDKMLKDVPSLVIREI
821	14722	A	828	420	3	KDAHTCPGCKGGFSGHRALKATCRNG FLTTTTEFLTHKCPPLGQEPWQHOG* RDSPPRRVSPAGTQWPPCHREACLA PSVE/GPS*IQEQKSLFFFLSLRNL/ NSVAQGVQWRSRSLGSLQPPPRFQPS CLS
822	14723	A	829	1	269	TKIKNLARHGDSCL*SPILLEMLRLEN

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						LSPSRGSGSEL/CQPARQGETLSQTNKQ TNKKPHOVQLPCFBIINFKEFITCLVLR LPGNWS
823	14724	A	830	432	1	GYNNQOIEDVDOTAFY*KKIPSRISLAR EEKSMGLGFKASKDRLLILLGAKVAGDFK LKPLMLVDPDSKTPRELNN*ARCTLPVL/V KWN/KAWMTAYLFTV*FIQYFKPTVDY C/FKILLIDNAPGLPRAVMSR*EESNV FMPVNTTL
824	14725	A	831	1	233	KKLQIKYLGINLMKYTHVVSICCKLLM KEINEDLNKWRDVLCLWI*RLNMSILH KLIN/RINLLQLRI
825	14726	A	832	3	477	YQTCEDLTQMLLKIFQKIRGEGIIIPS LYDASIAMPKSKDKRTKKF/NYRPISL MSIDAKILNKILPNQIQHQIFPIPE MKG*FNIR*INLIHLITKMTKTPMI SIGTEKVFDKIY/PPFITTLTLGLDIG RSLDAIMVARE
826	14727	A	833	3	402	RYQTPLLV*TVLITALLGLSLPVLTG GITIPLTDRRLDTFFDPAGGGDPLVH HLF*PFGREAHILIPGWIIISHIGTY YSGKKEPPGYTGMRAIISIAFLRVIV* AHHIYTV*IDRDTRAYLPSLHN
827	14728	A	834	7	395	DPQRVSCMALSSNSFFFFFWRKSLFFP GREGGQIWNWGTPLPGKRNPSASPPG GGGIIKAKAKPLPKPKGGGGGLEKPP*N QGGGPG*SPGKKGFGAG*KGQKSKG GGKKKGR\DP*AYILK
828	14729	A	835	41	444	DEVRVKKERENIYSVSUTKETESVI*NF PTKKI*GLDGITSEFTQLPKKKPK\IK KERTFSNPFDKTNITLI/SKPEPTTKK EN/VRPVSILMNI/DCIKLLVLANCTL HI*REIHDS/INTPAIQISFNIOKTN
829	14730	A	836	3	415	HAYYIVKPSF/WIFKGALSALLTYGLT M*MQFQSIKDLRLGLLNTLTIYQ*WRD VTRKSTYQGRHTPPVQKGL*YGIILEIT SEVFFFAFIF*AFYQSSLAPTPOLGHHW PPTGNTPLNPLEDPIINTSGLLIGVS
830	14731	A	837	378	0	TPPKPGGKIFLKK/SPGRKIF*PPGNG /PPFSLPLSKFFFFPKAFNFWGGGGPQ GPPPKGVFSQNPFPQKKRPQKKEKNF FP/PPGKMGGPPGGF*RAPPP
831	14732	A	838	383	38	GPGEKIFLKKPREKLSPFGEKAKFFPP SPLKNFFPPQGVFFLGGGPKRPPPKKK GPFQKTPRGF*IAQKKKKKNFPPRGKF GPPQ/RIF*KGPPPPPPPPPPPPPPPP NSL
832	14733	A	839	59	418	TKISSKQKQY*TTGPN*MAEISTTFED ABIIDALIFPNLPLWLHKKPDSCSWKVS VYCKLK*VVLSISATGLDIINT*LLREM KRVS GTWYIATDLAKTFFYI/PDQKEFA FSWG*KDIF
833	14734	A	840	5	335	TRHFL*INKFENLXMDTT*KLTYEGIE SLN/RII*NF/PVVLLSGSSTSEFYS LPKEEITAYKPIWREKGGIILPTCPA TRITLIPKPETCIMRKNKCPVLFMNGH F
834	14735	A	841	1	38	RRKLLEDHLSLY*KINSKWIRELNYR/F

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						ETIKLVKKDKGNV/QDTPGKDFMVKTT KTKIDKSDYIKLQSFYTANETVNRVKLO PIE*GKIFKNYSKGLLSMIYNELKQQ HRNNLI* KLEDHLSLY
835	14736	A	842	2	424	GRVGSIPLSQSLTQSKALTLFSFMKAET GQEAEEKVEANRGWFTFRKERSGLCNI KVQ/GAGGDTAASSPADPAKINDEGGHS /KOQIFSGNETAFY*KKMSSGTSIAREE KSMPIFKASKDRVTLIGANAAGNF\KL KMP
836	14737	A	843	281	3	FFFFFFFFFFFFFFFFKTLFFPGYWFISIFF LLFSISLLLSFGSGSVFTAFQPPFF*VSR YHQHFNST*FL\KL*FIF*IFLISI LFLFHQNF
837	14738	A	844	409	1	RCGGTCWPSFVLRLRL*KDHLSLRG*GC SEP*LHCHTFAWATE\DSVSKKKKKGI SCRHIVGSPFFHLKMCLLNGLLSFPTL NVIIYVVEFKPTILLFLYSICLSHLF SFFAKSINSKPESLVCVFNFS
838	14739	A	845	63	451	KNOEQUESETLPN\FYKASTITLIPKLD OK*KRRKEKKKKKK\EN*KPI*THRNII AKILNKILAHQIOOYIGKI IHHDQVGGI P/GAFDKIQYRCMR/TLQKMGIEGTHL NIIKALYIRPTDSIENREK
839	14740	A	846	60	460	RNNEPFLDQIVTYPEKWIYDNR**/PT QWLDGEGGPKHLKPNLH/QKKVVTVW WSASLTHYSFLNP/ETITSNYSQEI MH*KLOSLOLASVNRKGGIPLHDNRLQ VAQPVLOKINELGFEVLPHPPYSPE
840	14741	A	847	344	2	NFLKFHPGGGTFLLKQGYTGYSFPT* K FFFSLKPLNPLGRVGGFPFPPKGGFSK IPQGLISPPLRGKVFPFPPRLNLGPPR VFLKAP/HPPFFFGI\PHGLQPRMI*K PTRP
841	14742	A	848	439	132	RRVAAPPPSKNIFPPPGSYNCGGVNPOK SPPPK*GFPKP\SGVYKNPPQIEKVFF FPHRIIVPPGDDPKTTPPIFFCFNSI NFSLRGQLYVWDESGC
842	14743	A	849	94	470	LNFPLSFFLSFFLSFLESGSLSLSLSF FFFWKSGPP*GK/QKCLNKKKKK GGGGGQHPFTFPGGKKNPPGOGGGGS PAQKKP/EGGGPPGSKKNPPGGGPKK KPPKPRGGGGKPPFP
843	14744	A	850	2	396	FFKKENIQMANKHVKTITLLVIREMKI PTSMRYHFTSIRVAKILKTDNTRC*QEG RTIRILMLC*LQNMVLL/WKNQOFLT KIKIFL\FDPTISLLGIYPREMKTYVH SSFHIGNSKNNRTGNLNVHN
844	14745	A	851	369	36	SKGASDILEKPLF*EVGLPTFSPPLGE KMP/FNYKGGPGKISLLIFPKKFI GGHPPFPF/PFFFMDRVLLCPGWSAV AVSQTLTTSASRL\K*FSCLSYSEG*DG RIS
845	14746	A	852	1	367	PPFPKIKSPSGGPPSKRGSFGAPPRGG KFWFLSQKGWGGP*FPFPGVKPE/NIP *PPRGRVPL/HNLAPAPPFGPPK/PP PSP
846	14747	A	853	1	378	AMLATLISNS*PO/CDDPALAPQSAGIT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GMSPCARPTSCSFYP*ILLTVRTFIKIR NFFFFFTDGSNFVAQPGGEGHDHG***P QFPGPNKSFNLSPSRWDYGGAPPCFVI LCIFCKDEVSSCGSG
847	14748	A	854	369	1	SACFGLPKCNDYR/R*ATTPSLEIIIIYI ER*EKTTSSEPNANRFDTKLHHYDCSVM DF*KAL*NGDDFPVLSMKHMQSLNII\ FVFCFLRQGLALSQ/AGVQWRDGLFPQ QLRPLQSSHL
848	14749	A	855	380	335	NPGGRGCSSELRLCHCTPANAT\SETLSQ TKIOPKQOEV*LL
849	14750	A	856	373	1	LRITKILNKGGLANLP**R*KIHSQVE FIPMQA*FIIRK/TPSIKWPVIRTKKK KKSQMLISIDTEKIFDKIQHFLVLPKVI KLGIETGFINFIKSIYKKSTTATIISG LNASPLRLKTRQDF
850	14751	A	857	369	44	KVQNLVFEKLLNRYKVDLNKW\NSLCT RFRKLNIANIIMFKLIHRYN/SKVKIPI KIPANCFGIEDKLILKFI*KFKRPQIAK IILKNKDGVLDPDFKTYIYIMQYHLIC
851	14752	A	858	1	348	QWHAAPS/LARPPPPFRK*FCSLSLNS WDYRHAPPRLANFVLCFVG*GGIHL
852	14753	A	859	1	366	CTSPFTFNQKLEMLK/EEGMLKAEK* K LCLLCQKV/QVNAKEMFLKEI*SASLV NTMTI\RKQSTADMEKV*VV*IEYQTS HNIPLSQSLIQSKALTLYSSMKAERGEE AAKEK/LEASR
853	14754	A	860	12	366	PSTLGLRRASCLSLLSRWDR*RHMPHPA N*KNFFCRDG/SLTMLRLVL\NSWPQA IHSPPWQ
854	14755	A	861	424	78	NPRPLEGQTASPSLAPNF*TTLGKKVNP FF/SLKXNPPPPPPPKIWAQGGPPGPF PGGLNGGFFLPFRVKAPIIHKGAPPPQF PQKKKGRPVFFKKKKKKKKKKMGWTR AFQVP
855	14756	A	862	327	3	SHMFFAAV/GREISW*AMAPDQTKLPC RSAEDAIVKFLTOATGSIILLRILFNN RLSEQ*SI TTTNTGSSLLIIMAIKVI GMAPPHE*VPEVTGGSPLTSGLLVL
856	14757	A	863	1	341	YDRNKKWDIPGS*TERLNIIVKLSMLPTV IYRNVILIKIPMTFFAETEKSVKFSR DYE*PKQS*KEQNKWHTP*FO/QFFTA TVIKMVWY*NKDRYIY/DQWNR*SLGI NPIC
857	14758	A	864	32	324	LWPPFFFFFFF*KKKFFFFFFF*RKGR NFFFTPPPPGLNLFF/CPHPLKWKMKR APPPPPN*FFFFFFKGTFFFTQKGLNF PPLETPPLTPKGLN
858	14759	A	865	350	3	RVKNRPRFWGF*MYLKLPSFFSKRTN*Y LFPLKIFSPKTVWGIKIFLGLAL*NPFF CFKNPLWFFGF*KL/SFFFPPLYFF*KP LAPLKRFRSFFFFFFF*DGVSCLCRPGWS AVARSR
859	14760	A	866	342	118	GSVTQAEVQWCDRGSQLPETPGIK*S/H PPTSSYQVGTIGVCHPGLAMLSRLVLS SWPQAILSPWPTTVQGLQV
860	14761	A	867	1	354	VKPSF*PLTGALSALMTFGLTM\IHFH SITLLILGLLSNLTITIQ*W*RDVTPE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						STYHGHTTFFVQKGLRYGIILFITSEGV FWAGSV*TFYRSSLSPPTQLGHHWPTG ITFLN
861	14762	A	868	3	344	QIKNPDNISC/WIRCGATGMFLHCWNEC KLQLPLWKT*HQ*SRR*AVPLSGMFP/ NRYSSCTCPASI*KTFLSALFMMTLP/C LSRVENIK*SWCNQKL*Y*SVMKRSEEF SLKNA
862	14763	A	869	345	1	KQAGLKNVKITG/EGASVNSQR*VS/YL QTKKITEEGYLPERVFNAGASAVF*G KKLPQRTFISK/EEKAP/GSEVGKDRIL TLFLCANMSRFMISTALLYKAADQLSLK GKDKHRL
863	14764	A	870	340	45	FCSCFRDRVSLCCLGWSRAPGLK*SSCL SLPKC*DHRC/AA/VPWFQRCILEKQI QIY*CAERIL*SERPHTRHLDSSVTNIL PCDLSKVIWFKKKQIY
864	14765	A	871	209	72	KLWDIHTEYYYSATIKRNKPLKTYTWM DKDIMLCEKANLKRSHV
865	14766	A	872	3	353	SPFLGPPPPPPPPPPPPPPPPPPPPPP FCFSPKKPPP/PFFL*GQSPPPPP*RG FFFF*KKGGVFPFPPPPPPPPPPPPPP PKKGGGG/PPPPPPF
866	14767	A	873	3	267	DFTMLARLVSN*/WPGVVAHTCDPSTLG G*GGWITRSGVRDQPGHGEI
867	14768	A	874	1	346	PRRFFFFFVFLVFIYFKCVYLF*DKV LVCHPGNSAVPHGSSLQ*PLRIKQSSH LSLSS/WDHRAHMLVFSFYRDEVS PCLANFCIFL*RQDFSMLEPQ/VLXALCLP WPPSL
868	14769	A	875	1	172	KLLSSGSPPASASQAGITGVSHRARG LLNFPFC*CAFSVPGPCLGYPDTFTH/LC PPSFHQSVIASLDFSCLS*L*MSD
869	14770	A	876	1	348	LLFCFNNYSFFHGVPKPIAFFVFGPGC LPHFPFPIPTAPFFFLDRVLLFPGWRE MGPF*APPTSPQGV*GVFPPPPPO*LG RGPFPQGVFFFCIFGRDSA/LAILEP L
870	14771	A	877	1	203	GFHYAGASLEVLTS*STCLSLSPKSWDY RRGPP/*PGLSYFLYPSLRS*FICAMSI HIPPTKKKASD
871	14772	A	878	343	102	EMEDCFSPGGRCSEPRSHHCTPANVRE TLPSPKYLFLQ*KLNTKIYLSISTP* ELETILKILHFKMMNPLHNSYFPP
872	14773	A	879	2	359	RDITGDMQMETKHM*SFSTSLTSGYVH NSPIRPSKMKNIIDSTRYARGCAIRALI HCWNR*MVOPFGE*ISGSKKLNMYLS YDERPTFRYEK*K/P*VHPKICV*MEWA AFFLISPWN
873	14774	A	880	205	1	FFRGVTEGL*EFFYVESVI/AGGTTARR PLFFFFFFFFFFLWNSFALVAGAGVQR DLGSPRPPPPGFK
874	14775	A	881	150	2	CRARVDGVWPNRNSGLKPPSF/GSSDPF TSASQECIGITGAHHHTRLT*VF
875	14776	A	882	345	1	KGNQPKTEKRALFC/TLKKKKIKFNSP PRGNP*KFFVKKKILPKKERGFSPWNG KKEFFKKKKKKKK*AKDLNRNFSRE DVOMAKHMKRCSTSLIREM*IKTTIR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VHF
876	14777	A	883	2	355	DRLLFSASHLDLDTLYLLFGA*SGVLGT SF\SLLRARLGG\SGCLL*NDHIYNGI ETAHAFVMDLEIVRPIIGGGN*LGEP NKKGADMAPPRINNISF*LLPSSLLLL ASAIVEA
877	14778	A	884	262	2	PTCEQSERIEIKTKTQFTTESK*IKFVGI NLAQEAKDLYTETIKYKTLKIKIDTNK *KNIIYV\SWTRFRNNFKMLGWAQWLMF VIPA
878	14779	A	885	16	318	ILRADCADLFFFFFLGSGKKGFCFPRLEK RGETLLN*TLIFR\VKGNF*PKLPKIW/ DFKGNPYHL/AENFVFLKKGGLTLLPG LVLSN*IKEFFHMLPPKGVA
879	14780	A	886	298	322	KRRTP*YPPGEPHFPPPPPG*KARGAP PPPPKGGF\PEKKKPGVMVGTTQKP PKKTKVRVD
880	14781	A	887	353	3	PPFWGFLKTLFGKALWLFKGGFFFAHQK FFFLPSLPPPP\LGFFLRGLT*FKIFSP LF*KGAPQKGISHPLFFFLISPKPPPPF PPFFFFPPPPPPPPPPPPPP\RDVLL YCPGWGA
881	14782	A	888	22	341	IPCTCLRLHGXVHDHDSQLWNPKEOBE MRTLNNLAVLQSLQWLDIELPYDRAI ICAREIKTYV\QNCCT*FMLALCITAK KW/KQLKCPSTDDEWVSRMYTCTR
882	14783	A	889	51	338	ERSQLQWLMFIIPLSPFFFPETQFLFCCP QGRAWATFKIFEFLA\PK*QKPSCLTLQ TI*VYGLNPPPKNFVFLKERGLFHVGG SGRDLPPSGDPP
883	14784	A	890	1	225	GLRRLPENILNFGGRCGSELRLCYCTPAW VTERDTIS/RHTHT*NVFY*GSI*QLAN SCCCNMKNFNVICILRWC
884	14785	A	891	357	164	GKGCSDSLCHCTPANAT\TKTLSQKLL ILKKONKFRS*LDD*INMCTVWPCPHV FLFIRAAPLFSDWLYNK*NNRNT
885	14786	A	892	207	302	EPFSGIITINESHQEGITVLNVVTSSN PSKYNKQTLIELKGEKVSTIIVGD/FY THLLVIDRTSR*KR
886	14787	A	893	86	332	VMRVSCCLKD*ISLCHFTWAVVQS*L TVASNSW\VKQSSFLGLPALWEALGGS LEVRSLRPVWAT*TP\FCNKKL
887	14788	A	894	2	336	FFFWPPPTFLNPGGPGKREBGGPGGS PRGQKGGPGLHLTGFGGQGG*KNFEP GPGGRAPKGETRGGGGPTRPOIP/QLI NGSGKPKVTLNGAWSTIKIFLIKTPV G
888	14789	A	895	1	214	ARESLASFPLSPFFFLGLRFLPSFLP FYFSFLPSFLGFGFLPST*VPSFLPSF LLFFPSFLPWLWFLPS/FLPSFLPSFLP SW
889	14790	A	896	131	352	TLHESDSSEVPDFDKISDALAVEDDQES PGLTNAEELS/SSVRERKKKK/KPEPG L*EQSIKESDSYNSGGRIQ
890	14791	A	897	3	184	CSVAPAGVQCHDLTSLQSPPPP*SSSNPP TSSNPPTSAP*VAGTTGMCCHAWLIPV LVDA
891	14792	A	898	327	264	NRAVSLMNLDAKVL\KLISASQIYVIK

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892	14793	A	899	3	313	KMIH/HNQIRFTMRM*GQFII*TAINTY HKLIK*GRKHMIPLIYAVKIFPKI*YHN IMIKTLHLK*IKEPPGSIYSL
893	14794	A	900	340	1	TKAASHSQ\LANLQFLVGRH*HLKSRT ISPGRVGATAAVNSTAILEYLTAELVEL ARNASKDFTVKHTTPHYLQLAIRGDKEL GSLFKSTIAGKGVPIPHIKS
894	14795	A	901	1	252	LTIFFPHQLLGLSGMPRRYSIDPAYAT* NILSSVG/SFSFLPAVILIIFMI*EAPF SKRKVLIVEDPSINLE*LYGCPSPSPF
895	14796	A	902	326	1	LGPPFPKKEPGVFFPIFFP*FNNRGPV GPF*KILIGELILQDFPFFGGSQIVF PPF*GKIPPF*KVTPPF*GIGGSIPHP PLFFFFFL*DCVLLCHLGWSAVA
896	14797	A	903	1	352	KGIFPVWSCG*KGTKKGLSQGGQGVN PPGCIHFVKEPLGPFPAQGLIS*GRLI F*KGPKKGLP*TVFG/RRQFAPR
897	14798	A	904	325	2	RLEELKNDYWNEMKVKNTVEYPLNLEVE DIQKRDPDTWQCCDACLKCRK*PYGMDQ HLEK\WYMCNNHDSQFRYCNVPKDPEDM DLVHPNYGKPKYKPSKETWFSQMP
898	14799	A	905	1	329	IGLATHGAERTVRGQAKSLAVHN\VCE QKKIKKKKGGRGREFQNLKWNPKNPGG SF*RGLGQSNFFYLKQ/RLGFF*KKP PKI*ILAMEPPNKKI*KNKNKAHFF
899	14800	A	906	148	2	DVDKFLRLSLFTL*RPFGSYNIEG\TGQPYGGTMSEFNTLENNRIR
900	14801	A	907	384	1	ESKRSIFGPNPFPFPFGSGFSRSHAPLWL RSREPPHAKGVKKGFRFRPGS*MPID* SFQLONCLPQRVGFPSPPLPPGAPFLKISL FLRQESRSVTQAGV*YGLLQCRPRLK SFSCLSLPNSWDYNR
901	14802	A	908	3	297	TKIKSL*INHLIRAKTVKLEENMGINL HDLSSGRQQPFYDFTQ/SMINTAIKEK IMKLSFVMGSGFISQRTPLRKRQLTK* EKIFADVLIIGRRG
902	14803	A	909	169	373	ASNLASATDISNTFGPPSGSQGSGREAY VEAQTYTTFMFCIGQVYF*YMQQLVIS IYLL*LL*VTQKL/L\GRQEKFY*YVP AST*ASLPLKPCDEGGKVPFMSVADS/ DV*SLWLALIGESKFRCLVF*SKFLPSS ATYSPLEKCLFILLGCFVMICFCPCPL RRVL
903	14804	A	910	132	368	GRIFLVGQEGKARVSLFLF*DRVSLC HPGWSAVAQSOLTTS/TWTQNSSHLTP P*VAENHRCA/PHTPNVFLFC
904	14805	A	911	2	339	NSWAQE*AGITGSCHHHTQLTFE*AHDR QMMFFLFLKTNFTCPPA*RPWPLGLG TE\PLLPLGLKHFF/CLTLPNWDKGLHP P/HPYQI/CGFLRONGASLISG
905	14806	A	912	3	381	LNFCDTPLTRFVSTIQRCCLPLVEAGI RWRALISPLHPPT/YSLSSWDYKHAAPHPANFPPFFFKGSLMTFRGGG*IF

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						IYLLIYLERESY/AVAQAGGQGFNFNSG QPLSPRFKQFSYLSLLR
906	14807	A	913	394	1	MSGKGIG*KLQ*KFAQKVSQFVNAKEKL LKEIKHPTLMNT*MI*KRNS/LIADLEK ILVVWENKTGYSP*QTNRIQSKALIL FYSMMTERGEEA\KKFEARDDYFMRPKE RSRLQNMKV*DEAANADGEEA
907	14808	A	914	326	200	HNWLSIWKVKNSCFPLMPHTKINSRWIK DIKI/R/LHRIKILQENVGNHIIYKI*RO KRS*FRHNFLLHKNCKLVLVHKTNK*NH* KIYLA*CI*KFFAVF
908	14809	A	915	3	334	LVRVVKGSKFFWLLHQLGLYC*VISEF LNKMKYVLIHRIK*DHKNIF*MGYKKL *NVNIW*LVLPGFSSKNHL/WSGAVATF FNPSTLQDRGRRTTQCGEQISLTINMVK
909	14810	A	916	14	299	YQKLPOKKSPEPNAFTDKFYKIFK*LTA ILQ*LFQKI/E/KETPLPK*SNESNAL I*KPKDKIT/SKNYKPIVSNIHAKILN KI*GYQVQKQKLYSK
910	14811	A	917	3	339	SLQPSCLRLKCSSCLSLSSCWYKHKPP CLA/NFF/VFF*EKIGICTVK*NGDYPL GRRVTKRDHERGF*NAGKVLVGV/CGF ETQSRFVQAGGQGRNLGSLQALPFLGM PFSC
911	14812	A	918	2	321	GIISGIYKELSQPKMTDSSIKK/KDLNR NFTKEYVQMAKHKMRCASLVIREIK/ IKSTMH*H*TPTRMTKIKD\DKNTCKW *GYGAVGMLHQCW\NTKMVQPLKKN
912	14813	A	919	51	326	FFVFCLFSLVLSLNGGLF/PTFERIPS L/PYLQLI*LYLFFY*LKPIFLKFFRDR VSLCHPGWSTVA*S*LEASKYW\VO*S SHLSLLSS*DY
913	14814	A	920	239	2	DSLILSAVO*HDLGSLQFPHPLKQ/FL PSMWHYRCMSPLAYFLLFLVETFFCHV TQASLELLGLSNLPASASQAGI
914	14815	A	921	1	242	FRFRRLKRTFLFNLRQ/RSRSATQA EVG*HDSLSL*DOTPLKWHPSSET
915	14816	A	922	249	1	ALFCALKKTKTGTLWFTALFTIABYS HNQGTQPTCLSTDEEIKNMWHRHAMGYS AIKRNEVLIIYAKI*MYLENIMLSEII
916	14817	A	923	404	1	SRPQKGLGELKCS*RPKGLNKKKQKPKF TFFFFETKHFSPCQAGVQVWVG*SHPY LLHIIFP*VF*MFLILITV/PSRNKDL IGNSEKQIHN/WSSLYFYF*LFLRWSL TLVPQSGVRWRNLGSLQPLPRPK
917	14818	A	924	6	358	FFCSLLHGGETPNNSSPLPHWL*ETKS PPKPPHPLKKGKHSLEFFKIFLLKKGK PPFFPPAGPNPRG*NPPPPQ/RPPKGP PPKEKINPPPPQKGNFPKGRPPLGPF PKKGGGY
918	14819	A	925	268	2	HMYAPVRIIDLTAHLRFSAGKKEIPAGKL YF/L*RNPKNQIGNQKKKCLPRAGM VAHAMNPSNLGGQAGTT*SQALETSMG NMGP
919	14820	A	926	74	338	IAGITGVSH*ESKNSY*KQFL/WPGTVA HSCSNLGGQGEWT*GOEFETSLANM VKP
920	14821	A	927	339	1	LRLFACPLPRKWDYRGEPFQIFFSWH

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						FFKKQGFICPIEKGRSLNCCFOKEVLI *KKVILKI*PFFFFFLMESCSVA*AGVQ WHDLQPLPPVNSWDYRCPPSRPAKFCIF
921	14822	A	928	3	416	RCWENKIN/PFWK/S/VWPCVTKVNIH SPYDLTISLQYLPYRDEYLCYSKNLMFL IVLFITIGNYKQPKCASVG*WLRILWYL /YMENYSAIKMKN
922	14823	A	929	344	69	YKRSPL/LKSA*DGPAWKSPLRS*YKR SPLLKAKPDQIISGWASPLIIT/PRAL LQKLKPAASKF*W/NPKKKRALIS/KAI PSKKIKAEIMFPNFVK*YRDTATKTA* WWYKSSSL
923	14824	A	930	378	1	HGKKIDPRFIPYTKI/NLKWFDLNVKP KTIKLE*NIGE/TIFVIDHKK*NP*KK KLVN/WDFIKIKSFCFVH*KPAVGK*KR /QP*TRNRYVOTHTSDRGLISRIKELF *LNSKVINIRKWAQSLN
924	14825	A	931	479	83	SRKLGKGLKRGGFFPPPPKGLPGGVA PPGPGFCSL/KG/DRG*PFLKGVKGE KGKRI*EGG/EGKGGLPPPPKQKGSKE KGLFYAGKKENP*GSGPPPLPQPAKQ ISLKGKGVKPPPPGNLPLFLFIF
925	14826	A	932	36	440	TTVASLDEAQLPRKFNALFTF*HIK NGPILGKIGRKMYIAQ/GRHMKNHKK LTQVLNTHYVGPRIILLTGTLQNKLE LWALLNFLPTIFKSCSTFEQWFNAPFA MTGERVHLVEETLIIIRRVKVL
926	14827	A	933	8	398	CLQGKEETITTNWHLRYLPPPPFFWPK KGARKNGRPPGGSPKNQAPCPKPFEN PGEKTPQKRGFFPKPCPGPGPTGGQ GKPP/HPQRQILPFVPQAGPQGRKG* WNPPPPG*KGFAPTPPRM
927	14828	A	934	1	441	TRSHPRALKEVYTEINIVFMPANATSL QPMG*GVILTAKAYLRSTFCKAIAAVP SDS/SSDGGQSGLKFTLKGFLIDAI* NIGDSWEVKISLTLMWKKLNPIFMD FEGFKTSVEEVFADVVKITEEVQVED GTEFLQSH
928	14829	A	935	3	383	PGFRASDRLTFSSGNNAAGNFKLPVL IYHSEPRVLKNYAKSILSVLYKWNKA WNTAHLPTAFTEPVYETCSAENIF FKILLIDSVSHPRALREI*KQMTIIVY MP/STTSLIOPMNOG
929	14830	A	936	417	1	CFFSRDEVSFCGPGFSPSPD/HIDPPPP PSQCWDYRRDPLWVPHICFLIHKKRGS SHMGSSMDP*KPPHKWMSPPPVSVLY GSIPIVQVQIAPPETNPVYFFSPPPPW GGGRVCVCVCVSEVCOFFGGDENIV
930	14831	A	937	412	3	KPTRVKKINPPFFKNTKNGGVRGGSLY SPFFGGIGQKNGFTPEAKGSINLKFTPA PKSWGTOQKSLFKKKKKKILKFIWNQ KINPKQIKQS*GITLPE/FKLYKEATV TKTAWRYKNRPIDQWNGTDRNKATH
931	14832	A	938	1	416	KNRHIDQCSQTERPEIDSHKYSQILFDK GAKVI**RNDNLFNKMYFNNWSTC/RK INLDTLTYLFONGSQT*P*NIKLELNS MGGNLGDL/GMSQ*VSSSSSSRRIDHKK LVS/WDFIKIENICSEKGIKRMKSOTT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
932	14833	A	939	4	443	D DFDYNHHDHYAELGTRPGSVGGQSPDFQ FTPSRMGRGEGGTHSIL*CSSLGMGVIA DLSTDPTLEKRALEVAGPDQASAI ASPRKAGDGGHRRALPGCTSLTGTTG KSGEAGDQGGKPPGD/GPIGPTSLPGSGP SGSGSMWG
933	14834	A	940	3	404	LNFLLEFF*KRSGC*VSGAGMGCVLK ALQAPPRPTP/SLSS*DVWSLPPILA NFLYF*ETRGTGLTRMISIPQTEMPG LASQTAKLIFP*K/HRVLVES/HG*SAR AVHRGDLHILEP*TPGLK*YS/CISL
934	14835	A	941	397	1	FVFNQSVANAKKKFLKEAESTTEVLSGI RKONTFAADME*V*MVNIKDQPSYSIPL SCSVIQ/SRALTLDFDCTKAERNRGRKLO WEPAV\EGSKGWLMRFKERSHLHNKVKQ DEAVSYPELDDKMDAVNTKHQI
935	14836	A	942	441	29	SVTLCKHTVHVPTFLRGRKRCPLFGCCQ PWPSFG/PHPLSMSPV*PRPQ/PPIPLHS APPLALGPFIPMLSMAGLPFFQGSGLR NWKPPFPQPSLLQ*HFFPKLPKPIRGLR PFPPTLSIPLPGTRPRAKLGVMRSRL
936	14837	A	943	2	397	ARDAAPGEHLLQGLSARHGLRPPRDS RPGPD/PP/SPPHPLPLFAVPTVFVSFG DSWLL*SPFFPAPWASEGGACAPNPHAL VPSPSGQASGLRGAPSWKAGLDTDGQQ AGRQSPGPAPPSPPLPPSQDC
937	14838	A	944	3	449	LRQVWHEGEMPNKTTTLTYHYTPI*ITNI KNTDNTKSLWGCAEARSFTHC/WMRIMK VKPLWETVQ*YLI*KLQLPFPNPAVALW /SICPRKVKTY/CHRNKTRSPFIV/A LQVTAQTKN
938	14839	A	945	380	175	RAPAVPATOAEVGG/L/H*TWEDRLNPG GEV/CSEPKWCHCPPAWATKPNCSVSKK KKKKEKRNHODEK
939	14840	A	946	21	331	VAPLKVGFSKETI/IQSVRQSTCECKIF AYYPSDTGLITRIYEEL*RLNRKEKLS SVYKYADLI*PFSKEDTQMANR/H*K KCSTSLIREMRKFTTMRVDAV
940	14841	A	947	365	1	GGGFFWFFFFFLGGLIKGKIWAKKKT GPSFPQKKRGPKKKKPPGFFFFF*K GFVAPGGQWEGFSLQPLPGVKQFFC PRFLRK/DSRFFFFFLIKSNAEQPFTL YAGVRMYIK
941	14842	A	948	357	137	ISAHCELRPLPGSHHSFALLCSPLSRTP NLKQSLFSLPKCWDR/LATVPGQLL F*ARHCISIDPSLHLNNM
942	14843	A	949	53	352	REDNHKCI RNKMNINKWANEVNRCSSE ETQMVKHGEKLLASPIRSMQIKRYYL NSLA*KKEKSD/NTKLWQGFGETKSV* RYIIN/PYDPTIPLGIY
943	14844	A	950	937	3	KVSPYRINIK*VAFICTNNIAQEK/M NMVLTFIATNKKI/SYLVH*IKEVKYL YNKNYK/LKKGRDNANK*KGTPCS*I* RINIIRKMSVLKATYRLSAISLKL*ML PMELEKE/TILKVIWNKTAHLAKAITL /GSPNGGLTLPGLYKATVIHTW/HCY KNTHVDQ*/NRRESPEISLHFTQLFSD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KVNRSKQ/WKNCLSNRKYWESWLITCRR RKLKLYLSPYKCKNSK*IKNLTVKLKAI KIVEHQKSTVLVTGLWKGPMNTTIKUNA TKIKVKN*HLIKLNKCFCTPKET/T*QIC RQGRVWNKLPSNF
944	14845	A	951	246	1	AASTKTGVQTRTCT*MLIAALVITVKRE KQSKCSSVE*E*TMWYIHTMEYYSVTKR NDVLITTTWNLNLSMLSKKSHKG
945	14846	A	952	2	255	QGGCEKSTFLHCWEEQLWKTWV*FLK DPETDIPDQATPLLGTFPKYQSLYYK DTAKTNQPKCQMLVDGKIKKMYIVDA A
946	14847	A	953	343	3	GSITYKEMEPRVNNLQK*KASCTDGL*G EFY*TFENEIPILNLFQKTEAKGTLTN SRDEASIIIPKPEKCTRRKENDK/P/I SLMSIDAKLLNKILAN*IQQSRIYSRHT RLIQ
947	14848	A	954	1	349	AQPPFFILFILHP/IYCTFSS*SR*QKT LKTT*FGGFIFCFFFFFK/QAKCSRIK GRGPPIAAGTPELPLRDPPTSPT*VAG TKGGSPHTQLKFIFIAK*FYISF*HNGK FCSRRGR
948	14849	A	955	2	351	GLKNYAKSTLPVLVKNWN*KA*MTTHLF TAMSTE*FKPTVETYS/EKKIPFKILQ LMDNAPSHPRALNEMYKEINAVFMPVNT ISILQPMDDQGVISTFKSYYL/RNTECKA IGAISSDS
949	14850	A	956	336	3	PTKENFEPDGF/TG*FYOTFKELIPPOT FLKTSREYFSSSSSSSSSSSSSSSSSS SSPYRPI/SLMNTD/AKILNKILTNQVR LHIKKNTHDLVGFIK/WFNIRKKTDS NN
950	14851	A	957	181	1	RNDLTMLPVLVNS/QLRRSSH/LPKCW DYRFEPPCTA*GWFLIGPHNVSTVGS PRISRG
951	14852	A	958	3	293	GGLTSPHVITYQATVITKAWNG*RGVC MDQ/YNKTNPEPTDPCYKSLQMFSEVTK ATQ*RKDSLNVNIENWN*MSIHKSSSR KHLNQYLTPYTKL
952	14853	A	959	350	3	NKKKGQSLVFRSPTLFFFFFL*TEMG*F IMLARLV*NS*RRNMTTSGSQSVGITGV SNHARPKRLFLFSIIITIGWAGV/WNL TLVISALWDYRREPPRAVILLPFHIQRS RMPLSN
953	14854	A	960	349	1	GGFPPPLFFFFP/PPPWGKPPFFFFQYQ/ SFPPKKGKGPDPFFFGSPGWGHHKQFL VKSPLFFFWKKGKPPPPF*KKFFPP/VF QKQGRVKKPPYERNLWLLSPPTKKSPP KSTGS
954	14855	A	961	379	160	PGPGQGEPPFFLKNPQKLVGGGGRLF*AP LLRGVRQKNSLNPGGGALKPGS/HLWP PSWKGKGDFL*KKKKKK
955	14856	A	962	184	2	TFSPKKIFFFFFSSKFFPKGTFSPSR ENFFFFF*DGVL/CHPGSAVVS RLTATS
956	14857	A	963	1	328	AKLVKS*PQ/CCLPASASESSGITGVS HCASQSAGITGMSHHIRPKNISLYLG FWSFNKVLHFFCASSLEGESNNNELLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
957	14858	A	964	1	334	KQWFFLDKLGSTKLGNNHVCVNF HPLGGRVGGVFLGP/VVLNPPFPQ*GTP FFLKKNPNPGRGAKPVZAPRGG*GGKF LLPFRGG/PSMNPNCPAPPP
958	14859	A	965	206	360	QKSMSLHQQ*ODIHSSQAHKNSN\PGA VAHTCNPSITLGGQGMQITRSGDQD
959	14860	A	966	10	332	NFFSFGAPPPFFFGGGFFLKKGGPFF* KKKILGGPPPKKNPPGVFPFSP/AKNL GPPPPPPPPFF
960	14861	A	967	1	282	RKCAKDLNRHSTKEDIWISTECI*HC*S LRKSTLKPDRMPHY*ND*LYKQNDIDIK CW*GYGVGTGAVFHHVNSRMVQPLLNNW TVPRNVKFTL
961	14862	A	968	339	195	FFFCRDGVSPPCCPGWSETFRPKQSTCLS LPKCWDYR/RL*ATVPSLDLYL
962	14863	A	969	3	342	IKKGPHQLKPKPGVFFVFGFKKSYFPP PPPLFNPPFFFR/DKASLCHPGWSAVML SYFTAAYTSV\VRSSSHLLSS*EWRH TQFCLFF*F*FL/CRSK
963	14864	A	970	384	6	GRKNVAGFFPLSPLYTPHGEGLGPPQTF GAGPPAHKSHQKVGQRKPGFVPRPP AFLFFFFFKE*SVLEKKENNLNYSLFAY KILNKVQGETOCEGRAHIC/VCVVCVCV VSVCTCVHVCALIC
964	14865	A	971	427	109	INSQFELQEKIRISNLEDNEKII*SEKES KNRMARN/E/QSLRETWDTPGYTNIGIM ECPEGEK/GKKRRTIKKMAANFFHL MKINLHIQKAL*TPTRITCTGYGG
965	14866	A	972	389	145	SLQP*TPRLMLSSHLSSWDYRCVFP HLANFLYF**F*GFAMLGSSNSSA/SAS QSGGITGVSHAPVETFFKKLVADT
966	14867	A	973	170	419	VSFLFFFFFLERQYFFSPGCGGGEFG LLEPFP/PGFNFSCLTLW/RRND*CAP PPLPAYPGFLIK/TGFFLVGRGGLDLR SR
967	14868	A	974	212	3	QNSMIRYSRSMRSCLCTTLILSLNRS LKSPR*/WPGUVVAHCNPSTLGRGGRI TRSED*DHGQHGTP
968	14869	A	975	28	356	VFETSLFRNKKEIKVGTSLDPFRIFYFKP LIIESI*CLHGIGQNNANRVGNLQIDA /ECAENLIYKGGISIQW/SLFKN*CWS ITIHKEEKIRPLHCIKIKGTDFKCLS
969	14870	A	976	350	1	LFCEKVSLLCPKFFPFGMKKSTLLSL PKMRGYR/RLAPPQLEIFHFFLTSKA TPL/CLGRSLKRLNSQMFSPFTSEGVSL CSQAGIQWRDFGSLQPAILLWK*FSCPS LLSSWN
970	14871	A	977	4	343	PLHSSLGNIVRPHLLNNSKNNDITKCV* GCEKPGFLIHCIWEYMMV*LLWKTDWQF LIKPNIHLPYDSVAHLGIYPR*MKTFL QKL/CP*MTAAVFLIAKNGQLRCPV SK
971	14872	A	978	3	424	KMRROATDWEKIFAKGISDKELLSKIH KELLKNKKSPKQVACFKMGKQT*TAH LH*TTIYR/CRRVTHRKDSTRSWLLREL QIAT
972	14873	A	979	114	325	QQQGNW*IKKLAEDSNRDFSN/EDIQMA NK*RCSTSLVIMEMQVKTVRRYYLTLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
973	14874	A	980	339	2	SIAIIKQKKKQNPKK GPTGFKFNQGGPPPKGSFFL* KISPPS* NPPFFFGPQKGFKPPPPPYLNPGRNFF SKKPLFFFP* KKGFFKPPPPPPPPFF* GRVSLCCPGWSAV\A* SRLTVTSTSHVQ T
974	14875	A	981	2	377	QMANHKMSFSTSSAFMK* IKNKMRSH DTCIRMANINTND\CW*GCRSNKILMH SW\WCKMVQLL*TMV* KFLIKY/DTYH DPAISLLGSIKKKSCKCT*/T/CKILYL NVLFEMNPWKSNNWSMG
975	14876	A	982	1	457	INEYEAANTTEKFKRTLETSSSSSSSS PLVGLTKRKSQNWNEEDITTELEI/ TIIKDYSE* IYA\WKIEQSSSSSSSKT YNLGPIHIEGTESLNRPIMSSEIESLSQ NLFTNRSRADSFTGKFL* TSKDELPTT LLK\FOKTEOERTLPR
976	14877	A	983	332	2	TPKAGOMQVLFFQVGSKVARAPSSVVAL PPPPPFFHFCFPPPHCSLPPOIPPPFS RFFLQVKSQQGPPPSLLGWGEQ/NTLP FFFFF*SHSLALLRLECSGAISTAA
977	14878	A	984	365	2	KSSKLFNYPPLFFFLKNFGPKKK/SGPF FCFPKNFNRPVPGPNFNFKGFFFLKKG PTVF* IKKFWMGPLPLK* PSGVFRFFH FLIWDPRPRPPPPPPFLVERGFGHHVG QASLELLTS
978	14879	A	985	1	153	GVQWCNYSNL* PRFPG\SGDFPTSFAQV AGITGVHHHTRLFFFFVGGFFNF
979	14880	A	986	225	1	LYIYRERERERDRDRDVSHTHLYIHT RTHLDNLFCFPGWNAVA*SWFTVALNS WV\KSSRPSLPSSSDS
980	14881	A	987	2	375	GTDEYILIALIVVMVSWVLFFFFEKKA PFCPPAGKTGANFGLRAPPPPGKIEIFW PP*PSEEG\EFRGPNPSRGNFWFFKRG GSPL* PRLFG/HRP*GNRPP*/PQRG GNNKGDPPPPGGIFF
981	14882	A	988	55	335	HIYIDFVSGSWLTV/ISLLELTVFCY NUGAL*ASC\QASENI*SVSDPLPSFY LPKAGL\SEPAFMMHGHKILPEKVIH MLEE\TCTERP
982	14883	A	989	295	369	ILVTRNSEL*VLPEQRTFLFKAMALRS IPLLR/NGRPGTVAHACNPNTLGGQGG RIKRSGV*QQP
983	14884	A	990	2	240	KKSIMNLEHFMLSRSQS*KTYYMIIF T*KLQNRQIYK\TERIYIYIYIYIYL FFFFLERKFLFLFPRGEGGGPF
984	14885	A	991	463	0	GFRQLSCL\LPSSWYRHMSPHLANEF \TF*VERGFRHVQAGLELLTPNDSFSS ASQSAIH/GMSHCTQP
985	14886	A	992	82	365	ETCHQLYRSFLCSLFC/DHPSNKGH*DT MNCVHFIRLLNPSFFFEKKFRFVPQV EGQGSNLG* LKVLPLPKFSPCLTLRRS WGYRGPPPPPVN
986	14887	A	993	3	317	GLKQSSCLGLPKCDYRHKFPCTHIIF NTH*IIKVLNVSFPCI/PLCWSIALSD HVQ/PV*LYNMLVSSFLLLLFPFIEVV ILACLFCVGPSPILFF*YILTF
987	14888	A	994	350	139	LFRRLRWEHLSVGGGCCSEF*SHHCT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
988	14889	A	995	219	1	PAKATE*DFVSKIQCKNQDTFSHTF IL ECRTSKGVSAFLAL RPRRPLTKTKAKNHFTPTRMPIKDN NKC*QCGGEV/WN/CRMVQPLWKT/IQF LKMLNTELP*DRAIPLTGKE
989	14890	A	996	3	498	CLPWAAVARQPFSAHPFGFGP*LRTLA PDATAVNQALQGES*TCG*SPSGWPA VPTPVADP/PPSAG*GVVDPRAMPRIH PPGQHPKEKTYQPVAP*VQLSPTRCTP APMACSSLLLPALPPPAPAPRPPCPAPP FLPSRTSLPPRRSSSTIKSTPPGP
990	14891	A	997	2	419	ADTAAASYPDNLANDESSYTRQOIFN VDKTALYWKCTPSRTIAREGKSKPGFK TSKDKLTLGLGANAADDFLKPMLTYHS KNSRAHKNYAKSTLCFRN*NKAWTEHLF IAWF/EYFKVTVVNCPEKK/VLLLTN APG
991	14892	A	998	388	405	G*FFPLSASKFFFCP*ALKLWMEGCHIR PPQVRFPLQSSQA/GFISASLKGKGF ASMPANIGPPKGYL*PAPPFFPSFLRQ SHSVTQAGVQWRNSSLQPPPG/LRRSS HLSLPGSWDH/MPCPAPNCFICTGG
992	14893	A	999	1	423	WLHD/NLRQPAQWLQDEAPKHPFKPN SH/CKKVMVTVCWSAAGLIHYSLNPG TSTLEKYQQIDENH*KLQCLPALINR RQPLPCQDNARPRVTQPMQLRNLKGLCD VLPHPPSPDFLPTDHYFKHFNELQ KHF
993	14894	A	1000	2	406	SDLFRAI*ETTSVTVVDVSDMDYLETDE MIRDLNLTFFV/HLELQDSSGVIQAG ITEASTINAKENHMLMKGNRQRTQET AANOTSSRSNAVLOQTVRQSRVKMLIQ EVROGRLFMIDLAGSERASQTON
994	14895	A	1001	290	3	VTOLPETHVFLDRDVSFCCSGS/DHSS LQPTPLGK/YPPTSAT*VGCTCHIAQL IFIFLRDGV/SVAQAGVQWEDLSL*P PPPGFKRLSCLNR
995	14896	A	1002	143	408	IKKKIKREI*KYLDISKNN/DTYQNLWN ATKAVL*GKFIGINVIFKNRKN*NK*F NSTSGKLKLEKKEQYIKLISRKETIKI RAKINE
996	14897	A	1003	84	409	DKLAALPSSWTLHFGSPLGVTAPPPPP PPPPPPPPRVLEPVRSYLPGLAVPVV PRALH*PPHFGSLPACPAAGLLGGTRC S/QITLPPKKKPPFLADANEPNPPPP
997	14898	A	1004	392	2	EKNVHFQDKNLVSIWELQVPTQVCIQ NKTNSWGIAGYPHFLKRNORFPNALVK PGPFSK*TIHLVNLKNLFF*DRVSFCC PSWSAVVKS*FTAASTSL\IKQSSCLNH PSS*DCRHTPLLLFFVRMS
998	14899	A	1005	2	421	FVSLLLLLTSATVAAGAPTGRVTVPPFLS GNYPFHGAPVHLTI FCLHLEGVSSILRA INFASISIIIPPAITQTPFP*SGL TTAGLLISVPLVLAAGITILLTPSFL TTFFDPGGGGDPILOYHL*FGHPEVY
999	14900	A	1006	1	428	DIHWG*TIYRHWAGCASTFCTCLLHGT RGLVYGSFLYSET*SMGILLATIATA IIGVLP*GQISE*GATEITYLLSAIPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IGTDLVQ*I*GGYSVDSPTLTRCTCYF ILPVI IARLPALHL/LFLELTGSNKPTG LAS
1000	14901	A	1007	1	419	SPIVPIVMAMACMLMTERIILGYIQLRP GPNVGGPYRLLPQFADAIKFLSKEP/LK PATSTITLYISGPTLTLTIGLVL*TPLP IPNPLVNLNLGLLFIATSSLAGYSIL* SG*ASNSNYTLIGALRAVAQTI SYEVTL
1001	14902	A	1008	411	27	GQPGQHRKTPSPLSIFYF/ELAGGGDAS T*FQLRLRL*EARLSGI*GSEL*LP PCPPAWVK*DPVFGGRKKERLSQLRK LRPREVKSLLVQHYVAHKGNDPNPGPM ATQPGRSCTTLCVPLCHR
1002	14903	A	1009	21	377	MSLGGQDQSAOTTRS PQFAGFFGQRSIP DRIGLGHFLCVCKCVACVQVS VCKCVH MCACACWCTRTPMCECVQVCECVQVCR VSNVCQVCACVRVACVCSGACG/CTCV T*MSLACG
1003	14904	A	1010	1	412	HKANTSYTLTLVNTFSG*VKACPTTHK TAEVASTLTLEQIIPRF/GPAFISKIVK QVTTTLDVNWKLTFYHPOSSGKVERAN SLVKHLLIKLALKTRQSWVTLLPFLALW LWAAPOSPGTGINPEELLY/SAPLPLSN
1004	14905	A	1011	1	410	FRVAGASROENGA/TVILDRIDAREAN IHKSLAGSSGPGAGSGTSGDHGELVURI ASLEVENQSLRGVQLEQAISKLEARL NELENSSPVHRSTAPHTQQVSPIAPVEP PAEKPATPT*DDVDDIDLDFGRND
1005	14906	A	1012	269	32	NISRIYKELLQNNKKT/SISKRAGYLN RNFTKDI*MAKKPMKRCPTLLVIREMQI KITMRYFTPARMATIKKTNDNEY
1006	14907	A	1013	21	443	RIRKKNYSYPHYKSVIYVTFIIRLFPTT IFMCLDQEVISN*H*ATTETQLSLSF KLDYLSIILIPVALVATWAI IQFSL*YM /NSDPNFKQCLKDLMLFMTLVLSTAN NLCQLLIG*EGA*MISFLLIS**YARAD A
1007	14908	A	1014	1	309	SSRAATHGGACLWLQILHRLRWEG*LS VGGQCSCSP*LHH*TLAWATERDFVSK KKKKPQANP/VHETSCKKKKKKPMGLP PKSQRKQPKAQQTLP
1008	14909	A	1015	3	256	EKNQTLKWMDLSEHFSKK/NMQVGNRH MKKC*TSLI IREIQIKTMKYHFTPVKM AIWPGAGITGMSHRTQPSPTLLTHVV A
1009	14910	A	1016	397	3	LFSPPPKNGVTTTTTTTTPPRFPAPPPFFF PPPPPPPPCEKPPPPPPPPGGGAPPL SPPPPPPPPPPPPPPPPPPPFK/SPPPP PKKK*KKK*KKKKKKTPTPKKPKKPK KKKKRAARDLELVGRVGRV
1010	14911	A	1017	2	164	EKERRE*KREE*KERK/KEGEGEGGRE RERERKKRKRERKDRCMFIVHRE
1011	14912	A	1018	1	406	NSSPPKNKN*NK*QHT*EKNFANYIS DIELVFRTYNELLQ/LNKTGNPKNSF*K NQFKNGK*PNFYITQSF*RNKPI*KF/ AKDLNKRFSKEDM*IANKR/KTCTPLA IRKRQIKTTVSSFFKA/IYMWVVKET
1012	14913	A	1019	302	2	IVEPLGLMCLFLQNPRVKGPGPYFSK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, = possible nucleotide insertion)
						GKANVVFPTV\SKQPPKKPAFFVYQKQ LPLF/PALVDKKKVL/RFFFF*DRVLL \CCPGWAMQSWLTTSTST
1013	14914	A	1020	47	382	AKIALHSSGLQDRVSHHTHTHKRSNEI ELVIKSSPKKKSSGLNGPISFYCSFK* ELIPIFLKLQQ\VEAVGILLNLF*EVS ITLIPK/PROEQNSNXTIYRIPISLMNIG GK
1014	14915	A	1021	273	1	QSKERRORTQOEMGKTFHNNRENGTTFG FSQSLCKDEIIIIIFETGFRSISQAGVQ W/P/NHGSLOPRFRLKQSSCFSLPSSW DYMC*LPH
1015	14916	A	1022	327	1	KFLKGWFIYLLKGGFFVFGGGGWANYR SLVPQIYGVK\YPSAFASKINSTMGMP PAWVTFGMAQLINGD*IF/IFFLRQSPA LVAQGVQVHDLRSPQPPPGFKRFS
1016	14917	A	1023	3	407	THLTOR*/HNITGTFP/WV*GTGLSTVLM NFYLWM*FHFQSTLFLRLTLTKLTM QGWLDVTQQRSYQGHHTTPVQKGLRYRI ILFITINTFFLEGLF*ALYHSSLFPTLH *RGDWT/PTGIPLKPLEDPLLTNTE
1017	14918	A	1024	3	425	LPPQKKRGFPKIPREF*KTPPKKKKI FPPPGKNWPPK/RFLKGGPPSRFIPFP FFFLPSSPSP
1018	14919	A	1025	430	1	GGFFPPFPKNFFFLSP*IFG/RGVCPK FPPPKKRFSSKNPQGFNNPQKKKKIS SPPPVNFAPPRLDLKRPFFPFFFFF FFFFLEFMHPSFPTSVFQWQITSLFLCLL LLLQCCVCLIGMVVDQSSSPSHHLQ PRWL
1019	14920	A	1026	463	494	RKTGFPRLT*HLLDFFFFFHWKGI APRACGRGRNLG*LKPPLGWAPFSGLT PPKSWN*GAPPPPPFNF/CVF*RKTGFP RLTR
1020	14921	A	1027	606	1	AGGPGFPKVVFGAGWG/SLNG*S*LKG KSGKGAIPQSGPTVFPGIIPKESPLR PPGGMQGRGRPRWAGSGC/VG*DSVLR QP/GVTGEAPCPGASSPQASQAARRGSM GKGGAHFHVSNGCVLSAANPWGPPGSH G*/PGRRGGSQSCSPKG*AWWRPCLAG SHSSAKHKGMSSEGPAPRGRASIPVSAG SIGPIAARGF
1021	14922	A	1028	436	1	GGAPOGVLKRAAPFFFWKCNFNFVARI IKGKGGVLSRQFPPLGFKFWGPTPL/ SRWGFKEGLKPPGFWFFKKRWGFSMW RWV*\IPGPKEL\PPFFSQRGIGQGT/ HRPPIIPPSLF/CFEMETHSVAQAGVR WRDLGSLQL
1022	14923	A	1029	1	436	PPKKTIFSPKF*IFWGGGGPNFPKKKS FFSNPPGVFFSPP*KKKIFPPPPENW GPKIF/YKRPFFFF
1023	14924	A	1030	28	366	EDHLSGGGGCNEL*LCCHCTPAWRQNK TLSPKEKDEK
1024	14925	A	1031	3	142	FDGSAQGFETRLYCPSSWSQPELKRCT HLSLPKWDYR/R*ATTPLRLIVLELOK KLRR*CKRELLYTPRSVTPNINDI*HWGG TFVTINEIISIR*YIALAGLRLSSSDV LTSASQNGITGMSHHTWP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
1025	14926	A	1032	7	361	PALRPSARGQOYYDETNNKTLCRNAQND SYLPDPNPFSSRFSTL/DHSNHQLEAPDA *KAPFGLYWNCGARVCR\QGISAQ*TEA CGLGTIKPSSFLLPLKQGELLGYPAYNE NLKKKKKK
1026	14927	A	1033	472	3	TQOOLNVDRTPAFYKKMSSRTFIANAER SMFGFRASKEG*LLGANTTGNF/LKAML IYHSKNPRTPKNEAKSTLLVP*K*NNKA LVAHLFTA*FTEYFKPIEIQIITADN AFGHPR\MYKEMNVFMSAN\TSIL*PMY QGIISCRIPAAREIVKGA
1027	14928	A	1034	488	0	FLR*TLAQRSIGHSMT*SGEAAAE*KS EARSWSFLRFKEKSHLNKAKQDKAAST DGKAESYLEADTD*DNWTK*LNQDKT AFY*KEMPSRMFPAREELNPGFKASDM LTLLLRANAVGDVNLKPMMIYYTENPRA LKNDYKDTOLC/PVLVXN
1028	14929	A	1035	114	491	NYFKNFTFSNKLTL/CLL*LPLL*KLFN P*TF*LLC/I*HLA*NNNTLYSCTKI FS FFIFLFYKHLKFIYFFYFLDFII*GAY *SLCY*VVYFSCQFCQVLFHVFWGLCC HVLVRLLYFQTEDEPY
1029	14930	A	1036	114	496	LLRAITLYLYKISAMNLVSA*FIYLHL TYHCVF/DHPVOGR*LLNK*INELFCYR SPGF*WVFSYSHLSED*ALEEKYLRRS RWVK/DLNVTSETVKILEEILGKTLLDI GLGKEFMKMTSQANITKP
1030	14931	A	1037	381	45	KNRGRKKNS*LGGF(SDKFYKTF*KLIQ IYKLFQKNEKEGTL*NSRPISLINIE ANION/RAVLAMIIQKHIIKIRHNQV F/IPGR*G*NTCKSI\NVIHHKQRR KSIEF
1031	14932	A	1038	134	394	SFCDKFTNCISELCO/SYSPTYIIKIF VLPKIRSGSITQPGVQWHDHSSPQ*TH SWAQTI*FLSSQVVGTKGMCHHTWL/IF LFLFVF
1032	14933	A	1039	483	30	YDGGSEIINLVLESRLIGTEKFKHVNTD NLSRKTYVKGLKRGDTIYRVSAVINIV QQCKPSFCTKPTCKDEL/ATVSTTIY SETCTFVDL*QINKNDLPL/LQILAPP

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						AHII SQEKEIKKIQI*YKEEKLPFLTSS SLFI*VRNLMFAKKLLELINEYNKVER YKINIKVILLAKNTWTLLKF
1036	14937	A	1043	50	457	TKYQLANKNMKICSTLPPIRE/MQIRPH EISLTPIMMALSSECKQNKYWGCGREVE TLVHCW*CKTVQSIRKTVHREPK*LRK ELP*RLPPK/PGSQRDICTPMETAALET IAKRFPWKHPKCPSTDE*IKEMWYIQS
1037	14938	A	1044	2	469	LKQSSCLGPKCRDVR/R*ATVPG*PIL *NTTEDPNLTKN*ILNTNH/MCYSVQLI LGESNSTIKTSLSPSQASSHQNTTVQFL STSPSPKNCQWLAILPRK*GLTSLFCFA FERQGL/NSVAQAQAQNLHHSLSKAQPP RLKQ/FLPNCPTLMCEYRLQP
1038	14939	A	1045	42	200	LICT*MLIVALLVYARNWQIRRC/SST/ DEWLKNLW*IPMEYY*AIKEPTIGTC
1039	14940	A	1046	475	36	LNVN*LNHPTRKQKLAG/YVRKHDPFTIC CLS\QQRFPFKDNTNRLNKGWRK\TFH ANSNQKIA/GVAVVVSNTKN\FTRNKE* NYILIGKSIH*CIIIINICATNS*NLK I*NLKTEMKEEIHCSKITVED/YNTLF* TMDRQKSFHRMQ
1040	14941	A	1047	3	326	FFFFIIIIIFETERDSVSKIIIIKNNK DLF*FLVTQVTPETINQYISTLPLQSKT KWDRTGTVAHSCNPSTLGGRRRI/TLR SGVRDQPDQHG
1041	14942	A	1048	403	15	EVKNSFSYRLMTEIMFGYVSKLYNCD SGS*LS*SFNVCKMNR*Y/LEERGNTS FKSLLLMMKLLHSAIFTS*TPRGL* I YFIYMYVLETWSSHSVQAQGMQWHNQSL QSPSPGLKEPHRTDIVAR
1042	14943	A	1049	25	457	YMWNSHSCMFTLLFSSFFPPSLCFPI LRSFLFLYAEPLAFLLVKDSFILFV* I MSVFHLILKQ*NHNHNYFTLITFKCT VQW*VYSHFSVAKTAT\ISRTCLIPVS WDYRHMPLCLANFPL*RGQLALLPRLVL TSWLQ
1043	14944	A	1050	14	478	FEFYCRH*ITRWNCWGYELVQSLWKA TEQVYLKPDICVF/LEPGVSLMGYSKE LCTLC\YQKTRMFATLFAVK* *LPK SS*MVE*ITKL*YPHIMEYYTAM/KNE* ITI*TTIWMNI/TIILNERSQTQK
1044	14945	A	1051	2	465	GIDQPSKPIPL/TQSPOTKA/LTFFN VKAERGEAAE/ER/VEASD*FMRFKQ RSHLHNIKVGEAATADGETAGS\SYPE DPAITDEGSHTKQIFSVDEATACCKWIS SRTFAAKESMSVSKASKDRILTLILRAS AAGDLKEFPRLV
1045	14946	A	1052	392	24	DFAPRRKKRETRRSKINSLS* *KELEN QVKTNQKGRKQETIKKVELRIETLK TFPKKKVNSKRSWFYEK\INKLDGTLAR QINKKRKENQ/DTIRNNKGDITDPMEI *TTIRGIPPLWR
1046	14947	A	1053	204	488	CAVCTGISTLEWVDL*SLDPGFETVSH LFDVRQ*P*DCRRVTDMLMV*NLHPIV LFFLEW/DFVFLRQSFPVVTQAGVQW RDLGSLCLPPG
1047	14948	A	1054	498	2	SVVUCLFLSEGITSHYVPMIFKIGAKK

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						VHWWKSILFNKSCWRNLSTICRMKVDP M/LTPGKTINTNWKDLTPSAESIICK ENIG/THFDIRLGNFAWDMTPKA*ATK EN*IPWITSK*QT\FCAAKNTVN*VKR* PMD*E/RIFAKHISEKRILICIVIKGLE LN
1048	14949	A	1055	28	209	IDGRSRGLWW\CVVLASQLLWEABAGGS LEPKSLRLQ*AMIN/DCTPPW
1049	14950	A	1056	163	479	TSFLGSQSAGITSVSHCFPSREVFFKL IHWKQGGQVALLVATPHSPCCPYRLAPI PRAREHDFACASLI FVCLLVHVLMLPRS VAGRGVGGGLG/CGGR*1, +TC
1050	14951	A	1057	2	1258	ELFPHHQPSPRAASLVVAKA\RDKVP GGT RRPVPTDGRPEOFALEPHHS CLGRH QGPERCRIMAASP*EAGN*PKDK CHP GERTETAAGVHTGCGCKGPAAGGR* AQ GGSGEAGAAGGAGAAGVGGAAVGGSA GGRWAGLLGQHAG*GEGPCROHGPFP GVSAGOAASFKAAGQPGFGT*GAAGQ PGRG*GPAGPRGGAAERAGAGAMPQ AQAGAAEPAGEARPGADYGPANHPGA RTGAGGAEAGAGAAAGGLPRPAOHR\AQ IHGPVPLGTGGRSSS/GGI PDNMSHRLW QRHRSHGAEASQGRHPHPGPTGGER/GL OSMLS KIREVAQOGLKVLGRALGDO EEAPIQOQVFRLCFGLNLR/RPPHMRP *AVLL*NIPHISRREDVMDPMPPSPIC PL
1051	14952	A	1058	2	437	ERSVRTACCKQSRGLSSLLCPFPAPRLS *TGSFVTGSSALEPRSPHPQP\PSLRPR SPGPQLHPLGPRSPSPSEQTVP SHPA RPLSPSPERTQG\PKAQ*SQLPPPSLAL AQPAFVGGREEVASPACPSWKDKSLR AVPGSA
1052	14953	A	1059	47	456	TRCYCTLLRLDAPGKLWTRKN*VVASTY ARTDRKSSASERPLLPLRGPQLSLHES LTSPSCLAFSANTHROLRGENYHTK/C DMAKPV/HN*TOAVVQWHDGSPRPFP FGFRSSCLGLPSGWDYSPLWHEQTL
1053	14954	A	1060	484	13	FPTSASONTGTTGVSQHAQTIY/LFVE MGSPGV/GPASLKLTPSRDLTPASRAA ESVSAHHH*FLNFL*RWASGFVAPSW* TFLL/KOSSCLSLPVC*DCRCYNHWAMP HSVFSSQFLSLFPFNFSFLFSSFSFK DRISLCRPGWEFHQTQWNR
1054	14955	A	1061	1	494	GSPPGHVCGRRRSALENFGQPCSLQPGV VSGATGAI VRVORTSSAWATAAAGAYV E/TTRFRYT*KAGVGCDDLWGAWLKADG LGETKAETHLDG/PPEDALYGLIEGDD TNFTIQGEVHWCYTGTLPDGTVFDTNI QTSAQKM/NAKPLSFKV/GICKVSH/G WDE
1055	14956	A	1062	3	395	SDPSPCGGIRFDEMEKPLENYNLPKLKE /DKINDPTFVK*IGSVMKIHTVBP/PS HKCTSEFY*TFKE*IAPISHKLF*SRG INGATPFWMEHLOENVIPK\TEKK*T YRPSLWNLN/KLWKLTYK
1056	14957	A	1063	402	260	WYCFPKV/LLRFSVYSSPFEVWAGSIK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: of USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ABLYMLRPLFPRTREVD*IF*ICPV/LK GSPKNKDFCP*GAKTFEYFYPATLGLNL KI*IFRQW
1057	14958	A	1064	66	379	EPGRGCGEPKLRQCTPAWVTEEDPVSGG KKKRKRERKT*REPSVSRPESH/PFSQ EAFVWVQALSRVLPNPFISGRSASGLGK SEAIKSLFLYLAVCSSTTEQA
1058	14959	A	1065	223	437	KSCMSCDNKIFFLRQQLSCSLTQAQVQ WHYLGSLQLPQGGPK**SHLSLLSNWFA RR\PPR
1059	14960	A	1066	414	65	NKSPDRNELAS*KCTQ*THTSIARDPFA KTQWGNLSLFWNC*DNWISTSKRIKL DPYIIPYTK\TNSKWIRDLHVAKITIKL LEKNGPGAVVCPNPSYSGGLEARS LR PAWAT
1060	14961	A	1067	418	1	LWVFFSRQSL/DSVAQAGVQRCDLGS L QPPPPFRKFRPSCLSLRSRDYRCRPPHV ANFVFLVET\GFTMLARMVLNS*PCDLP AAASQSAGITGVSHHARL*FCGP*YIHR VAQPSQSQI*DDHIKKFCIL*QPTPPR S
1061	14962	A	1068	24	440	EV*NLVSENYKMLLKEMRGDLNKKWSTP *S/WI*RLNIVKMAVLPKLIYRNLPI RIPDEFFVKSTS*L/CKFIWCKRLRIA KTIIF*K*RTK/SGDLILTDPKTYKTMV IRTI*Y*QKDRCID*WDRIES/PEMNFY IY
1062	14963	A	1069	442	26	LRNQVSTPSSKTPRFFFFFLKRLQITGAQ RHNHSSL*PRTPGLKQPOSTASGVSR TI GASHHTPLIFFYFFN*GKEGWGGSCFV AQAGLQL/RLQMLPPQPPLKCWN*RHK PPSLTYPILFKRTE*SCFSKEKATRIFF
1063	14964	A	1070	294	46	KNKLRKRERKENNKKAKINDINKSM L EKIHDKN*FFERNKIDKLLATN/RIT KKTQIVLFWNKIRIDITTYPTIDNKV K
1064	14965	A	1071	141	469	PKKQGVLTQNALPFRVGGKRGELCBKK KKERERDRITISITIIITKLPTKKTPGP DGFIDELYQTYK*ITSILLKVPLKRRR CFL/PYSMDPAVPAIALNPPP
1065	14966	A	1072	49	472	EFQITIK*NSFFADTEKALVNIENQNSH NMPLSQSLIQSKALTI\FNSMNAERVGD AEEKLEASRGFWFMRFKKPS*HKVQGE AANLDVEATASYPEDIPETIDEGHGSK /QIFNMDEIVFYWKMSRTFPAERERSM PG
1066	14967	A	1073	82	419	LTVGFRETRSSSWCSPSPKRALHALRF TPALKF*FFFWSRSLFFFFFLRDRVLLC CPGWSPTLGLK*SSCLGLPKCW\YRYE PP
1067	14968	A	1074	1	407	LEDGFPKITQSDKKEKKRI\KCK*NLQ EVW\DYVKHSNLQVIEIPE*EVKCLNENL FEEVIEANI/PHLASLDIQIAVORTQ RGYIARQTS PKHIVVRLSKVNMQEIKILN LPKEKHILITYKGNISRLTAKPSPKPT
1068	14969	A	1075	3	396	LHAYHIVKLSP*PLTGALSE\LLMTSG L TM*FHPHSITLLILSLNTLTITYQ*WR DVTRESTYQGHHTPPVQKGLRYGIILFI TSEVFLFAGFF*AFYHSLAPTPKLGGH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
1069	14970	A	1076	250	47	WPFPTGITPLNPLEVPLNTS VACONAFCTFSCYWL*NLLCRK\MDLD ISLLP*TKVNSRWIAGFNVRALTIKILE ENIGSAFGNRHSQ
1070	14971	A	1077	2	393	PLTGALSNLLNSGLAMRDDLHSTILLY LGLLTSTLTIYQG\WREVTQESTYQGH TPPGQGLRYGTMLFITSEGFLYTGF* AFYHSSLAPTQLGGHWPSPGITPLYPV ESPLNTSALLA*GVISIT
1071	14972	A	1078	2	500	LHVIGVSEGEEN\GMQNKIFEEIMGPN F/PNLVKYINA*/IQEMO*TPNGIHLKK TVHRYIIQLVRTNNKERILIVAREKWH GIFGGTML*MNDDFSSEFIKARKIEMMF LKYKRGISSSAKHC*SRILCVAQISFVS KG/EITTFSDKKLRAPFIISRPAHRAK GK
1072	14973	A	1079	419	1	LRWSFALAAQAIVRWRNLGSLQLPFPSS SNSPGSWRLQ*ANTAPLRSSLGNNKNTL SQKRRK*KDNSEWEKIFANHASDKGLVS K*TKNSINSTITK\DI*WTKYLNHRHFS KKDIKMANKHKRCST
1073	14974	A	1080	468	2	KLPPPRGNGSSAP/LEFFFTPKGGEFSP PPP*KFFSPNPLIFGCGFPPIPPPPK NFFFLNPKGFFFSPP*KKKKIFPPPP*I FADPPFFFKSPPLFFFFFFFFFFFPF FFFFFFFLRTRGRTGRTRGRTG
1074	14975	A	1081	467	1	PTYKFNAITPKIQ**FFKKIENCTLKFL /WNLEKPOLAKTVLK*NKVEGFTLPDFK /LTVTKTVWS*HKDRHRDE/WK*TESLK IKPYKYDQFFFFFF*FSFL/HFF*YLT YQHHKLIENRMPKPFNKERLBNK*CWEN WISICKIILKDHLYLTPYTK
1075	14976	A	1082	387	3	LKQFPFPHKSFVNKNKGVSLLCCPG*F*TP GLKRSS\HFDLPKCWDFRCEAPVLSLLN NIK*L/CORGLIKQFPF/SVK*K*AP SWSAHLAETFFFFRQGLTLLPMPGVQWH DPGTVOQTPGHHK*SSHFSL
1076	14977	A	1083	2	435	FHPPTNMGGSFPPPP*KFFFSFKALNFG GGVGPNFPKKRFFFPKNPRGGFIYVPL KKKNFSFPPPLKLAPRV/SFKRPPPPFF FF
1077	14978	A	1084	447	47	FSRKFFFFLAPPKRGFFFFFPLKNFFFP GGLFFG/RGVQFFFFPPPKGFFFFKPRG VF*PPPKKKKNNFFPPRENLGPPGVFLK RPPPPFFFFFFFFFFFGRRFVK
1078	14979	A	1085	438	2	AKNHKGFSPFKKFSPPFGGGGIFIRGQ L*KSFFFFFKPKFLV*KPPFKIFFF/I FFFKQRLAL/CBPKNKGVPQGFPIF FSRVGKELFTPNPKNNGKNPPTDGI FFFCFSFPL*RGQLTSHRLVLSNWA*A ILFLQPPK
1079	14980	A	1086	43	265	IKHKLEYTKIKNFCASNSNR/TERQPM WEK\MFANLISDKGLIPRIHKQL*LN/ TKQNSPI*KWVKDQLQWPLYL
1080	14981	A	1087	11	412	IASGLHDFNNKKKKKKKGGGFLKKFP GGPKPNRGGKKKIFSPKGGEKTPGGFL EKNPFLGGGKMGONPPKCKPFGEKKNF *GERGEKPKFPGGKKMSPSQPE/NKAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide Deletion, \=possible nucleotide insertion)
						RDDEPPE
1081	14982	A	1088	2	292	RSLSASADSSSLVAASLAGVRDVRSTCW PQWS/AV/VQTL* SARLGLPKCWDYRCE PPCLAEAPSTMRSGKASCTLETVWEDKH KYEEAERRFFYEHEAT
1082	14983	A	1089	376	3	HIGLYIASCKTLLKEIKGS*IDILCSWI ERLNTVKKAILLKLYGFNTIAI/KILS GLFIETERMILKLTOKCNRSQTANTILK PNKVGRLALPNFKTYTKATVIQTVWSWH KDRWYFFCCVPTQI
1083	14984	A	1090	277	407	QIKAESRHHKQITSMRNVKHCSSENYS *RKPAPGYIIIK*F*K*LIKRKILNSGR LQNRPIKEE*RYAYQDIDSEITIKVR*EN DIFKVL\KEKKSQCPRLLYPLKIS*IEV KYFFDKSKLKEVITNRSVP*EMLNIVLQ /INYSPIYEP
1084	14985	A	1091	421	2	GHPEGLFKG**A*NEKSL*NCSFFNY*S SFSNMQTRIKNV/WPSTVAHACKPSTLG GRGGQIT*GOEFETSLANTVKP
1085	14986	A	1092	369	3	FLKETRSVPVNT*ENLIAD/IGERVLV VWLENQTSNIPLGSLIQSKVL/TFNS MKTER*/EKLQKFASRGWPMRFKERSH LH/NIKVQGEAESADVEAAGVYDPAKT IVKGGYTQ*QIFNVDV
1086	14987	A	1093	71	506	FAEDNGL*LHPCSCKRHDIAVFYGCTSF VLTPGL*PWFLTQS/FLNFLEFS
1087	14988	A	1094	118	385	SDLGKDFMAKTSKAQAARTK/IYTDWI KLRSFSAQ*TKQSTE*RRQSTE/WKEK IFADYSSNRGLISSRQETQTTQWLKKIN KNALCTL
1088	14989	A	1095	419	1	DAKIPGQVVAR/RIPRPIKILFCPDQVW FIPGMQGGHEHIGKSINVAPIHMG*KSF NNIQHPFMI*KKKNLSTGCTHEGDTQH /R*MLHEHTTNAILNREKLKAPLRTGI RQGCLL*PLLPSIAVKT*P*AMRQEKEI N
1089	14990	A	1096	34	464	NSSKKKKRRI*PHDLGLRFLDMTPKT*ST NGMMD/KDFIKIK/FCASKDTINKVRE *EKLQIIYL/DEKRLVPRIYKDSYPIRQ LKKWVNNLNKHCFCEDTQIANKHKECS T\SIRE*QTKTR*RSHFISTRVTIKMS G/N/NKYWQGC
1090	14991	A	1097	458	28	RIIRVLDLKMCTHNFDSLEEMNOFFKKSR WFR*NR*FE*SYNH*RN*IHNLVSKSS GPDFTGFEFYQTCHEELAPILQNLQKM ESIRSNSFYKVRITLIP*GDNGS/TKKE NYSVVSFPMNDAKVLKILAN*I*VFIRK REFH
1091	14992	A	1098	41	500	FWIRHLSRHHQKQNR*MDFIKIKNLYA SKDITVKEVR*ST*WENYFQI/RMFDTG LVPRVYKEFI*LSNK/DNHI*QWGGKAV SRGFSKGTQMAKKHMQRCMSMFVIRKM *I*KPKMRVHTFPSSMT*EKNKDNTECFK SDGGYGLLIYYWGI
1092	14993	A	1099	1	484	RRAPFFFFFKRSFPWARAP/LQWAF GLVGNPPPRQIPPLGLHPP/SCNPPK WGYKGPPTT*PKGLIG**KGGGRINLXK IPISRCPDPPAPTQ/KVQIGQGTTPPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PPFFFMVSCSVAQGVQSCDLRSLOAL PPGFEQFSCRGMPKMGSHSPHP
1093	14994	A	1100	144	260	ILLDLSALGHPEPEFNTKGIEVVVLP NTMYIIQPLDQ
1094	14995	A	1101	265	457	DPAAPLLVYTTREI*MYITKRYTAALF IKTKNWK\RPKCPKSGE*INKLNYICTM EYCSAIKNE
1095	14996	A	1102	387	40	RLRADILRLVYNNFLQRLKQRYLFTG POYRFLFLELWLCVVCVVCVVCVRANF *IISRDKVLLCCPV\CFCLNPPCVCVC VCVVCVVRACAIINKLLVETRSCSVAQS GLR
1096	14997	A	1103	465	208	QNMTKTFQDYRPSILMKYIARKQOYRYR Y*RMLHNYQMGTFLGLRGWFI*K/SII IHIN*EKKIMILIESEEFDK*QSL II
1097	14998	A	1104	57	250	MTCSRMQ\RNILKRLRYSEKL*EENSTS RNEITILSEEDSFYNKLEN*MKTVKQK KTKSKTGVYKMAIKQISEFKGKTSNF Y*EQINT*EKKNFKEWSL
1098	14999	A	1105	2	378	YVDFRQCGGTLKGVLKGEFTISNEKAMP GRGSPSSVSKD/L*CONIKTIESKKTCL IOKLIKVKARIEVERESRTNEEINETK/ SQFEKI\NKID*PLARLTKKKKTQV LKSEK\GNITTNHTEKRV
1099	15000	A	1106	291	1	VSIIYVSYNLDSCKGQIRKSCDDQYIFK RLYFFEITFLKFLN*K*VLKKIRDNVLL C/YPGWPQTGPKQSSCLSLPSSNDYRH VPLHLAPINYLW
1100	15001	A	1107	24	397	DIDHVVEFETVYHVQAGLKLSTDDP TALASQAGITGVSHRTPSSGHPNNTF EPPEASLSSSHPLKHSVPV*NGAGL/Y GSSKLLSCVLNGPISLVHSTLRLKGGP QGNISQISLMAPP
1101	15002	A	1108	64	414	AQLTPTQPGRAALHKGHV*RKTAPTCL FMAEKNOAASFFLPPFPCINKR/HFK KKKKKKKKKKKKRTRQKKKGPEKPR KQPGGGLLISKILVVA PPPFFLTREGP PPIFF
1102	15003	A	1109	62	475	FEPLFYLMCLNLLFPQLPRHFFLFLTV DLVNTWGCPLPSSPO*EWLLAAPHRSTP PFLSSGFARROLEPGAGARG/HHTQA LHLFFFFVLRRSL/DSVACAGVQWRGL GSLQPLPQCPV\ILSSPLSLPBLV
1103	15004	A	1110	76	477	EEFKKLYKRENTSINLISDKELTC*IN/ NOTFNIQPLKTKMPTKDNDLKTFTNED TQKYTVIHQ*R*SHMKR*SP*LFT*KMO MSTALRFLYPPITMDRIQIPENIKFWRG CGILHISW*TRKMFHSL*KAFWPF
1104	15005	A	1111	1105	3	KEERSETLARGKLIAGA/VN*KEERSQ INNLTLLHKGKKTNDKPSKR/QE/I*Q IRAEISRIRPRKKKEKNNEFVFLKINKN FKTHSYIKKKREISNTKIINKRGDSTTD ATEMKKITRD*CEQPSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSPPKKKIPGPDNFTGEFYQTFQEL MPALCKIFQ\NVQKPEGDI/PNPFYQVN IYLVPEPDE/QPFFVITLKLVLVYGN/Y

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USPN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						L/K*IKIIEKLTANIILNGEKLSFPL GSGIR*QHLFLPLFITVLEFLRLIISQ EKVIKRMQIGKEKV/KILFTDNRM*WV/ ENP/VNSQNGIKMKFNKVSQYSNTHKS VAFP*TNEQSANKILK
1105	15006	A	1112	37	466	DRAAEFFTENPFLLELISKASKVBEFVSI QRPIVFLCISNQLENEILKIQFH*/PI SVASKNSKYGGINLRKYL*DMHIDNK/P LNKNRGGGLCSWSATSVLPKLIDNFAIS GNVSRFFFFGGIEKLNLPINKYK*VRV AKTVSY
1106	15007	A	1113	33	436	PGLN*CNKNRISTCKRMKLDPLNLAFT KITSKWQIDINIRPVTKILKENRGKGL QH*MMQ*FF*I*PQKQ*TNRTKSDFIK TAQQRKQNERQSVWEKI/FANQISNK ELLSKIKFRLPLDNNKOLT*KWA
1107	15008	A	1114	2	391	PLTHSRMAIKETK/NYKQW*SGGIGN LGNCW*ECKMF*PLWKIVLQFLEKKRN TELP*NPLIFILGTH/YKRNVCQMTE ALFIITK/SWKQPR
1108	15009	A	1115	3	458	IRDPLEAVCPFADKLKHAGRTTTLFRA VRQGPLSL*KLLFPVQLSHVPRGGVYR GSGASISCGGLHPVQAS*LLCLPTQASA MADAP*PPASLPCCSSISDCASSERGS VGMGPSEPGMGYNLLVCRLLRPLEKPSI RVGVSLSFRVHM
1109	15010	A	1116	204	13	PKMKTDSRWILGLFF*FLRQSL/SSVIQ AGVWRNPGSLQPPPPFRKQFSLENGCI PPHGLVVS
1110	15011	A	1117	34	454	IHISVVEFLTSLKYLGTLSQYNKKTNIL IK*MGKRFNAHFT*EGI*IVNKHMRPLP TSSVIREMQTKTVGFRSLVTRAGIKQ TDS/NQAWVRKWSNSTLLCWWKRWLQ PTWN/TANQLLIYKMIWQLHFYAKQDIY VN
1111	15012	A	1118	83	451	CFLKFFLYRELISFELL*Q/VVRPSDAF RRKPPPHVAFFSPDS/FSFLVFPFGKI VFFLGDALKVLIT*KNFFFFGRD*VLL CCPGWSRTPALHSSCLGLSKCNWSTTR P
1112	15013	A	1119	316	441	FFFFFLKTNFNFFAQVGGHNRNLG*LK LPLPGLKQFSCLTL
1113	15014	A	1120	67	312	ROIDOWTRIES*ETDPREYSQILFDKGA NPIQWRK/LFNKWFHWNWSTSTCKQIKKN LDIVLASFTKTS/SHRLRENLYIHI
1114	15015	A	1121	27	490	GTOLHSREKKNSPKN*YEN*ILTCKR MKLDSYFIAYTKINSKWKLDNVSLLGL LAKIK*SPCKIQNY*TSRRK*KGKDLG Q*FLGYDTCKATE*KNK/LNKNDYIKL KNFCIA/NKTNRMKQPTVWEIIANI ISDKVLISICKKTNR
1115	15016	A	1122	490	48	EHTNNKRDTLVDIGKVLVI*TEDQTS N/IPSNQSLIQSKALT/LNSI*AEERGE ATE/EKLEASKGWFMK*KERSHLYNIKV QGEAASADEEATASYQEDLAEIIDENG KQOIFNSDKIALKQKKM/PREKSMHPFK VSKDRLTLREF
1116	15017	A	1123	2	259	IYGQLIFNKGVKTIQ*RNKSVFNRCYWD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						N*YSIWKRM\GLDPYLTPTHTKINSKWIK DLNIRTKTLICSSWRKKKRENFLLKKRKL
1117	15018	A	1124	206	24	CSIFFCYLYFYLYFYLYFYLRQSL/DS VTQAGVQWHYFSSQLPLPPGT/GLF*RT SYSWDF
1118	15019	A	1125	3	351	RGRGFTILWQAOTPDLM/HPPALASQS AGITGVSHCARP/ICLFFKRGQF/NSVAQ ARVQWWDHGSLOQLPLTLR*YYHLS\SW DYRRM/PAMLGFFVFPYAYPGITLLPRWP WISGLNELP
1119	15020	A	1126	2	349	STNHKDIGTLYLLPGA*AGVLGTDLSSL IRALGQPGNLLGNDHTYINIVTAHAFV LIPFVIFITIIIGGLGIWILP
1120	15021	A	1127	362	2	RVSLLHCQGSQTPKELKSSCLSLPKC*D YRCPPHPALVTSITEDSKNFSEYVITLL F*NNIY*TMFIEIP*YHIGALP*DLQ LSTFF*SF*N*FFVCLFRQSHSVAQAG \VQ*CDLGS
1121	15022	A	1128	1	349	IYFLTRSHSVSRAGVQWHSGLSP*FP RFRKRSPPLSLSSWDHRTWG/HMPF/H SSFSSSLPLRSGWGKGGLWS
1122	15023	A	1129	367	24	INCVFYPCGKVTTKPKYTH*RGKFI INIFHGPFKLT/PVCPGEGKNSETLYVPC FLPLSLAIKSRPLGVFLV*KGPLSPPL QGNVGVWVGVPFFPSAFVIFIKKLVLSP YYKN
1123	15024	A	1130	61	299	IPRVNDYCYVREHLSFLFFFRKSLV/ SVTQAGA*WRDLSSLQPLPPGFKQF\SC FNLLKNHCYRDVLLNLTLCLIFKT
1124	15025	A	1131	2	261	FFFFLLVFSFLLRLFLPSFSSPPSVF FFLPSSFL/CLVSRDLTLSTQTKVQWR DLGSLQLPSRPFKRFSCLSLPS*DYGR TPLW
1125	15026	A	1132	2	381	EFYFFF*SSQMESPIAQGVHNRDLG/ SIAPYASWVQVILPQPPPGPFESFSL RFPSTWNRHAPPRLAKKRNKI
1126	15027	A	1133	2	221	PSLLKLKLHRSRCL*SQLLNLRNENR/ CVPAMVTK/GETPPSKKKKNPPPKGP GAQTETPGPGKPKGKIKV
1127	15028	A	1134	331	2	RGPPFPPLKPSGVFRITQFKNLESRGGS ERKQSPPLGPPTRRGSLSPKPPPEKGL TVFFFFFCKGWSGCCPG/WISRTPG LK*SSCLGLPKCWYRHEHPHAPL
1128	15029	A	1135	3	391	AVNTQWNRK*KSLLADVEEV*VWVIEDQ TSHNIPLRQSLVQSKAL/T*RAKPSMKA ERGKEAAKGKLEASRG*FMRFKENN/RL HNIKVQCDTASADVEAAASYS*DAQIT GGCGYTKQOI*FNTDETAFY
1129	15030	A	1136	107	350	TYSIVAIWRRYFFFIIFYFLRWSLAVI QACCCHPGNWHDGSLQPLPPGHPKPSCL SLLSS*GYRCPPPCQA\IFIFLVEMG
1130	15031	A	1137	35	297	TLMHYTRNVKEKNTIISTEAEKAFRIQ HPHM/IKYLTNIKAVNRPASTIILSG* NLKAFPLKSVTQGCPLSPLLFNILEV LSTRP
1131	15032	A	1138	378	1	PFPTKINLKIIDLNIKHKTIKLLEDITG ENLDNLGHVDYDILDPTPKA*AMKKILIN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VALC*NHESFCSENDTVIRMRK*ATDRK KIFAGDMIKDCYSKC/NEKAEVNNMKKN NPYYKWKADLNNLL
1132	15033	A	1139	271	361	KW/YWNPPIHTISQVCL*GPEIYQHVYQG MTKQRCQGNM/WAKDSLENKWC*NEWI FF/C/RI*NLNSYLTTPYRKIK*KWIRDQ NITVTTKLLEENMRFSFAGIGKD
1133	15034	A	1140	28	340	LLYF*YKRGFTMLSLVNSRPF/CDPP TSASHTAGIADSGSHHARLFELEK/EPA FGPAGAKKGNFG*REPSPPFGRIPP/ LPPPGNWD\YGGP*PPKPNFGEF
1134	15035	A	1141	94	128	GSQMPRLVU*MTIRHLATRES\CYSR\ VYFRFIEFLHFDIOSTGOKSHR
1135	15036	A	1142	85	492	VWVGLLLEGSFSKFGNTEFGVLLSSG GFSANRLFFVYFLRQSL/NSVAQAQVQ QWRDLSSLQFLPPGK*VLKQGVCLFV CFETESHIAQAGTQWCDLGSLOPLSE FKRFSCLRNSRLRDIEPSEGNCC
1136	15037	A	1143	372	3	KMNR*PISIKETDFIVKNLPK\FGPDG FTGILY\RHFKKEI IQTVCNLPKQTEKE GMLS\YKASIAQIPKPEKDKQTKATD/ YKPSGIEAKIINRI LANGIQQYI\HDQV RFTPGMGWSNIQI
1137	15038	A	1144	56	482	TMKTLLYWQKNG*VDQWNGIESPEIDPY K\YIQLVFDRAKTCNV/RKDSLNVKWC TYAKKKKTLNLFFTPTKITISKTYLKNW N/SVNFNLNPLGKTLGDLGFPDRDFKFLN TPKAKSLERH/MDTLNFFKGKICS*KNM VKKNKKT
1138	15039	A	1145	190	482	RQGLALS PRLECSGVIIAYRSLRLVGS DPPTLASQIAGITGIRHCPWPKTLFLAS VIMPAHNS*PSLSPVPSP\SLPSPPLLA SQSRSSQ
1139	15040	A	1146	138	485	IFFPSV\TIFLLALLFFS*MYLIFVKS SLSYSVYQF/SFLCFWSPISDPKSRF SLLSPVCFVFPFNNVLLCHPGWSAVV *S*LTAVSNS\LLKQSS
1140	15041	A	1147	101	426	GDWKKFYIKHSEKSPFLFEKKKGVL EYSSFDI**AIKVIVHISRRK\KNOL ANLTDAAKALNKI*HPFMKTTQQFSNR SPLHLRKGIVKPP*ANMIIEKQIIF
1141	15042	A	1148	458	15	VFVCLTKICKHRKGTAKKRYNFMGLPLV MRSVVDQNGTM*KMTIYAPNIGAPKYIE QILMGANREVNSNTILLGDPSIPLSTL/ DKELPELNF*NTKDLTDIYRTHFPMMA KYTYFAGTHGTFSCMCPVGFDIRVLVE FRRTSYGLDW
1142	15043	A	1149	1	507	KGPPAPPVYKKKFOGGPKKFFP*SHFP KRPRGEDP/YKPRNLKPPWAKKKNPPFP KKKRGKGPKNPPPWKVKPEKSF*PSPK KTKIWPPPPPGGQKKKKPPPPKKKKK KSVSSSPKNI/YRSLFCNLKKSFFT*F *NLMP/TKLPV*EFPPPPNSE*SAF
1143	15044	A	1150	436	32	NLCMYVMYLIYVRTYVCYISYISYIL IDLSLYHHYLSICMCSVSIYPIYLSLY LCISLIYHLFNLCIYISYIYLIYLS/YVC M/SSI*SMYVCYIYIYVCFISISLYLY IYLSIITIYIYLYLCMYCLFYLSIEF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to last amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1144	15045	A	1151	3	657	QDCKIQNEHKIQNTLFLYTRNAHRIKIF HLHSKKILAVNLTKHV*NFYAENYTTLM KEKI*IERNKDLHRKQ\NLNPCIWIVKL NIVKIPVI\PHR*RSLTPIPIIPAK\FF GDKEKILKFIWKGKGR*LRP*KIRIK GGLNLPN\LRLLTVTVTKIV*YWKERD RYLNQ\WNKIENS/EKLPKRYVQLISF VFDTSG
1145	15046	A	1152	430	438	TFWVKKFFLLNLPK*INPGFKKKKKNRG G*KRP/SGSOVLKLRGKIALTPGKGG IRDCFPPPPPLRKKKKPIRP*KKKKK KRKRDPFPGNHYSYSYRHS CYFTLLHL TLQIFFTSRSPVMSCRINL
1146	15047	A	1153	104	478	ELLLEGGSPCLRAESKAGPAGRLVPTLLS WRVQSPGVLCWABEECEEPSTGEDAPS LAIRRTQLKFIIRNHLPSLSMAIPQTNN DNVRYKKK*CWGGCGEIG/T/LHCWAE /CKLTFP
1147	15048	A	1154	171	476	NSSDYVYVFLRQSTFTLVQAGVQWHDLS LQVTSDDPDLR*FARLSLPKCNDVYRE P/RMSDSNYFLK*VPVN*KARA*LLRIF SSCOAG/ASAGTSLVS
1148	15049	A	1155	3	562	PDYQVARRROAPADRCQPGPAATICPR* PKARSSMMNRSNPTVTRTAGP*PSWKIG AASKSQTDGDRKELIPNRTPHN*VST AAIK*QVRPYLTQKVPAG*TPCQHQLQ GVRPLCRGPP\RPFGSPAVIDNRQAKLK TPTQ/HPADPPEQKRPPARPFVGRHAEV KQPGPPFPAGPRAPSTDGL
1149	15050	A	1156	67	417	TLSCETPGQHGHEAPS/PTKNA*IALPL SWARLYFPAPARFTARGGPVFTSKRVP SPPNRRGWRPDP\QFCHAWNPSKFLAD KIPPT/GLPPNKEPSKENVNPGLCPCL L
1150	15051	A	1157	446	87	PDCINVISCFLTRIYHVFFFL*ROGLTK LPLRVMS*AAQALPP/SASQSAIGITGV SLHTRPIMYFSSYYIIFGDTVLP\ETQS HPAAQAGVG*CNLGLSQPPPGFKRFS LGLPSRMA
1151	15052	A	1158	1	938	FFFLFATYLFNKGK\LTGRKQSD* KHLKQYVYIKKILTSXU/V/KKCPISL ATREMQILTGIIKCC*RCESGIFFTW *ARALAOILWKNV*QHILKLSMCITYNP TILFLGISNRKVY/CCPK/DPCSRMSR AAQFVI
1152	15053	A	1159	370	3	APKAAEAGAAVMTGGQVNLNSWVVLGG VTTT/CPTTFIMPNDTV\RGDILELTR PLGAQVAMAVHQLDIEPK*KKH/LV VTEEDVELMYOKALNMVQNNKKAAGIM YTFNAHAIDEFHR
1153	15054	A	1160	55	471	SPPPGLFKKIFFWFLSFYVWF*PQRFCE LFAPFKQESNPLKVVPPFALQNRKSG CSPM/SARQES*PLFPKNLETPFPFGSK FLKFFFFFF*DGUSLGHPGNSAI/IDSL QPLPPGFKQ/SLCLSLPAS
1154	15055	A	1161	3	467	GVTNQOIFPVDKTAFY*KPSRTFMARE KSMGGFKPSK/DRAGDFKLRSMLYHSE NPRALKNYPKSTLPVL\KNKANMKHCL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QPPVETVCSGKKIPFKILLVIDNVPCHP CALMEWYEIEINVNTATNTTIL*P/VT SGVIS
1155	15056	A	1162	216	464	SSSEGPGSPGELPYGAQEFVMKAPGGTIV IR*T*FFETESHVAEAGVQWCDLSLLQ LPPLRFNQFCLSLP\SWDYRPERHPAN
1156	15057	A	1163	29	433	AVEFGGSDSCSPQHPLNFPFGSPQHSFFP LIGICT/REE*GWGGGLPVPCPPALFYP STPSWGGICVCYGRGGVAPFP*HPPLT* LGGGSTPTPSALPAPGAPRHPGHPLMLVQ TLFPWGPHTPARKPYINKVLSCVDF
1157	15058	A	1164	486	11	STCLGLPKCWDYRREPRFRLRCRPFPLN ILLFLKFTLSEINPTTFAFF*LVFAWYI FFSLFSF*P/DLEHYI*SGICVDTM*VG SSCFNFPT/WSISSF*LVCLDHLVFFLF FFFLRQSL/DSVAQAGVQGDLSLQPP PPWFRKFSCLSRIPAHFEMSA
1158	15059	A	1165	467	131	NRSLEWAKMYKTYDEIKLVTNLPT/RKS PGLCKITAKFYHIYKDGVLVLLNLQEI QVGFPHNS*YQ\IILIPKYSegTTKKGN CRDIFLVNIETKILHEIRAI*VHKQIRT LE
1159	15060	A	1166	455	32	EEGVLYAKRGCKSGLLHQTVNVQV/N LEKFLKEIKSDTPVNI*MIK*NNLTAD KEVA*IQDQTSNNIPLTQSLIQSRALT LFNSMKTERGEEGEEKFEASRG*FMGF KEKSHPHKHSASKAASADVEAVASYLN S
1160	15061	A	1167	26	418	KINDYVKQTNL*ITGIPERGGEKVVNLE NIFEAIQV/ESVPSIFKEVDQEQEIOR ASSSSSS
1161	15062	A	1168	64	313	KWCKGNSYISKDLRELKYLGV/OLK*VQ /DL*SENYQILLKEIKEDLNKWDIPCS *IRRLNKKMVIFPSKLIYRFNAIPKILA A
1162	15063	A	1169	464	36	QQAEEAESL\DPGGRGCSLEKSCHTPA WATEQSINK*SIINGSIK*SKKL/CWEN TLVKHIFHKRLTSRIYKEL\QQLNKKTN NSL*K*EKDVNRYFIKKIYEDI*MANEN IL\IKLVIREIQINLEKLSWFCCECC FVLFVF
1163	15064	A	1170	290	487	GSLPHHTPKR*PFLE/CVFETGSRSVT* AGVQWVNHGSLQP*PPGLKRSSHLSLPV LIFLFSVEMGV
1164	15065	A	1171	2	413	GKVFIF*FSTLH/GCNMK*SRSL*ALR FIFLFTARGLTGVLVLANSSHLITLHDYI YMGTHFHYVLYIGAEFATIGGFIH*LPL FSGYTLDDQTYSKIHYITILIDINLTFFP MHSLGLSGRPRRY*DYPDATYTRYLS
1165	15066	A	1172	381	2	PPKLQKNFFFSSTGKFPFLGGGRASFPP KKGFFSQIPRRFFFLPKKKKIYFCPP CFGPPPTFFLRAPPFFFLLLFCPSL VGVKFFEL/YFLFIFRDTV*LCYPGWS AVGOSMLTALTRP
1166	15067	A	1173	9	405	NLDKKGKRNSTPOSWFOANPMTSFTSKK KKKKKKKKGGGALKKKPWGAQKPKGK KKNFLLKGG\EKKTPRGILKKKPFPGG KKGPNPPKKKPLREKKKF*GEKGEKPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
1167	15068	A	1174	410	0	*KFFKKKKFFPPSKKTP PSYPPPTRGCCSPSPQIFLPPBLLGV FFPSPPLKIFFPPRGFKFPGGVVFFSF PKKVVFFKNPRSVYKNPKKEK*SLQP PG*VWAPPGIFKR/PPPPFFYIFS
1168	15069	A	1176	319	3	KEARSVFRVEGRG*KNFSASGPPGGGNP GGGRPGRGNFVLKKGCGPPPGKG/SP FFDF/GGPPPPPPSGGGSGVNPFFPF FFPFEMESRSVSQSGVPDADAWAD
1169	15070	A	1177	385	1	SASGFLPKCDYRHEPTRPASVSVTVTS SRLSGA*ARSGKTLVFWAQMVFK/RIP LTKYSDHSREPSLLQCMQSTPSKAEFT VARADKRLCTAKSSTAKSIAQIKCQND AGRSQESLHVSGRV
1170	15071	A	1178	147	808	KLKEKKLLEENAGINLYDLRLSGFLD MTPKAKQKKENLXMDVTRMKNCSASKD TITTFYNVRSDDGLV/SKYKLEAGSITE RQPNF*KDLNKFDFK/EQAKST*KTTE RLFIREMKTITT/ME/VHPLSTRMAKI* KDSNR/RLCRKGTGLIHCW*GTAPANLL KNCQPLPFF*GTWVQPLKRLNLELDDP AIPPLVICPKEMKT/C/CYITECTQMFT AA*III
1171	15072	A	1179	1	398	SRSRHCTPAWVSVTLVLKREKKEKKEE KKRCPCYIVSHQSL*KPAWQL/RNVK/ LELPYDPAI/PLLGKCLKET*KYAYTKT CM*MFIALFIAKKYKQLKRLSTDEWIN KMWYIHA
1172	15073	A	1180	3	389	GYDRVIFNP*PLTGA/LRALLLTCGLAM *FYLQSMWVILGLLTDLTLYHRWSDV ARKSTYQGHHSPPAQKGLRYGIMLYMTS EVLGLGLF*AFYHS/SLCPTPOLGGHW APTGMTPLDFVEVPLNT
1173	15074	A	1181	354	2	ANSDACTLDGHRALPLQLPPCGYSISF AAQSTVPMPLLLIPPHCNRTPSLWHY SPASNTNPSFY*TAPEPPPIPRNPN FS*KFYIYVWYTSLLTCSQPPVSSPNF TOPSVL
1174	15075	A	1182	3	384	GANVSG/DL/KLPVLIIYSSNPR/ALK NYARSILPMLCKQEKKEKKK/AWMTAH LFTAWFT*YFKSIGET/CAKEKIPFKIL VLIDSACHPRLMNECKEINVFVPVN *HSI/LFCMQMDOGALETYSKS
1175	15076	A	1183	1	410	PPLP*KFFSPGGVGS*KGRFVWBPB*UG VLPSPP/IIFFTPGNMGCFSPSP*KF FFSPKGFIFCGGVGPFPPPPKRFFSKI PDLVFFSPDFKKKIFFPDPVNGPPRV FFKRPPSIFFF
1176	15077	A	1184	406	62	PPIINMLCSLAPFFSPPLRLGVLPFFP LQNFFF*GVYFWGGGPHF/SPPPKKG FFPKFPWVFNPPPLRKK/YHNPFGPK FGPRVFFKAPP
1177	15078	A	1185	337	383	RSYISFQK*VKDLNKHFSKDDTQMAN/R HIKRYSTLVIREMKIKPMTRYHFTPTRM AVPF
1178	15079	A	1186	3	471	LAPSDK*ENRLPGNRPL*EVRSPSARQF PHLRSEELRPAATPSGK*GASPPSSHA VREGGGQPPPGQPPRPGGEGRLCPAAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1179	15080	A	1187	2	406	TGG*GAPLF/EPFPPGLGG FLVETEFVCYVGOAGLELLTSRDPPASAS KGAGMTGVSHQVQVQ**S*LWT*/PSSV EAGTSPGLSFLSSSWALSQAQGLCLAVPS /SGSRGLLVGALLLWTKPSQPLSPVPAS QRLSSLSLMPPLPQPOHLLHTSTIET
1180	15081	A	1188	160	459	NFMTIDMLCSAVVTHFCSSGDLQFL*KL FKSQ*ENNLINKWADLNSFTIFS YG*K LAHEKMLNIIIRIYFTAINS*YLTITTV KVKKETKCK*GCTATGNLIHCCKNV*P LRNTAWQVHKILANLYLPHAPILSDM NSRE*KN/CHAKMCWIFI
1181	15082	A	1189	232	2	KAPFFFFFFFFFFFFFEC*SGSHSVSWA GI*W/PGV*WHHGSLOQPSRLK*SSC LSLSSWDYRVVPHLANLKK
1182	15083	A	1190	2	402	PRVRASGSPSPFPFPG/L/SHTSFSPQ* VFSWSPY*TPCLSLATLASVLSL*QRS PRTLFTITNKC/DF/PASHSSCRIPAGL* ALGRQGLFSCFFCFETESHFAQAEVQ WYNLSAQSPSSPEFK*FS/CLSLPSS
1183	15084	A	1191	19	390	WCVPAVPATWAEPRFRSR/RSKPLTRGRQ SKLSLY/NKKKKKKKKKKKKKTGGGP *KKLLGGPKYKGGKKKKFFFKGKKKS LGGILKKKTFFWGGKKNPFPKKNKALK GKKKFLGGRGGNPP
1184	15085	A	1192	485	112	QRFDPR/SAEAAITVFLTQATASITLLI AILFNNILSGQ*TIITNTNOYSSLIIIM AIAIKLGIAPFHF*VPEVTQGTPLTSGL LLLT*OKLAPISITVQISPSLNV
1185	15086	A	1193	55	385	THAFADAWADAWGLFRGILTENFPNLQK YINIQVGG*RTSSRPNTKTNRDLLII ILPKVKDKLSKKKKKN/AENKKILKYRG GPP**KPGGAQFVGGGRKSPFFFGG
1186	15087	A	1194	408	3	CCSA/LLGASQLG/SRGSGVRDPLEEA VCPFSDQLHAERTTALLKAVRGSHLSL FRLLLSF/VCLCPAPRGACRGQASLS CGLHP/RASRLCLRKAWMASVPP ASLPDCSLSDCCVSNQ*DSGRV
1187	15088	A	1195	5	371	LFSTNHGDFPLYLFP*AGVLGTDL LLTRAEGLQPGNLGNDHMYNGLVTAHA FVIIFPFIIFIIIGGPGN*LVPLIIGAP DVAIPRISNISF*LLPSSLILLACAIT EAGAGTG*TVY
1188	15089	A	1196	76	404	PTPLETHDQSKVSRKYNIKQVAGFLY MLSTRITGI*\IKSTSFPPASPKVKYLT INLTKCVO/DLWKEKKL/NEIKEDQNK* /NVFPSWIKGPNIVN
1189	15090	A	1197	50	334	ILHMVSIPTISITV*HLLPAG*AGTHIG* LPPA*FWVMG/RDRVLLCHPGNAVQV S*LVVASNSW/VK*SSHGLSKY*D*RH EPSYPASGKTLN
1190	15091	A	1198	250	1	OYVLVSNT*SIIDFLQLFKQCIPTVGF SK*CIQGFIFKN*LF*/FCLFESESC SVAQAGVQWQDLS*QPLPVFKQFS
1191	15092	A	1199	2	402	TDRHRTWLI*FVFLLEMGFHHVRAGLG LLTSSDPPRPKLNFL*R*GHAVM/CPG WPHE/TCGLPKCWDRCE/HTAPKPHR FLFFFFFFSEKNFIPVVRGGG/WKLN*

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1192	15093	A	1200	50	437	MEFPFPG*KGFFCGPFPKYWN*KAP STLYLERKEQISLSVIVSSPLPSTSTG PTAAQSSISGSPSLPFPHPHAGDAPAG LG/YGGGSPGPPWGPS/SGPSPR*ALVC PTDPSGAARGGRGG\SRGSCCAPAGPAG LGDHRPGGMSEGPAAPPKSS
1193	15094	A	1201	86	313	PPFPGGYPHPSFXXXXXXXKSSLL PGKCGPNPKVGLPFPXXXXVSPKXXXX XXXXX*NPPHSPPRAPGPP
1194	15095	A	1202	105	485	VQQTMMARIYVCNKPARSTPFTKQILL DVLK/YIDTQTIILRDNFTP/LNSVMSW RQKTNKNDLNDLMLQLDLIDISRLH VSTR/YIFPSSLHEITYSKSGHMLSHKAC HNNP*KSEILLILILHHC
1195	15096	A	1203	1	476	PHGFPFPFPQDPR*GGEFSTRKGFPPQ PGGFPQAWPRAGQPPGKT/EPVFPFP KHP*RRNPYPKFGSPPLGKIHGSGPG SGQPR/PFRWGKRAQPTFWAHPPIFP FF*GULLCHPDWGTVARSR/PPQPPPC
1196	15097	A	1204	1	269	VVEFTYNLGIK/WSKDKMRSFTKEDLM MADEHPRRC*HHLTPRPTAQVKLELEP NE/WQCGGAGPATPCWGDAAFPVQLLQ IGRRFLKK
1197	15098	A	1205	459	42	KLKPMILYHSENPRAFODYAKSNLSVLY K*KNEAGLRAHLFTAGFTENFKPAVETY CSE*EISLQI*LLI/GHPR/SIMEMYKE MNVVENPANTISILQSMQGVALTVEYH YISNILEAIDNTENFLIDLKCANAWVG PG
1198	15099	A	1206	408	1	EMKTLTMSGPMPTKEVSELED/DIN/ EMHRKLQCREKR/IKRN/EINVQEL*YH YKRCNHVMRMPEKEQRKEEIFKVMAR NFPNLATNNSKVKEAQRTPERIKTIYI YIYIS*LQAKKEKESILKETCQKTSKPK
1199	15100	A	1207	7	383	LDIGCFWNEDKSYSSYFLSATGLKLYF SFSCLIHCFVLVCVVRHAK*CI*SRAS* CVCVHK*CI*SSAS*CVCVARTNGI*/ CQCFVLVCVCAQ/CI*SSAS*CVCVCTS GI*/CQCFVLVCVVCV
1200	15101	A	1208	405	214	ABAGRSLCPGGGCGNEL*SPFPCSAWVT \SETLSQKQNPHHHKKTKQVGRGSSYL PLWEVR
1201	15102	A	1209	384	2	GVTHH/ARARFFC/LLDTGFESVFOAAV Q*ANHGSLQPPQGLKPSCLSLPSSR DNK
1202	15103	A	1210	403	2	VPSIQNGKSLTYFYDFPFGKLFKTLKLL DASFVNVCVNVEFRTFALSTQSLCLL SLFLIF*TINCNCFLRQN/LRSVAQA GVQWRDVGLLQPLPEPFQPC
1203	15104	A	1211	156	405	ESKQMLIQCKSMLYC*RI*TV/CLVC VCVCVCVCVCLTCGTRVCIVLFIIVL NCK/PLCEPCC*CNQGWAFWLLPVIST RN
1204	15105	A	1212	70	408	KAFSLLPQGVSPGFLCNFRPRNFGGGP KKKPPPPQRVVTQGFNPPPPFFFLWG G*GQD/PPPVAQG*MDPPPRPFK/GRGP RHEPPPPAF
1205	15106	A	1213	410	3	KKSMFGFKSKDRMTLLLEAQAAGDF\N

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						LKPVFI\YHSENPRLKNYAYT/PVLY KWSNKAWMIANLFIA*FIKYFKPTVETC YSDKKIPFKILLIENAPDHLRALMEMY KEITHAVFMPANTTISILQPMDOGVILT
1206	15107	A	1214	3	340	KIRVEVNNMYNRKLEETIKKLSLFFEN INKIDQFLPRLRKTRQKMQINKIRNEQG GISINIMEIKYSYKEML*AIICKKLNHL HEMNKL/EHRVPLKLTQVEIENLNITYIK K
1207	15108	A	1215	1	57	EGLKTONVNETKS*CFEKIKIDKFLARQ NFKRKRFKFRD*KGDIIMADTEI*GII RAYV*QL*GNYLENLEMEKLTVTNLP KLNH/DLENLKKPVTT/REFKSVIKSLP LKKSPLHDSFTAQFYOTFEE*VSVLKR
1208	15109	A	1216	350	1	QSSFFSYTNPFLHLSFLFCFDPFLFYA SVLATNSLPLFPQISRYVPA*PPERERE RERENVL/CCLGNSAVMQS*LTPALNY W\VRQSSLSLQAS*SYRCGGPPHPANIF HFIFCR
1209	15110	A	1217	139	358	KNFTFFVVEAKRLFPVQAGGQGNLSFK FPAPP/NLRG*SASSPSSGDYRTPPCP ANFFFPKKNRISPWGGGW
1210	15111	A	1218	361	50	WGDHGLKQPPLRSKNPPPLASLVGTG Q*LG/HPVAPFFIGLIFFFFLRRSL/D SIAQAGAQCWDLSSLAQAPPFRFTPLSCL SLKCKGNPVFVITWMNLEDIMLS
1211	15112	A	1219	1	361	LKQHVSNVEKTAFFWKQTQSTFFVARE*K GEILLSNRGECLQSQFGQPLLIGANAA GDFKVK/PMLLDHSEN/PKALKNYTTS
1212	15113	A	1220	292	362	HIPVVPATQAEVGGSLPRKSRP*PPR LK*SSHLSLNSWDYRNVLP/RLANFCI FLCVPR\FKLLGNSHQNASVSQSARITG VSHHAWPILKCLKLVCLFEMGSHYVAR AGLK/PPGLK*SSRLSLQNCWESRREPP HPDITI
1213	15114	A	1221	372	3	KIFFLLPFRPKGDFPPTLLIN*RHGFSP PHVFKPPLNLLIGALKKKFFLS/LPY VKFFPKRALPFF/TFFFRDRVSLCWS *PPGLKQYTHGLPKHNDYRHESACLAN NHNNNTNFFFEFE
1214	15115	A	1222	3	291	RSQDQDCPGQHSETLSLLSLTFVNLNLSL CNL*TLSLIPVKIQKLANHGGVRL*SQL /LRLRLQENHNLNQC/DCIPAWATEKDS VSKKKKKKKGGF
1215	15116	A	1223	379	19	HMOILTIMRYTPIRMAKMKKIGYTK/C W*GCAATGYI\WECKMVQSL/WONTWAD S*KLNTHLSYDIAIQFL/GFYSKKIKAY IHTKPTCT*MFTATLIIKSQI/MKQVKCL STDKWKQNRGIYI
1216	15117	A	1224	387	40	KKTLSTP\PEKHPTPLFLHFFPKGKGGA PPSFKPPPKHPPEPKGISPPFP*IPPP PIYPPPPPAKPPDPFFL*SPPPPPPPFP PPPP*TPPPFFSPPLFFFFFFFFFFLLLR LLV
1217	15118	A	1225	21	477	IYSLRITVRLQKPLRDPVRVPRVRKEN YSSV/SFINIDRNVLNKL/SSQIQQYI KKLIRHE*FWF/IPGIGQWFNLKSVIV TVVWKQKWKHHTISQVTEKAFDKIHY

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						LALILTKKKKKKRALPOSFIPGDLFKK PNGGFPGLKMMGRAPGE
1218	15119	A	1226	1	398	ERINHTLFFLAEAKRLPTGISGRGRPA IPHNTFQAPDHAHLPAALAAQHRAGGQ QAPPPG\SSPSSPYDEVKREGDVTASH GLRNGWGSP*ATSLVLNNLMYMTAKYG DEVPGPEMENAWNALANNEKW
1219	15120	A	1227	3	238	DAWVAGHDG/RTP*SOLLKKRWEHRFS SDGRVSDP*SCLCTLAWVAE*DSSSKKK KGGPFKGT*FNSRGGGRNYFFYA
1220	15121	A	1228	207	2	NRVSPCCPVQWHDHSSLG/PRTPLGKGP \SASAF*VAGTTGVHHHAQLIFHFFFF *DRVIQAGVQWRNL
1221	15122	A	1229	15	413	RKSVNVIHHSLEILKKKNYMIISIDTKE SFDKI*YPPMTKLSN*DSLNLNNIY/ AKP/VANTILHSKRLNAFPIKQGLQGC \PPFLFNIILEVLASTKGRKEIKSLQIR VEEI/KPLSLFADNM/IVYIENPKES
1222	15123	A	1230	363	1	AADPFACRPVSPHPFLYLVTSSQSLTS VSPKKQPPSAGMQLGVGDSLSGWGWRGT KKTRLF*FFKTRSLSAAQTRQWCEHRSQ P*PGLIKRSSHLSLSPS*NHRHMPHL AN\LCLEV
1223	15124	A	1231	3	402	QANSTCFSDFFSGVQAGLEPLTFGDDP ASASPRCRDYRC\QPHQAQLLTF*ISI LILV/CIS*MKDYFICTYFFNYS*QII FYRRASDFFFLRGLRGLSPHMDHGSLO PHPPRLN\HPPTSAGVGTGT
1224	15125	A	1232	3	396	FLSQHGFLFFPAGIDKLLTKFWKDN* NNYKED*RGVITLP/QYKAYSATVVIK MVHMQSDKHVDQWNRPRNPNYMSQ *FPL*YVSQRNENLPLEKNPMNVHNGF ICNSRKQSRYPSTGEWVKL
1225	15126	A	1233	3	395	LPKCDWYRR*PFPBALF/LFF*KHKPFL KMQVK/WRKH*TENRLVMYFSEKGD*L KDQKLYLDNAFQIFFTFYVMVRSIL FKPNIR*LTLSSVKMAVFLVETGF/THL ARMVLIS*LRDLPTSASONAGI
1226	15127	A	1234	416	2	KIDKILITFIWCKRPLLAKIVLKKKNK I*RLPLPSFKTYGKMV/TK/TKWGWPK NRPIKGTGF*VQKKKTPTHYGLVDFDSG ARTITN/WY*DN*IST*RMKLDLYLTI YKINSKI*LDLNVRAKTMTFLEENIWI LD
1227	15128	A	1235	384	22	FPOET*NAIPVNTQMVWRKONSHPANIEK VL/VVVEGOTSNNIPLSQSLTQSKALT LNSMWKA/E/AGDKAAEKMETCRGWM RFRERRHVINIKV*GEARSCGSLAAGS PLKHLLHNTLIC
1228	15129	A	1236	379	2	SPYTKTHSKCLKGLNVLRTFKPLEENP G/VMVDPDLPQKKFTS*APKAWATKTKI IQWGYIGLK/AFCPAKEAIPRVKTPWSE SEGIPAGHAFYEGFIFQIFKGLQPFHSH KKDKLILKDLLLSADIS
1229	15130	A	1237	1	407	YRVQAGLKLTLT*SAHLGLPKDCDCGR EPPCLTI*AL*SVFSLVLPVLKILINF F\CRDGGQTMPLRLVSNWPMQIC/LW PPKVLGLQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
1230	15131	A	1238	3	380	ELSQRTCCMDIMSYYKRAIVITMAWY*FKDKQRVQQNEVESPKTLLLYLRLLWYYEGDTTDKG*TF\NKWYWDSWI/ST/CKNM*FDYHFTQCICKIN/SQWM
1231	15132	A	1239	1	396	FADDMIVYLENLKDDSSKKLLELVNQPSKVSQYKSKV/NVHKSVALLYANSNQAE/QIKNPTPTFTIAAKQK/YKQKNLGIY*TKVKDLYKENYKTSLEIIDDANKWKYIPCWSWGRIDIVKMTLPAI*RFSS
1232	15133	A	1240	392	58	SFSLRLARLVNSK/PSRVLPSSASQSAEIIQVSHYAWPSKLSF*LTIDQTHLSNMLFIYVFFERRSCSVTQAGGQYGHSSLOP*TPGLKQSSCFGLPKCWDYRLALPRLM
1233	15134	A	1241	500	204	LSLSLFS*DGVLICLGWSSTPGLKRFSCLSLRSSWDYRCVPSSQTNF/VFLVEMFGHHVGQAGLELLTSSDNARLGLPKCWDRVRVPPRPAFFLFFKG
1234	15135	A	1242	2	397	NFMINNLKKKALCPVVFTGEPYLPFKEETIP*VIRISLSL/IFSIFQKIETEGILPNSFYEGCIIILSKPKYDI*ENYRLTSVMHIDARFLDSILANPIQCCIKVIHCSHVAFV/SGTDWFWNIQKSM
1235	15136	A	1243	12	362	AGPYHVQDGLKLLTSSDDPPASASQSAQIKA*ATVPGLSPLNFCVRFMESWSWKRP*RTS/VCSALAKCDNRNASQVVDKLPSPFT/RM*SPCLHPAVSAFCGSASVLPGIIVTTSV
1236	15137	A	1244	183	383	KQAGRGGSCL*/LPRCWDYRRELLHLAFMPG*LKK/FECKDGLTMNPRLVNFWPPIVLLPRPPKVLG
1237	15138	A	1245	410	2	PSRDRVSSCWFGWS/PNS*PQSQALAKCWDYRCEPLHPAFC*MNFLKVSC*HGTS/DSKY/CQHVSPKNKDILSNYNIIIIPKKFNIL*YIWFLDFFFFETECSCCW*HLSGLGPPPPGFK*FSCPSLPSSWVRHW
1238	15139	A	1246	440	46	KTEGANENKSTPYQ/SLWADAKAVPRRKFRALNAYTRK*ERAQCNLSSTLKRKKEONKLKADRR/QIMQI*KLKGVENKQTKTIQQIH*TKSWFEFKISKITYEL*QA*RKKEGETTITNVNKNRYSGRVG
1239	15140	A	1247	266	340	RKCWPGVAHTCNLXITLGGQGGRT
1240	15141	A	1248	3	391	DAMADANGSRKRAVLFPPFWGLFGGGLKTGFYFIPQVERGLNFD*WNPPFPGLRGSSPPT/LPKQWEPGGGPAPSPNFWPFPEKRGFPQVTQAGFKLWN*GDPPAGPSKGVGITGGTFSPHPLFLKKR
1241	15142	A	1249	3	323	MHHHA*LVLVFFCGDKVSLCCPS*STPDLKRLSHHGLPKHWDYRC/RATTPGFFSLFFFFFNPPPELLPWAPPSYSLKQNKIFLKRFLLEPLAPPKGLPLKRAKRI
1242	15143	A	1250	3	405	QPDSSYPQGRLSAPPECEGGFWLILPHACAPSQICVGPHGASILSYQERKQKVLSCGEHCKLSSPVGLVGQSCFWQQDPADVQWVPPFRRTQTGTVAHACNPSTLGG*GRRITS/RPGVRDQPEQH
1243	15144	A	1251	407	2	PFLKTKTKELF*GPAIPALGVSPFFEFFFLPYKRKEIKGIRTPMRIAALFTIAKILNQPKYPSVDI*LHKRHTSNTLLSRMK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						H*WIKKT*/HTDMMEYYSATIEKNGILSF AATGMSPKDIMLSEICQAQKNRY
1244	15145	A	1252	1	253	VADVRESLDPGD*GCSELRLCHCTPAWA T\SRRTSQOQLKKQENNTT*KTYGIQLM NCQIANYSCKLLYFRKMSNLQSNLKKKK K
1245	15146	A	1253	3	372	KKKAQKSGTIVLPCNPSSYSGG*VGENA\ WARSQPLIS*KQO*QQNQOQTTSKTD PYIYG/YLIHDRGGK\NTQGWDRLLNRW GWGIWLTQRKIKLELYLTPYTRTNSTW IKDLNVAGCGGSC
1246	15147	A	1254	2	410	KNLTPIVGLKAATN*ESIPPQT/SRKKK KKKKKKKKRGALKKKFKGGGGGKQNF FKGGKKKKLGGGVKKRGGGKPGGKKK RFGKKSFFSRGGKKKKNRSSSSSSSSSS SSSS
1247	15148	A	1255	61	487	GRPGPTHAFVVIDSFFMGNEARFINHSC DPCNCEMRWSVNGVYRIGLYALKDMPAG TELTVDNPHSPFNVEKQQLCKQGFCKR GLIGKSGRVNGLTSSKNSQPMATHKKS GRSY/RE*KKNKKRGRGRGQSGSSFG MOG
1248	15149	A	1256	118	5	MFIAELFTIA/RWK*PKCLTDEWINK M*YSHTM*HY
1249	15150	A	1257	390	1	TQKNTPTPKPKPTSQQHQKNEPTPFPG FFFSPPGK\GGFFPSPLWVPPGFFPPP VFKTRPPEFIFGAP*KKFFSPPRSLLNF FFLRGPSPFFFFFFFFFF*VGKEGSSPSH ENPLFVPTGEG
1250	15151	A	1258	378	3	GAFFFFFPKPKGFFFTFFFPFGPGFFF SPPPFIPPPQIFFFGPKKKKFLPPPPQ KIFFFLRPPPLFFFTFFFTFFFTFFFTF FFFL\DLL*NVLSGTSAPKKNQELLGMV AYACNPSTLGGGG
1251	15152	A	1259	462	287	RDG\FHHVGGDGLHLITS*STRLSLPEC WDYRCDLPCPAIPAVTLVQIYRPLGLE SKA
1252	15153	A	1260	446	34	NVRAET/IKTLEVNTGVNLHDLIS*/GKA FLDARPKAQVAKEKSRQPSLHRLR/PC ASKDPIKEVKRQPT/WEKINHVSCKGL EFKIKHELLEKLSNNPI*KWDKDLNGHF SK/ELQIASKHMRRCSASLVTRKCNIEIV DPD
1253	15154	A	1261	2	383	GSQRKWFLEMESTPGDNAIDIVEVITKG FMYIMNLVIXAVAGFERIDSNFERSSSV SKILSNSIACVRI*IFCKKSQLMQ/QTS LMFYFKKLPPQPPSAATTLISQQLVTL RQDSPPAKRL*FTDGL
1254	15155	A	1262	476	50	FFFFFSDTSGSHVV*AVQVHHDHSLQF *PPGP\SDPPTKSSSTREFF
1255	15156	A	1263	143	472	TGAVPTRPSNN/RFPAMIFF*NAQGLIF AEFLASQRAILWEFFEXAYHESVLKSA KGLAEKCPGKLHQRVLVQYDNLALHFSH QTRTTKSTROFR
1256	15157	A	1264	179	489	YIFPFLSLFFFLWPRPEYRGATIVHCSL NLPGSSDPTASASSVAGTKPH*YIFPFL SLF/CFSVAQA*VQGGNHSSLOPQPPGL K\YPTASASSVAGTKPHPLIFFFF*KKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						FLVCFVQAGGQGHDFG*L*PPPPSLKQGGGLTLRIGDYRGPP
1257	15158	A	1265	1	536	FRGCGWSVRRAPGTASCYLALAGPPFGQCPFAAISCPSPLPWGS*TE/PYVPRRPGDPSAAP/PSW*VPRPGVPRNVPGRGRVGDCCQQAQDIQAAASLWADTAPDSFGSASVRAALPACVPEISGS/SGLPFGAALP*VAA/RPTTGRHVDTHPRQISFCGQGEGRIRAFPTLYLEVYPGP
1258	15159	A	1266	403	2	TSLLHPRGYMKLLRGGFISAPCGMYRLPRGSSLHPRGYMKLLKTGVHRCTPAVHAPSQTGVHLCTPKWEHTPS*RFISAPLGAASHVT/GSLSIQHTIYIFVFCLLRQGL/NSVTQAGVQWNCGLSLQPKLEQAQVILTK
1259	15160	A	1267	2	401	FVLNPGGRSCSEPRSLHCTPAWATRAYLQLGKKKKKKKERGEENKQGPRLPLKREVGTPGQKKPL/WGSGNAGQKQPA/QKKGKKKADHKGQKGN*KRKREGGSGTSKNNSRGTGAKA*NPTIWGGGGKXI
1260	15161	A	1268	49	416	LRGRALDPRLLRCEGDLGAPAPEVALRAGTCWTR/CTL*APRGA/DRSWPPRS PMCKAG/DECQDGLPG/MKAWSCGLRTRQCPWP*PKLPCGPGHPAWRT*PLPOTA/CGPGPAAPCAG
1261	15162	A	1269	420	47	GPFGWASFRNLNFPKARR*GEWKTPGESGGAFFSPGPKNF\AQGN*GRPPNPPPPGPGKGGIQTGRGAGLKNPFRFWGFPNPNK*GGGTKKKEGPPPLFFFLNTDFCNLTIKRDLGVGAHL
1262	15163	A	1270	404	1	AEILELKNVIDILKNVSESLNSRIDQAEERISELEDRLFENTOSESK*KRI*KNEARQDLENSFKKANLVLVIGKEEVEREMGVESLPKWIITENSPLNEKHITVQEGYRAP\FNSNKKTSRHSIINSHTK
1263	15164	A	1271	387	2	KKERKKEVITIFVLLLPK\FQNIQVWL VRELEKKFTGKYVV\FA*RKILPKPTOKRCTNKKQKRPRIHAPTAHVAILSDSVFGEIVGRRIRVKWTQQLTRVHSDKAQQN NVERKVQTFSGIDKCLR
1264	15165	A	1272	1	393	FRMGRLPGGGAPHFSDGVAGQRRSSPHRRSRRGAELLTSQTGRGLRGAPHISDDGRPRDAP\PS*TGWQPGRGAPHFPD/GQPGRGAPHIPDDGRPRGDAPHFPIYGAAGQRLQSRHFGPRQAGRWRL
1265	15166	A	1273	3	317	SSVETKGVMIASFSSREADNHTAFIRIKTNASDSTEFIIILPVEVEVTTG*WKDEIESCFVFSIAYSGKVNKNC*LFFFP/APGIYSSTEMLDFTGLRTQGGKIF
1266	15167	A	1274	92	368	LCPPGGRAGQGQNLN*GVPSPPGPKGFWGPTYGGGGGKRTRPGGKPKESFD/PGPGPPGGTGKNPAPKNF\FAQKERGPFQNGGPGNKL
1267	15168	A	1275	401	3	DMCDWFKEFSDTTPKA*SIEKQLTSF IKIKSSCSPS\KNTIKGLTROEKLWGKIPANMSDKGLVSRITYEELS\KN\K*KLN P*WAKQ*DHLLKKTH*QICKERYSLGKKIKTMYRHSITIMCIKITHS
1268	15169	A	1276	298	426	GATMLVLLF*LAFDLRQSL/NCFPQAGV

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1269	15170	A	1277	421	1	QWRDLGSLQSPSPWFK VSFKDQKL*INKENHPKIKWKKICNOPL POIRYMDANKHIKIFSTSLAARETNMKI TT/RILWKTWQPFKKVSIYLPLEPAIS SYLFTQEK*KHIDGSCSPSRVATAKLLA LQWRRPSSWNCMHQRAGSWKQIGAPPSFK L
1270	15171	A	1278	1	218	TRSGVQDOPNQHGETLSLLKIQKLSYSG GVCV*SQLLRELKQKNC/LNGPSRHCT PAWAT/EQNSI*KKKKG
1271	15172	A	1279	88	396	TFLFSSSSFFFGGGVPCPPGLRPG/PN FASLHPPPGGPGGFPPLTSPPRA*NWGPR PPPQATLGAGGLEGE*IFPPGRPEP*L WGPPPPPPQRRGMWMTPL
1272	15173	A	1280	94	399	TDFLFL*TDFLFLCLCSLKNKIWNFEFR YGGFSLGVSNTQALPSPQEVNDATKQMK KHLKLA/KDKISIVRCKTKMGW*LLGYR SSWQVKRITWQLVLVNLMLAYRAVEGI
1273	15174	A	1281	236	2	TGSRLVFFVYMTGPAVYLNHHLRTHQGS HLCTFFCPEMESHSYQAGW/VWRDLS SSQPPPPRLKRPSCLSPSS*DY
1274	15175	A	1282	37	410	KKTKLKKKKLCPGPGVKEFFNPFYVLS KVFPKKERGLFFKVTFTSLTPFFKKNP KIGGSGGPPPLWFFFFFY/RDRVLLCH PGWNAVTRS*LTTSDSSDPS/CLRLPS SLDY
1275	15176	A	1283	404	232	LSSWDYRCLPPHPANPLYF*RRGFTVL ARMV/GPRDSPASSSQSAGITGMSHCAQ PG
1276	15177	A	1284	3	402	MQKITWENYCTPVKMF*KKK/SRTKPR C*GGGTTKILPCWGDYKIGE/PLW/K SVWQFLIK*NNHLLYDPAILPLIFYTRE MKTYYVHTITKYCNHNEK/CMQGTEALF /TLPKTE/SQPKHSST
1277	15178	A	1285	1	253	LRGKFWLHS/SILKRG*SQINN*TATL IK*KKKGKIKP/RSRRKVIIMNRNK*D *KQNNKFNETRWSWFFKNMKKIYKSLVR VT
1278	15179	A	1286	400	105	FNFKKKKKKNREYSE*QY*QAKYLKRN FTKNI*VAEKHMKNQYVVKEMLI*LTN RYYYTPIK/MAKIKLTDNHKCOQLKPSY MVGKEFGKFLIKLNM
1279	15180	A	1287	400	119	TVFHHIGQAGLELLTSSDPPVSAQSAG ITGLSHW/PASSSFHNSHSCVPLEPHQ VAGLDSFGYEVKCSFSN*VPGAQDKNDL SEN
1280	15181	A	1288	157	386	NDLOFHPFYCLE/DLFCQSLKKAGMGMW DLGSLQPLDPRRRLCLSLPSSWDCHG VS/PMEG*PCIVTHIVLVEMGE
1281	15182	A	1289	400	124	FDAFAKGGGCGSGSPFPFPFG/AKIFP PHFSQ*IG*KEGAPMQQPIFVFSKTAG PPPGGGGQIPTPCGGPQPNFGIQGAG APGPGGGGF
1282	15183	A	1290	419	3	KNFFFLRGGFFFFPPGCRAGGGF*FPFP FFFGQKKISGPPPKKRGPGAPQKL/R EIFLVLKKKGPPLPWCGFLNPAPKNFA RANFFKRGGSRVGPSGGPNLNLGGGW FRFFRFFFFFLVFETEFRCPCGWSA

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1283	15184	A	1291	397	39	M WGQVWAKDWIHLGPKTGCGPPPLGVFG CP/SLIPPNLFFVYI PGGLKIFVHKNP FPIKKEPANWIATFPFGVFL/CFE ETRSHSVTQAGVQ* RDLVSL*PTSGFKR FSLCLSPSSR
1284	15185	A	1292	399	1	LNFFFLHKGKLCNLIGSDDKVPAPSIYP EPRICYVFSLLFEIIFSPDPNKKIRIYK KHVSRIRYDKLLKFNKNQVFKKWKADLN RHESKDGQIQKKHIRNC*TLAK/EMQ NTTTWR*HLMRNKMAKIRKTI
1285	15186	A	1293	412	1	ARMVSTSRPLGTPIHRSQGGKNKRVSP TRPNPLFLKNPKKPKSRD*NKPLLK KKKWSGCPAQ/SCPGQNP/SPKQOL PPSPSTPPSRPSTLAFPMAS*LAISPA HTHCCWRELSGTHTLSIPCLKLGRP
1286	15187	A	1294	229	1	FFFEATESHSVTQAGVQCNPGKFRSCF GLSSSWDYRYAPRPV\ANF*FLVETGF YYVAGLKLSPGDLPALAS
1287	15188	A	1295	401	2	STLPVH*KWITKAWTAHL/FTAWFTEY FKPTVQNYCSEEEKIPKILVLIDNAPGH PQALMGNMKEMSVVPIPV/NTTSLQ\A ADQGVITFLKSYCIRNLFQHQCTPAWVT QLDSVSKK*INIFQGMVAHAN
1288	15189	A	1296	1	336	KKTPRRKTHKEHNGEK/LRAFLPSRGI KQ/GCAF*P/YILNIVVA/VLAKEYGKE IKASFRKEELKCLFIDMII FVEIPENS PQKL\IN*FSKVAG**VSTQNSVAFLEF FFFF
1289	15190	A	1297	3	384	HTNMOKVLV/VKTEQDSHNIPNLQILI QNKSLTLFNSI KAERSEEA*EKEDSR GWFMRFKKKK/RISITMOGEAASAVVO AGTSYPKDLAK/DEGSYTKQIENVNET VLV*KMI/PTEDFVVRDKSM
1290	15191	A	1298	3	395	SRSVTRAGVQWHDGLSSLSQSPFPFGKFC LSLLRSWDYRLSPHQMGIGFL/VFLP FFPQKGVFLGQPGAGKGNLQ*WNP PRLGEFFGLNPPKQWQ/HPFHPQL F/CCFFRGKGGSPRRACRANP
1291	15192	A	1299	260	4	GFTVSSAVFPLKCLLDYLVSSVLLYC LWNFKIQKSRFYNLSPLVSSFKNSH*N SNI/WPGAVAHACNPSTLGRGGRITRS GD
1292	15193	A	1300	91	219	LSRLSANDY*HVPTHFFVEMGFHRVQ ASLELLS*GDPPALA
1293	15194	A	1301	277	441	TVEF*GVQSKKEI ELCLFEDDSVYE ENLKELTKN/LLK*ISNYSKVAGYKVN *KAIIVLHSTNEQ*NFEIGNTILF/TIS TPKYLGINLTKYAGGLYEYENSLMNEI KELNTW/RDILCS
1294	15195	A	1302	256	482	YNVYFKICIGPSTVAHACNPSTLG*G GRI/TLRSGVRDQVQHG
1295	15196	A	1303	182	460	VGREFLDMTGKFTYKFLYRKIN*SSS KLKTFVLPKTLRD*KAKLTGRKYL*I TYPVKGLVSRCKKLSKLSKTKTQLKK WAKDMNRHF
1296	15197	A	1304	1	468	FKQFSSLSLLSSWDYRHPTGNFCELAPY KQNAPS CSNVFTDNVPVIST*QGLQALS

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1297	15198	A	1305	880	1026	PNVNEQSPWRETKTAVDLGCVIWKFCQ VFLRKKPKTKTGQ/HEQQIPGF/CFFSE TESHSVTQAGVQ*HHLGSL*PLPPPFKR NSTTRTSDYDGP/HVPP/HPA EEHGAGLSGSQDAAGGVAPAG*GGWAQLW VTRRASFLDKTHWPVDEQNGLSLYLTIE ATAYGLMQKLELGRYNETHAIKWLLEK QELGGGFRSTQ/SDGDPRETTVVALEAL TRFREAVPPFKGIQDLHVQIRAPKLTALNV NWYIDHSNAYQORSAKFLAQDDLEIKAS GNGRGTSILIMYHKSPESREDNCNLYH LNATLHSALEENKGGETFRLRMETRFQ N*EATWTHEVSLITGCFPHQDDLKCL TSDVERVAFQYKTKTSTSDSTVVLYLEK LSHEKNTELGFRVHMLQAEFLQAAVLT IYDYYEPRSRRCSFYNLPTQESSL RTHYQFQSLKHICLTGGALNFPDVRKK KRGOTGVLEYEGVQGSSTVVTYKNWLSYE DANTYIVK*KTL*TKQEB*IIICANPK MKIKSVSMVKESLPYVHVIVDDEGNVLP PVEERNVTVRIKPTQLCLILNCYLDKCE KTAVS*QGDIFYITGDARMKDGYFWFM GRNDDVINSSSYRIGPVEEESALVEHTA VLESTVSSPYFIMGVEGKAYIVLTRY SSHDT*ALTRVLQEHVIK NAICPNGSKSGLGSGCSVTQTVGRV*D HSSLQRPPLGLK\YPPTSAS*VA\GPQA GVQWHLGLDSLQTPPG/FKRFSCLSLPS SWDY SAIPVHT*RRRKQTSLNADMEKV*VVWI EDQISHNIPLNKSIIQGGKALTLFNGMKA KRSEAEAGGKFEASRGQVMFKERSHLY NVKVGGEAAGADGEAAASYPEDLAQSTD EGSYTKQNFSDIV/TFYWKMSRIF IAEFHHTD*GDMGSP EVLSTLTGKGLIKTKNAK/CWQDCGK RTFHCHWGYKLVQWKR/VYTFPYNL AIPLIGIY*/NMRTYSHKRTCTKWP/I NSLFIISKWKKHLRYFTREWIK/*VS HTKDYYSAIKRNKLDMPNMMHESQKHV PGGKGGGGTTPAPFPFPFPFKVGFVW* GFPRPFLFKPPPNKAPFPFGAPHF/SL PPFPFRVFKTFTFTKKKFPFGGKKKKP PPPLQGGKKMGSAKFPSSGKKPWGISP QI HNOKNEFGPVVTSYVKVKEAK*IAKTRK LLEENIGVNIHDIELSGFLAMP\EA* AIRLKEIKLDFIKIKNSCASKDTINKVK KTGRPGMVAHYNPSTLGG RGQQDVLPG*RGQQDVLPGRGTYSEYGL IFSARNPSMEV*SVNHRPFHHGVF/HQ NCSDSGSYFISKECGN/WVSACGIH*CC LVPCLPKAADLGE*WNGDFSLSGKEKKK EFYLIINTFSQ ENKLTNHGKTNGGAGSQ/PPECEPRTH LORGLEGRGGGEPWGGQPD\PPSNSSL KNPQAGVPFSSSLGKVKRDRS VSDSG EQREAGTQ*TFVNGKKKKKKKKAKKA
1298	15199	A	1306	3	726	
1299	15200	A	1307	230	486	
1300	15201	A	1308	463	440	
1301	15202	A	1309	463	59	
1302	15203	A	1310	438	29	
1303	15204	A	1311	2	310	
1304	15205	A	1312	19	348	
1305	15206	A	1313	2	424	

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1306	15207	A	1314	375	3	AYS PDSKA / PSSKSSPKSS KKRTLLIFLMMMDAI / MNKILAN* IQQH IKRI IHNDQVQVFPVGMQGFNIQKNINV IPYY*LFY*CYINRIKDQTLIIISIDTE KNDKIQNSFIVKTLRK\IKENFLTILKRI TY* KSSNNKKNID
1307	15208	A	1315	403	3	LEGVSFFFPRVASQSSILGSCNPPLPRF HHFS / CPHLLSKWYRFPSPPA\FFFF FLKTGFFFFCKNFALCSFP* KQASPPPP LTVFFS / HIFPFFFPFFLFLRWSFA LVQAQGVQWHDLSLQPPSLGKRF
1308	15209	A	1316	38	427	PFXPARPTPRPSANQPRFKSBEFLRP AASPSEX* GASPPGSHPIWEKVSVAHQ PPRPGGRWGVNPPPGQPPRPGGGRRLC PAAPTGK* GAPLPGQPPRPGGRWGYP ARSAASYGR* GAPLSSRP
1309	15210	A	1317	43	399	LTFFFFLGEGARPPFPWGPGPAHGGTTA PLFWGQGNPPP* PPGESEPS / QGPPPP GGMVFFWKKGSPRAPGGWTGGKGLP RPPPPKGCE* RGNPPPTPKFLGFTTFQ KKGKNSGP
1310	15211	A	1318	437	54	MNEQGERGLSSLGLPAR* D* GKGNVKE GR / EGVTFSPREPKESLRWSTPQKEIV GVINHPRGQVRDQAGSGCEGFPALRAQ TGGPPA* EITRAGEQKAGGSGKAQTLQ RETRPPRQRRGGGSASL
1311	15212	A	1319	351	133	GGGWAEPVLTQVGRSGRGTQPLPDGAA RQRPPPPRGRSWAEAPTSGTRPGRGA PHLPDGRPGRDAPHL
1312	15213	A	1320	474	11	KINSPOKKKKKKQCSIRKLA* / DQNR HFIEETQIPNKHMKRSSIS / LAIKEMQ IQITKSYCIIIRLCK* LIKNSDSIKCWQ GCRET / GSLTHCWRLKMNSTALQMVK
1313	15214	A	1321	485	33	CPASRVAGITGAHHAWLIFVFLVEMGF HHVGAGLE / LPVSWNGGHL / RLCLLF GYCGQCYKPS* RRFCVSPYIRA* K* G FVCLFV* WVECCVTRLEFV\TRCNISK LQP* IGPLKCS / PASGF* VARTGLYHG VNHVSNSTALTSGLQ
1314	15215	A	1322	451	145	THFGRPRGGVFKVRKLNFPWLKENPL FIKKKKKKPGGGGGPPTPSEG* / GKK KGFNPEKEASNPKFPASNPTGLGKKK KPPSLKKKKKKKKVYSLIF
1315	15216	A	1323	470	151	GKAERHDPPGSRACSEPRSCHWTAPANAT / SETPFKKKKKKLCISWPGTVECSFSVR T* * I* LRQVLYLFLFPKNVILYFICL HDKANMVMFLDFKYFCFLFD
1316	15217	A	1324	64	367	TWEGEGSWLTSQDRRTAPLHPSLDNRVK LRLKKKSGVGLSPSILLAKNQKKPAP FTMA / SK / RIKYLSINTKDKVDLYNEN Y* TLMKNLKGAMCSTSL
1317	15218	A	1325	193	381	AQLFKTSMGNSETLSLQKKKREKS* LTL PSSWDYRHPPPRPVNF* FLGEMGFRV AQAGLEL
1318	15219	A	1326	410	7	GFFPYF* LPK / SLRC* GRDFYNGSGGQA RWLPVPIPPPLEAQAGSP* GRSRLPTW PAWNSPFLKKPTFLFLKFS* GRRIALT PKAKSVNWDSPFALQGGSPKTFPPK

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1319	15220	A	1327	295	3	KKKLRIIGPGVVAHACNPNLTG VCHFGIYFCVCSLYFTCLYFFFLFL*V TLTFLVYFDFTLVLIISL*YFNDCSRD CNHIM*LLSLPVLPHCC\VFVRDRVS LCHPGWSALASSLL
1320	15221	A	1328	2	392	RQASRPP*SAPPAPAGKSGSGE*PFPSPK /PFPFPKVVPPRGFPFPFPAGPPPPPP KKSPFPKTNPPPPP/IKPPPPPPPPPP PPPPFPFP
1321	15222	A	1329	378	7	TDDLILKFT*ERYKPNQF*KRTKLKDSL PDFENYKAKVVKTRN*YKE/KHIDQW NRIESR*QIFNIASII/HIEKEYLCNKK CYRTTMEEEKNNMLKPL*TIKFNSK*I TDLNKIKTITWLKL
1322	15223	A	1330	403	2	VEGFRHVGAQGLLELTSGDLPTLASQC WDYKHEPLRLGELRSLTAAMQDPQVS PNK*IKKK*1/P*SEQFSGI*SIHNVO NRFP*PPDTHFHSKVKPLTHYVSPHS FLSPFPNGQCLSVSMQFSL
1323	15224	A	1331	1	389	KMKSQADLEKTFPKHSDKGLGVGLYK ELL*FN/R/RCOT*OLKGER*TNSTW GMSFEWVSKHMKRCSAFPVLVREMO VH/TSLFVERYHYTPTRVAVIKQSDQV W*ECGIRTLHC*WCKMIAT
1324	15225	A	1332	392	3	NNFMPSA/PPPPPPFFFGPVRVFP FFKPPPPFFFGPQKKKIFSPPPPLKFF FFLRPPPPFFFFFFFFFOKNLKGGF F*PRPEKKKKPPPGVFFFLFLRCSV ALSPRLCSGAISAHCNLCI
1325	15226	A	1333	394	1	SOVVGPTATHYCAWLVRKFLGHFSKTTI SAPLLK*TSRAETSKSFS*CPKMER EGRRMFLGKSLKQIVLL/LISGSCVT AS*FL/CFQTESHSVAQARVQ*HDLS LQPLSRLKRFSCFSLPSRTRG
1326	15227	A	1334	416	1	LTLPLKPTPVNTRKENYRPTSLINIDAK IL/NILAGKIPQYIKVGN/NMGLTPMO GLFNI*K/RKSVNVIKHNREKKKILL INA*IVDFKPTMI*KNWQ/GEYKEIY SNILNLGKMLKACHL/KTRIN*GQLSP DAW
1327	15228	A	1335	391	57	WQRVNCNDKNLYQKEKRQDNVREK/WAT DLINFTHEEMQSVNQLQKTHPSLVI REWIKTTSY/HLLAKINDNSSY*G CGGMGT*CCWVSKETHALWEIVFPIY SK
1328	15229	A	1336	285	2	IFFPFWRGSH*HLSLINKSGRNERAH \KDNGDFSQIISKLKMYKKILNOTTI KYMFPKKHRTSIKIEHILOKSGSLNLC QRISVLQTRV
1329	15230	A	1337	34	391	AKIASLYSSLGNRKNVSKQNKTKNCN LKN/IKTAGGLGVVAHSCSPSTLGLH DPGV*GREL*WCRCTPAWASG/ETLSQ K*INKKERKKMKNCWMMNSLIQLTS PSFTKTWSS
1330	15231	A	1338	292	1	GGGSKT*PGGEGAINFKKPPALFPGGKK EAFSPQKKKKGERA*RDISED*MAN KHKSCPLLMIEMQIKSTMRYRFP RMEILKKQKNS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1331	15232	A	1339	369	16	DPWQNEQLSEVTCFPGPRASMFRT*YK VITAAIMAYSGSPRAVSCIRALMTTGG/ IMDNYKHERRRLKPL*WEGMVAHACNP STLGGHGRHERVGRVRSIPDCVVRVAAG VKASI
1332	15233	A	1340	394	1	TQSGVORHDAGSLQPPPRKQSPHPSL PSQDHRRVPPCPARPCCSHDSVVLREG PCGRW/HESGRVFLVLF*LSLMRS GGFKKGFPCTSSL/SCLPST*DVTCSS SLPSAMNVGLOPHIFMHGF
1333	15234	A	1341	400	161	KIGPNLFCFSTKRPWKIDTQFMPFGKV F*/SPPPPKILFFPPPSGPFPLPLP PLPKSFFPKPNPNLPPSFGFDLPP
1334	15235	A	1342	377	3	NRHFPKATKLKSKHLKRHLPLLVIREV QIKTNI CHNIATRLAM* KADNTKCWE SCEPVLTFY/C*WEYKLVQPL*KMVWQK PKVCVPYYLAILLQHIPEGTCS/CY* DIHKRLLTAMLFAM
1335	15236	A	1343	170	369	RCNENKITREVFGEI FVRLDNKERNTS FFYFYFLFY/CWR*GLALLPRLVLS*A QVVLWPWPKML
1336	15237	A	1344	385	2	SDLRRSTHLGLPKCWDYRC/RATVFGRL FIFLMVSLKHKSFKF*RPYILFFLSL MLVSYLRNH*LIQGHKDLLPMFSSKS MLVLTSSRLSLLLFCPLFFVLRLQGL/N SVTQAGVQRHNGHSLQPOP
1337	15238	A	1345	1	281	HPATKMKRC*/SEMCTLKPOLNTTTPD HQNG*N*K*LVNFKGHW*EGAVNWLHC W*DKLAQPFWKIDLSIKAKISMSYSHV VRKIFKLKXK
1338	15239	A	1346	176	1	SVIWNKEP*IAKILKKTITVGLTVP DPKTYKAMVI/KTV*SNLQDRQRQWY RED
1339	15240	A	1347	398	2	PRPFGPVRRCFSL/TATSGSSPSPSP FYLGYDQGFPLPAVLNRPGLFWGPHK KNITLPAQR*IGSS*TAPEFF/SLS FLLFSLLFDTSYSYVQAAVWFNHS LKPQPPGLKLSOLLRLGW
1340	15241	A	1348	9	395	GLQNPVCVGLVSGFFPPPPPKKGLGV PPKKK/RGPNPNPGVGEFLATGPPFWTG PLKKNPAPPRALFWGPPPPPPWGG*NPP PFLARGSPFFKKFGGDPFFYRTNFRG PNKRGPPWLKGNPPPK
1341	15242	A	1349	119	1	ENVFRNM/WFGNMHTCNTSTLGGQGEW ITRSGV*DAQQ
1342	15243	A	1350	58	396	GIRVGKVCFIIFFGFFFFFGKGVSLPP GRETGGPPL/LIKFPFPGVKGIFLPPPP GGGG/CGPPPPPRVIVF*GKGFP*G GGF*PPAPKGSAPPPPLWKNWGNRIFG GR
1343	15244	A	1351	396	1	GPTKGPGLFDGQQFPPTLKQNFPPFA LFFPPLGKRLILGGF/KPKGGLLPPT* KPLRFPKGGESDCKPFKF*GRIVCFQQS LCFPPPKKKKTAFGRKFKKTLTLLFFF SDGVSLCHPGWSTVAQCL
1344	15245	A	1352	1	250	RRL*SQLRLRLRQGVNLGSGACRS VCSSRSRICTPMAATKRDVSKTKCR RHQHVGLTLVRLRPGVWIRHCGCHWWP

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1345	15246	A	1353	249	3	CGATLCPKRYMKITPSFFVEIDN/AILKFIWKFPGPRIAKITLK* KQG* RTHIFHFHNILQKAIIVKTMWY* YKHROS PGRVAH
1346	15247	A	1354	15	416	LLTLSSSLRYTHHNGRT* SFIRENIIIFIATTNLLGLLPH* FTPTQLOFINLAMAIPL* AGAVIIGFRSKIKNALHSLPQGTPPTLIPILVIIETISLLIQPIALA\ARLTANITAGHLLMPLIGSATLTI
1347	15248	A	1355	2	416	IKYLVNVRPETLLK* /ENIE* NPHNIGLGSDFFNLTSNSQGIKEKIDESDYFKLKSCTESDITNRIROLKNERKLCQITCDKGLIP* KKLK* LY/ KQKTNH* K/ WSKRLKYFSRRDIHMAKRY/MKCSTSI IRENKPK
1348	15249	A	1356	426	85	HARLVL* VVF/ LFETAYLSVAQA/ GGAM AQSAHFSLELPSSDTAISTQVCYHRT/ RLLF* IFCGYG/ RLCCLGWSRTPLKQSHSLPLPKCWDYRNEPLYARPLYLSCFPENARLG
1349	15250	A	1357	2	301	GSLLLEVKQDQLGQHNKTPSL/ IKEYILPIYTOKM* KNLTRHGMCL* SOLLARL* ED* SSPGI* GCREP* WRHTWPWTIQD SKSRGGEKKQVIFTHYT
1350	15251	A	1358	2	389	FLHVQSGSCELPSTSVOLPASASQNAGITGVSHRSWLKPSLLDVPSPLTP/ VSSAVPLISYLATGWROAAIAASPIFLHQLARPAQPARAAADS* LPADSAFFPKQWTC* MFTGALFKKKKKPCFVAKK
1351	15252	A	1359	309	3	KWDHITLKNFCTAK* TINKVQRQPMEW* K/ IFVNYVVDKGLITRIYKELQLYRKKKSNNLIFKMSKS\SSLAIREMQIKTTMR YHLPVRLIVYVLPKRARS
1352	15253	A	1360	300	2	KRAF* KMPSTRTTAREGSGMPCFK/ A SGWATPVIPAL* EAKVGESLEPRSSRPAWATRRDSCLF* K** INK* KLTLGLGANAAGNLTLKMLICHXSXS
1353	15254	A	1361	396	60	HKVTRKSDGMLCHSGFCSINQLAFCECLFQPGGPRGTPLP/ PYKPPPKPTPKTGPGGGGLYSPFGGGGRGNPPFGAQGF* PPSPPPPPPGGRKKI FLPKKKKSLIFF
1354	15255	A	1362	37	385	ALPFSFSPFFGFGMGKIFFGGGGRAGGHSNLPPEPPPGGGAFFRNLSGGGE* RGPIS\SGIFGLKKTGVPPGGRGWFKPPAPKEPPFPAPFRGSGQDPLPPVPLFGWCKKN
1355	15256	A	1363	12	421	EPWEPOTLGICTHLOTLFHHYQVLMKMLVTVRYHLTPVKMPPFRKTFDTAGM* KKKGCYQSGKGGNLI/ HPPWAL* MSIVKKKTWGTFFPKIKQELPWPDAIPWLGMPKEGNSVFQRMGLPSVIGTLFPFIAG
1356	15257	A	1364	278	3	CCTGEKLETFLLR* ATROGCPHLFDNVM EVLANAVRYEKEIKGIQNGKKVKT\SLFPGDEIV/ YAENPHKS* PKNSL/ KLKSDCSKVNITQKPIAF
1357	15258	A	1365	265	330	WFGAXAHACNPSTLGGGERIT
1358	15259	A	1366	379	1	KRLRMKYCWECK* IQGKRTVWHFLKRLKLELPYDSVILLTYFLKES/ PVYARDI

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						CTPKFIATLFIIA\RCSLTHD*TKKMWYLSIMEYYSALKNE/YLPFATTQMNLNEDNIFSEESQA*KHGVFIFF
1359	15260	A	1367	1	376	HLPGAESQPPFV/DNSWDRFAGRTQLLWTPA/DPHSYG*GGAGPHPCPSQPGCCAPVQSCS*APSEAQSLGAADS/GPAATLPA RQLITKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKDDSGK
1360	15261	A	1368	2	409	EEAMPKAKMG*RPFPAPNSQILNAKKLLKEKTSVTPVNI*MRK*NSLIADMKEV*VIWIEDQTSNIPLSQSQIQSKVRMLFSMKAEEREAESEKLEVR/GWKSAGFMRFKERSLHNKVQGEATSTDGEGA
1361	15262	A	1369	220	416	PQPLEDWQMYTTTLHNDILVNDGELSFGQGCSELSLCHCTPI*MT\SETLSQKKKKMGQARGLS
1362	15263	A	1370	310	289	AFR*AFHSKGSK*H*EKKN/VNPTKT*NFCTAKDIKKMKRQPTKWEVIFANHIYLTGILIS\KIYKELRTQ*PETQSLK
1363	15264	A	1371	3	322	HASERTHRRGKSTETTTAWATERGVSQKQNTNKKTK/RNTGSSIHNVSDFEKQVTQTF*SSMQMSNPKLRYLTSVIEMN IKPEYHFTPIRMALIKKTDNTKC
1364	15265	A	1372	3	332	GKEVS*EDIMMLHVVYAPNRRASIKHMKQNLIEMOGEI/DE/HPTVIGDFS/TPLSIIDRSGQKI IKDIV/ELE/STVKQLDLI/DIYRTLKRYEYVF\ETLSKFTATINCILGHKV
1365	15266	A	1373	381	2	CSVAQAGVKWCNHSLSQP*TPGVK*SSCFSLPSHSDYRHE\PALFFKFFVQMGS\TML*FS*ESCIKGRQPCSYTYLHSPPIFSSLFPLAPESIKRQPSFFFMESCSVTQAGVQWRHLSSLAQ
1366	15267	A	1374	1	385	YKKGINAKIFNKI*V\ESAISHDQVGI VLVLQGLSI/RNKSISVTHHVNRLKN/HMLI*IDA EKAFDKIQSSHGKIGIKGNFFDLLKSIYRKPMANVILNSEKMKCLPC KC\RTSGGQCLSLPFLFFFF
1367	15268	A	1375	1	357	CSGVI SPCHGLKFLGSDNLPALASRVAG IIGMTF\HAQLIKNFCOCWWR*CLAFGG*RFKTKMCPITVK*NSIKMK*NRVTCMSG CGDS/RQLGLRLWSFGLRNVQCSSEF*WHGCTSACL
1368	15269	A	1376	1	375	HRPKFKSISLLEENMGESFHDGL/GSD LDMAPIVQSIDRDKTSDFLEIKKSCSG GTV*IMMKQATDWE/RTFVKHTSNKSGI MYEEL*NI*KL*NNPI*KWAREFSRHL/EDTQMATKHKM/KCSTAL
1369	15270	A	1377	260	400	KRGLGRTVFVFPKPKNGPFFFPKPTTSKGRKTLMVNPE*PKYYSVKKKKKKKGGGLPFPCKIFFPNLTITQTTFVFPKTNPLTLK KRKKPPKKTPTFWGHFFFERGTTKTOGG KKNFPKKGWEKFLGLQKKKNAPFFFP KQPFQR/WRKTLMVNPEP*NLKQNM
1370	15271	A	1378	403	1	TGVSQALSLFFFKYFKPRMVEFLVEPSR*KGPSVYGLQIFFSPKVPFPCPNAF/SLV*SSPPCLSLHLPLAPAGVLPKRSLEP PMLQSFSPMFARIG*QIILLFOSLL

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1371	15272	A	1379	195	381	S*FFFFGDRVSLCRPGWSAVAP AERYQTSRSTADTRISCLPT*SAEI/VFP DSGKKTGNNNNNNNNNNNNNNKNNNNK ISLSLKP
1372	15273	A	1380	361	39	PPVKETAKDVNRFPKQPMNTST*SDA* VDEVVCL*FQLIGRLK*SRRIA*AQEFK AS/HGQHSETLSLKNYLKKRFTSLFL REMQIKTTTRYHFTPIRMARK/SHHTKC *CGLAMLPRALNSWAQAILLLHFSLP I SWNYRHTTSSTQASLHVLFVIGLCGNRL LTSFAVSVFTGG
1373	15274	A	1381	400	90	LPSSWDYRCAPPLLANPCVF/M*SGGFT RLVNSM*PQDPPTASQASAGITGVSHHA WPAFFIMWFSSSYSR/TMH**QHPIV*K LHICPN**KS/LSCPQVTTIIV
1374	15275	A	1382	1	431	DNIPKKSAYVYITLFPKGV*DNVEEAY SGTLAISIC/ENIHLVCSLSDBEOHST AQTJANIITVGLATLTLAKSKNLK CT**NPKLSYPLP*KLL/KXKTKNTIV NQLQIKAEPLVEILHNCDDQDPETWLG GV AHTYN
1375	15276	A	1383	2	432	ELSADVSFFFIITPLSGVL*QNWGLA F IPIELRSPTEVTFSPVNGGPFVEISLS Q PTHFSDHQNHVVRVERNMKEASL/QVDO LTPNTOPAPADGHVLLQLNHLFVGGA TTQRGFLGCIKRAL/RMNGMTLDLEERA Q VTPEVQ
1376	15277	A	1384	1	421	NPPALASQRAGIADICHCAWPLRLSLK P QFSNL*SKKFALGDV*SSNIL*YIYIFF EMESRSVTOAGVQRHDLGLQP/LPPKL SLLPPKLSLLPPK/SASCLRLAGSWNYM HVPPRPANFCIFSGDGVSPCWPGRTPT P G
1377	15278	A	1385	2	416	IFSVDTEALYWKMMPSRTWYL/RKEKSM SGFRDSEERLTLFL/GLNAPGELEIL LI*HPEILGPLNVYKFTLSVFY*WINEA LITAHMFTAWLTECFKPSVETCYLSEEM PFNILLLIGNAPGYPRAPMEIQEINI IV DSVFLTPGGQNEKLNKNDG/DLTKLPR LA*NSWARQSSCLAFSKCDWYQREPPCL A
1378	15279	A	1386	170	1	
1379	15280	A	1387	47	418	FWGFFFFLLKKKKAALGWTPPPPGQGG PPPPPPRPGKGGGPNPPTIIGVFGQR GPPPGGGGEPGPPPGPEP/PAGPPTGG PQNWPPAPGP*KGF*GASKGAP*KGVD P GGERSQVPMRGA
1380	15281	A	1388	58	503	RPTFRPGNYIMIKEFIPQKDRTI*NVYAP KNLALKYIKQLINLKGKRDKLTLTVAN ISTCP*VTDITSR*KICKGTELF*QPA DLIDIYRTLYPTAA*YTFSSAYNYSK IGNSIGHKTFSN/CKRNDNTQWLFSDHN GIK*EINII
1381	15282	A	1389	2	401	LVSQVNSKNRILKIKNSPTVPH/RCM IRKQNNLIADMETVLVVMIEDQTSNNT SQMSQTQSKALTLSNVKAERGEEA/EA GRGWTRFKERROL/NLQVESEPPS/AD VEAVASYPEDVAKIIDKDGVTQR
1382	15283	A	1390	294	3	KIVYDFDNDVKNCS*KTIVDFDNDVKN

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						CSSKTVIEGKVSDDCKKIFSKHISDKYLI SIIYKELSNLNNQQPN*KWAKDL/NNM SSKHKICSISFGKMQKTQIRNHYIPT DAW
1383	15284	A	1391	3	422	PLFKKEEGTNFPFPFPGWGRFPFGGKSFS PFPFPFPFPIKGGPKVSKQGRPFPPFPF F*DGVSCLCRPGWILFPFPQVTEALLRGFL ALSSCLFRDLKFFFPF*R*GHLLSRWDY RHEPPLRLIS*RKTKVKGLIMLTRLVL
1384	15285	A	1392	3	400	FLYIYKDIYR*YKTFPQNNKLIKTIYFK* EKDLSKGLFTKDVQMINMH*MGSTSLII KMQKKTTHKHSLSPECLHFNANITC WKLOPACTLILR*ECKSVKPL/WETP *OCLQLSMOENYH/DPATPLIG
1385	15286	A	1393	409	2	IVHFSKEDITHSTNEHMKKGLSLVKEV QIETTMGHHHIVRRVXIKTDFASAN TKC*GYCKTRTLNS/YWECKIVQPL/ WKNILAVAYIKHTFFPPIRHLSGSQS HFSIYSKEMKTLROKDDIFMATLSQ
1386	15287	A	1394	409	24	KSTFFFEKGFSPSPGGQWGFPPPE PPPPVVK*FSPTPPKNWGRPPPSW/P G*LFFFCSPGGFPPLNWFPLPLR*SY PPGLPKRWGFKQKPMGRG*RAFFCPPI SKKLWSGKKKKGRPLAI
1387	15288	A	1395	83	411	QRDSVSKTKQKINNKRSTDRLNRHFTKE DRWM/ANKHLKRYST*LVIREVQIKTMM RYIYISIKSKINKPDHINCQGCGRPG TLIYC*WE/CKMVPSLK*TFW*FLKRLN
1388	15289	A	1396	308	14	NFFFFYSWSNIIYQCKGTAFTPISDKID FN*KIISRQK*QYMLIKGSKIN/DITII NTYTSNNSSPKYIKQTLTGLKEIAPST IVGVFNTLSIIK
1389	15290	A	1397	321	1	KQ*CSIEYS/FKYTR**SKL/WPGAVA HAYSPSTLGGRGGRIT*GQEFKTSLA
1390	15291	A	1398	183	48	KWPGAVNHACNPS*MGQGGRI/TKSG V*DQHGQGESPSLVGRVR
1391	15292	A	1399	18	422	KAGMAILDKVDFRTKNIIITE*/EKHFI ITKGSVRENSVLNV/WPHYRAGHMK Q/LIIEHVELGEHTIIVC/DFNIFSV LNRIKESARRR*NT*NTNHLNLDVI Y*KTQTTNGRTTFFPSAHKFTIILHI
1392	15293	A	1400	28	339	YSCDHSNVQFQFGLKOSLCOPPE*TAG ITDARHHIPIPIF/LKRSFVFLAQAGTQ WRGLL*KKKVGGFKKGSLTLPCRGDY RRFREEKILIPGRGFCNELI
1393	15294	A	1401	390	1	FGLGKHLVHMTSKAQSIEKTD*LDFLK IKNPNFSKDTIKGKROARNGEIKIPRH QS/DDFF*WADLTFPKEDKVMANKHIK RCLRLLL\SMRYHYH*NKTDHTKC*R ERG\ELELLCCW*EYKMQ
1394	15295	A	1402	149	402	RFWIHLYKRVPFPLLPVITWKEKRGF VFVFVF*DRVLLCHPGWAVPWS*LTAA STSWA\K*SSHLSLPSY*DHQHASPLC N
1395	15296	A	1403	1	403	KRKSVPPLIC/APRC*APCSYRPNLPSS PGPHLDVPGPTPTSPRPGPARGPAPAA RPKEPAEPGKEERRGL/PAPGG
1396	15297	A	1404	342	3	KEDNLDKGGSPKQITFKVN*TALP/YT

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						ALYSKKIPPTTLIAGREKLMGFKASKN R/TLLLGANAAG\DFKLRPLMIDHSEL*/RPKSTLPVL*KKA*LRAHLFIALFTKH FKPTVE
1397	15298		1405	498	66	KNYAKSTLPML*KWNSKALMTAHLFTAW FTK\FFMPTVETCYCEKKRF/SFKMLLL IDNAHSHPRALMEIYKEINIAFMSAKTA STLKPMDO\KVILAYKSSYLRLNI\FHKT TAALSSDSSDASGQSKFK*INWGFTRTR GRTRGSAR
1398	15299	A	1406	3	411	VSPCLCGRSQTPEIK*SSPLGLPKCVDR RHEPLYLASMGLVNCIPINLQCCIPF*A AWWSLLLGC\PIMLMLNVTCDLPSVLQ PRAPGPR\HPPVVSAS*VAGTLGTHYAW LSMLLGSTL*DVFFPLSPILIPSEE
1399	15300	A	1407	361	2	IRVPQKKIKSPGKGHKIFSF*RAQPPFF FFSFFFLRQKESHVSQAREQWHDHGS LQSLRDPK*FSH\PPPHPPPTGTTPLE IYIYYFLRQSL/DSVALAGVQWHDLS LHDRVRPRV
1400	15301	A	1408	393	2	PGNTISVLKASGGLFFSPDLGKKGFFS QPFFFGSPRVFPFPPFPFNPFFFFCCP L*KIFFSPPGPKLKFFFFKRAPDFFFFFF FFFPDPRVSL\CCPGWSAMVQSRFSATST LRAQAAIL
1401	15302	A	1409	393	60	LNUNPML*SYLDRKHGMLYHILQSKFEL SKTSKAQAKEVTLCNDYNKLMKFTAK KTL/IKVKR*STE*KKIFVKY/STK/G *TYRIFNKLNKNNTQFNKRAETSRKMAE
1402	15303	A	1410	422	2	VNDRKMDGMNGWKEGR*TQKKKGGRK REKERSMFLGRKQREKEREEREKESQ KERQKRGKARKEQREARKQGG/EREK EREERERGERGERGRKSS*TSKVVVK IILLAVKMLVHLKSLHLQKVCVSFSRS
1403	15304	A	1411	398	64	PGFFFKKIFVENFFGPHQFFFPFPPGK KNPL*PPQRGGP*\RFGVPFPLKKGSK KKFPPPPRGTPRQWKKPLPKRPGFFP GPRVSFFCLIEIGWFFWAQVPKKKKK
1404	15305	A	1412	391	125	EPAPFFFPFPPGKRGFFP\PP*EGYPPG FSPFFFLKTPPGNFFLGPKKKKFFFPF GKKICFL\RAPPFFFFFPFPPPRQA ICPIE
1405	15306	A	1413	3	387	TPDLK*LTRLSLPK*NDYRRATTPQVLE PFKPPASLGSISM*YIISVCLASKIRLL FDSSFSATAKHPLTISAFAAWLSPPA LIQPHSSSESLYSSYCPVILLF/IYLF IFLRQSL/DSVAQAEVQWRD
1406	15307	A	1414	409	1	KRSGGFFFYF/SPFFKKGSAKFFFLGSP VFFPPPSPP\GFFFSPPPKRGFFPNP FFWGAPGFFPPPLF*NPDPDFFWGPKK KKNFPFPRGKFFFFFGPPPLFFFFFF FFFFFFFFYKIISIKGEIGRSSVR
1407	15308	A	1415	3	385	HRPPPVNGLSPRPAFAAEVGPVPAVLAH QHHAQFLARP*LPPhGAGLRTCSPCLSL LPNPPWPAPVWPEPP*ALPPAP/AVPG PIN
1408	15309	A	1416	2	238	PGGRGSELLPRCTPAWVT\SKTPSOK

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						RRKREKPGSL*EKTLLFFCOTLVFGPKKK NGPPLLGRVMAKRRGGFHPPLKN
1409	15310	A	1417	3	394	NKHLKRCSTSSVIREMOIKTTNRCHFSE *KHW/IINMCW*ECGQTELSALLIRC*\
1410	15311	A	1418	307	357	WDESMVQPLWERKEYLKEITAESSWDPA IFLLDIYVPRNEASC
1411	15312	A	1419	341	3	LETRTAEKKKRRAGFEK*NLETNRNGN TISQMLRDVAKVREKFLANMA* *SKK KEKP* INMLSLLELEKDEQTKPKVRR KKKILNIRAETIR*KNSSKD*KKSWF YFVFLVGRGFPPLTRMVLFWHDFEPL PP*VIEGLFH/LPAERPGAFLRKMVPPY *KNKIPPPRINTFFFLKPPPPFFFF*DR VLLCHPGWRAVQSWLATASTSQAPAIL PPR
1412	15313	A	1420	405	1	WGEELVPSGRVHELFSSALRSERDTSV CSCGGQCHCPGAI PGAAKACRGDPAS RVGVBETGSTMGNNGFFSFFIFKPYFFRD RVLPCHA\AMAS*LTAAST*\VKSSF CLSLRSSWDYRCVSPHLANFKTF
1413	15314	A	1421	1	399	OPTLLTELGLRVPFPHPATMNLV**IN TILHYSYKNYFLFLFRQGLQPLQAGVQ WQNHGSLQL*TPGVSLSSWDHPNPANF FIIFLERQGLTLLPRQVLNS*AQ/CNT PASAFQAGIIGMSHCSWPYKN
1414	15315	A	1422	168	414	EWREKAGESLEPG\GGGCSLERLCHCTP AWVTEQDSSYKKKKKTPGGGKGVF/C* K LGGGINF*KRVCFCGKPTKKKTGGEA
1415	15316	A	1423	369	1	EHFCKSQDRDSVPKKRYIYYFMSVFMP INLTNMWIKFLERQKLS*QIEEAIENLNS IY*/PNESEFII*SLPITKAPGPGYTE FYISFGKEAMQILHLKLFQKRG*RHFSFN VLKTLSSKPEK
1416	15317	A	1424	403	1	KTEHSRYSTIPORYCGSSREFPHFLV HMKVMFLPKCAIALCLKOVYTFEETE SCSVTR*/EVQQDHGSSQOQPPRFQ\H PPTSASQIAETTALLENFKICIFYFLRQ SL/HSATOA*VQWRNHGSPQAPPFG
1417	15318	A	1425	401	3	FFFFKKNNFFFFQVEGKGRKLS*QFFP PG\LNKFSAPPLPGGGN*R/RPFFARLF FFFL*KRGSPLNGGGLSPFFSPP\R APKNVGFQGITPPPGNFFFFFSSEAES RSVTQAGVQWREPGS\QPLPPGF
1418	15319	A	1426	386	27	CRINGVLILC*CECKHAQTL*I*FGNFL QKQLDLTCDSTIPLGLIYPRDMKTYVH KKTCT*MFTAALLIITKSWEKLLRPS EWINSRHPYDRIVLSNYETHNVNKIQRH YAAKKTIV
1419	15320	A	1427	398	2	GLQVHATTKFFKFFVETGSCYIAQAGLE LLVSSNPPG/SSFFKCDWYRCETRRWPF LFKFSLEIFVF*LNHLFCLHLFLFLK LNLPCPMYLFIPALYLSLALFRND CDLSPHLEVKYFSKKDL
1420	15321	A	1428	401	70	HHAQLRCFFNSFVEVGVSLLCCPGWSQTP GLKRSSHNLNFSKCDWYKR/AAILTPSFF *IALF*ENPPNCHSLPTPLSPPLAALG NSCLHPWLPQPFVKGLSDSFVCMHPGS
1421	15322	A	1429	388	131	RGGGCLQRH\RGFKQENWFNPPGGRSS*

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Start codon, /-possible nucleotide deletion, =possible nucleotide insertion)
						PRSMYCPFWANGAAGGSLSQKKKKKKKKK KNYOKILSTQKTQKSRVFIWVSKHCTRHC CEK
1422	15323	A	1430	184	413	VSFLFDYFLFF*RW/RSHSVTQAQVQ* CDCGSLQPLIFYFLRQSL/NSVAQAG/ VGLSLQPLPPGPKQFSCLSLLSIWD
1423	15324	A	1431	76	533	SKRTTGRQFPDLPTRPPTPQGFALVA HAGG*WRDLRLSLQPPPGKFRFSCISSV LWCTKAFNFDFOIYFSFS*I*GDFSFE VNFFLEMGVSL/PARAGKLGSGKLP ASASE/SGGIIGVCHWAQL
1424	15325	A	1432	373	29	RQGFPPMGRVVLDSLKKKKFOIPNSKIF PGGGAPLVIPPSREGEAGKFF*P\GOGK AIKQNYC/HCPPTWKGEGNFVSKKKKKK EKIMHQK*RCVKDQO*T*MLLPSLKS IYYFK
1425	15326	A	1433	389	73	TDCPAIGNRHRDPVRPLLLSPHRKI/YA NLTYIIVRLTLTQSLDLM*ISPVLV LTVGVVGVVGVVGVVGVVGVVGVVGVV MYPTTIVKVNQISIGQKQKKT
1426	15327	A	1434	402	39	QAGLQLLASSDIPALASQSAITGVSHC ASPSISL*APLGLDTPSDPCPNLDSF EEHWSGML/SECP*TGIDLSFSS*VYV GYGFLDHRKVPFFITSYQSYPTPTQL IADVKFEQLV
1427	15328	A	1435	105	387	EFSKVAGYRINTYKSTIVILYNSNE*FEN \KKIIPPIIASRRKYLKI/OFKAVOD FYAENYKTW*RIIKEDLNK*KNVLC*WI GRL/NI/LKMVLLP
1428	15329	A	1436	242	2	EGGGFFWVGT*PNKMGFPQIINKLF/TR PPENF*KPF/LPPIAFSLGLGVFFFF *DIVSLCCPGWSA*AOQLLAALATSPG
1429	15330	A	1437	411	0	LLFVAQCECKWFSALGGPGVPC/LPAN QQPSVWVP*QS\EHVTVLQRFCLWPVLG PAYGQIWEPPVSTLK/PDPPGFK*FS*V SLLSAWDCRCP/PTDANFCISRDVA
1430	15331	A	1438	41	412	FFCTD*GSLCCSSMTOTSGLRSFHLFS PNCWNYGH/RASVLGLIFFFFLRKKT/C P*KKFL*NEDLLCCQGLLELLAPRDS PALGQPSVGTAIVTPRPW/LLFL*TONYLN SSRVFSPAPLKYEK
1431	15332	A	1439	1	406	HAYNIVNPSPVSLTGALSSLLMTYGLT HGCFHSITLLIGLLTNTLTIYH*WRD VTRSTYQGHHTPEQ*GRYGIILFIT SQVIFPTTRF*AFVHSSLSPTQLRRHW PPTGTITPLNPLEVPLNTCVLLR
1432	15333	A	1440	3	422	MEKVSVVWIDGTSHNIFLSQSLQNSAL SLFSSMKTE*GEAAEEKFEASRAWLMR /PEERCHHNKVVQVQ\EAASGDEATGSY PDDLAKIIDSGYVKLHIFNIC*KPTDT DIVDETALC*KKPSTYFLFFFLKQSLAL PP
1433	15334	A	1441	375	2	KVSSPRAENVILYNCPPIFFFLCQD/CH SVTQAARQWRHSSLQ*P*VGL\ASQVAG TAGAHLPSQNLIGRGIRSLA/SVAQTG VQWRNIGSWQPLPVRIKGFSSLSKSSW EYRCPPPCPD/LFIFL
1434	15335	A	1442	397	122	GOASLELPTSGDPPASASQSVRTGMSH

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						CARPILGSCISLFAYPFCFLKCLF/CC REVILL*CSGWS*TPGLKSSGLSLPKC WDYRCEPP
1435	15336	A	1443	3	299	WEKMFAMLYLSD*ATVSRPYR*LLQLNKT KYLKLKSQS/MNRHFTRGDAMANKHTK RKSTSLVIREIKTRVHYLLKRMAEVQK /SVKWCQECG*GGGKCG
1436	15337	A	1444	10	410	CTLFLSISPDSSAGGICIMLLPONTLNFK ISLALGVSDKCFNSFLIMTIVRNVPYIH GKXCLCYSCGACNTHMFLMHTHILK QPFLRRLGLTLLDRLECSGAT*AHCSLDL LGSDDPP* *EMFYIYMW/EMFYLLPRV CTHTYAHIDAHHTPBTIFFETGSHSVA OAGVQWRNYCSLQRPFGFRSSYLSLP GS*NRRHVP
1437	15338	A	1445	431	9	GPAQSLDSSVSPLGTISSTVKNRHNAYL AGLSGGI/PCDCFGLPRVWGSIGICQWH WAVSPTLS\PTVRPPLFRETLYFT*V*V PPLETCQP*HISHCRCVINWCEDHTPK KHLVCVHACVVCVVCVCLGRSRQS EH
1438	15339	A	1446	85	416	PGCLSLPKIWDYRCEPPRPHFFIFSSI OGPLTDFFLTPLEQVOISPTAKGFLKKI PFFFF* *RRGVPILARVVFKS*PHDLAA SASQKFGITGVSPhVHPFLY/CSSIQG PLTDFFLTPLEQVOISPTAKGFLKKI P FFFLRQGLT\ROWSTHLGLPKCWD*GCE P/PMPGLHCEFFKG
1439	15340	A	1447	376	3	IKSEITETESRKPIEKIS/RAQSCFCGM VYEIDKLLARLDRKMKMTQLNIRN*RD EINTDFDIDIKRI IRENYQDYGTGFNNL DETDIFLERHQPLKTQSEKDNLNSPIT IKDIEITV*NLSTG
1440	15341	A	1448	2	192	SKWTNKLKELP*DS*KKPEGNLMDIR FGNDPLDVTPKN/MATKGKIDN*TLPKF KMLMIRN
1441	15342	A	1449	411	3	VFLPFLPFPFCFLNFF*KGKGFFFKIFF* KKKGGEGPGLGPPPPPGPFKKIFF*IF LKAPLFPVPTLKPL/CPPKKKNWNNP PPFFCFVVKTKQFYFFFFFLRNRVLL CHPRWSVMV* SCLAVASTSQAQICP
1442	15343	A	1450	413	1	EA*TGECNPGGGACHEPR*PCPPPPWA TERGFVSKKKRQKQK/ SRIMECFQDNLK GFFQIFSVMKNKQGR*FWTK/VKMTKY NA*NVNGS*YWKRENEECYDVVKLE QSILS*YVKKAR*XPGCWMAAIPALW
1443	15344	A	1451	4	384	DPATFLPGTYPRENKTYVHITKTCTOMPA AVLFTVAETSKRPKCTPDE/VNKI*CTY I/MTYYSAMKRDE
1444	15345	A	1452	3	390	LDPDHGSSVSTPRGVITIGRGFWLLFPW VSFFFFFLLKRISSLPPNRRGGQNLN NKSPPPRGF*NFLA*PPQGRKKGPPH PGAPGDKNP/QPFFFFGEKKKIFNPPTG GEKKKPPSPFKWGGGGPN
1445	15346	A	1453	37	381	LILYINVCVVCVYIYTHYQMGSHVAE AGVQWCLGMW*P*TPGLK*/FLSSGD YRLTLPHLANLYIIFFFFEQGRQ/FFLL KLV*NSGPKATLPRVIGTLHTHFRPYR

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1446	15347	A	1454	3	400	GDLEFF TEMVLHTEMVLHISVWDPLDRPGRGVT WMLMTAELFLYGGTEAFSSSFV*GPCS ETVECFSD/L*A*GPP*NT*SPIYRFAS FLLAFCIYLETSP\SVTQSGGK/WQD LTSLOQLPPLRK*SSCLSLPSSNE
1447	15348	A	1455	77	398	RAEIVPLYSLSLGNVRPFSQKMYITYEQ LHAHTFGNLAEMDKLVERYKVLKFT*E EI\LNSPVSIKERE\AVISLPKOKETLG PDSFTGGFYIFKEELMPLIQLRFW
1448	15349	A	1456	397	69	CPPGLSLPLWA*AVPP/RRPAPPPPPF AGIDAGLDDPLQQTTHA/PPAAGSAP AGCAAGPARGAPRGSRPPRRGSAGAAP PWPPAAAAASSAGGSSAPCASSPAPPT
1449	15350	A	1457	400	2	ALFFWAPKKKKNFSPPPGKFFFFFKGPP PLFFFFFFFFFFF F*RRPFIILFYFLNGQNI PRDFFFFF FLRDRVSFCQPGWEMV\QLTAA*TP GLKQSSILSLPS*DYRWVPPC
1450	15351	A	1458	343	11	QGVHSRKYKETSILNS*KKNPTKRWKD TNRHFTKDNIQENKQMDVOARCQS* F*KQ*NFKSYAL*PKSEI/KKSVGTGN WRNSQIYDKLSTLQNI*NISSRLVNFPE
1451	15352	A	1459	109	401	QNYROLQWDRISTEVIDPCKYGLKLEP QSAKATEWRKDS*NHQTS/WWKESRTR KALEBITRKVNLSLASISVKTVDVHVIV *LKKKKKKRGRFKE
1452	15353	A	1460	42	424	CPAN*NSFSRDR/SLPMLPRLILNSWFO VVLL/PWPPKVMGLQ
1453	15354	A	1461	419	69	IFPLKKKKRGGVGPPLYPFLGAKRGG SP*KQNLKPPRPKHENSFFYKRRKKGG RGGAPFFFPPLGGKTKFFLPK/IKVS FNPNLFPPPPPGGKKFFFPKKKKKKK SRNTVWF
1454	15355	A	1462	1	277	CHTNFLCMSFPFAISHRLPMPHPVSR VAQAGV*WCDLGRG/CSELRSCHCTPAW MTERDSISQLIRKKKLIKIKKKKNKK SVIFLGGGS
1455	15356	A	1463	382	3	KAGGSINQNSPPPPPGGEKKKKPPPKKK KKKNPFWGGRILPHNPPPFER*R*KI FLGPKFLTPLGPKIKPLFFFFLKKKKK RMTY/HSVAQGPLLNKDTLQAG\LSKA* RSPPKSSWGQSHEN
1456	15357	A	1464	561	86	NDPILSLKAEKTFGKIQDSFLIVSSIA/ NKPGIENGLLS**KASTKQNPIMLRA/ LNVPFLRS*TRQVCLLSPLLFNIVLEIL AHIISOKEIKIKI*YKEKPIPLTFS SLFI*VKNLMEFAKKLELEINYNKVER YKINIKNILLAKNTWTLEF
1457	15358	A	1465	3	221	RFRHVSODGLDLT*STRGLPFC/WND YRLEPPCPAKTCLILNGSC*VFLCYLSC FKAQERPSONSWGAFVTL
1458	15359	A	1466	2	396	WNPANTHTPLGKTKSRFSLPECWYRRE PP\PGVLKFL/IQYRVTOHVGLGDWV QDHHPHIEICLHKSVI*NGIVFAYNLRT SSLTLPYLRRGLF/SAPQAGVQRHKL LEPLPFSKRSS\CSSLSKSDYR
1459	15360	A	1467	349	413	RLGL*PRKIDT/DHSLRDXDTG/WFGAV

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1460	15361	A	1468	403	2	AHACNHS TMAGHRRQIPRSGV*GQPGQ LFVBNWGGIGFSGFHPPLRLKXFFSPTP PKS*D/YRGGPPPGYVFFFLKRGFSP FGKVLTFKPPPGVPPPPHONFGFKRS /HBSRALFFPKRVF*YVFFFFEME PRSVPOAGVQWHDLSLQALPPRM
1461	15362	A	1469	423	3	IEFSFFAFSKDKGAILGSPSTLFPFRFNN FFCPDPTINKDIRRGPPPRPFFFRKRG GGFPHWAGMELSNLQEGPPSPQ/SV GF*GRN/HPPRAQFFFKKFF*CYFPF FFFEPRSVPOAGVQWHDLSLQALPP RFM
1462	15363	A	1470	13	427	RTRGLVDFDKTEFKPDKIKKKKA/GPFL RGNRSILKKJATPQNLFAPNPPPKFI KKVLSLDQKNLNPMPRMGNFTPSLLK* NKSSKQKITRDFRLTSLDQDGL*KIY KTFYFKTEYTFSSAPHGY/S*FDHKI
1463	15364	A	1471	378	1	FVRPPFFFSRRFPFKVGGPPLPAPQ FFFKTPRGNPLLR* KPPPQTPVGGAGK SPPW/VPPGPPKGGGVFFQQGL*KIS PPGPAPP*LVWGGESPPFKKKSRRGVV AHACNLALWEAKAG
1464	15365	A	1472	412	33	SRLSFFLSSEPHGPPSPGLGFATNKVAF C*/PPPPF*PSPPPKFFFF*GPKSVIYF YQR*PPTSRIFFPKGGAGPP/PPFNGFV NPKKK/LKPPSKSPPAKFNPEGTKL GFFKKKKKKL
1465	15366	A	1473	116	34	DWNKPLVLSNVMIGLMSMIITLLQLL LL*/LFFFK/WELTFPGGKFHQRVDSFQ GSLGRQFLLTKTEYHIFLLKVPNS KTEGAGLAT*IK
1466	15367	A	1474	42	428	EITMESINRFDUITF*NFCL*CVLMSKI NRQASSW/ENV*NOYVGEKILIFLYKE CIQINK/KLRPKIDTQVKDKQISEEGM QMANQHMIQC/QPSLVNKMQIEIAEGH HLPYINKDSKMMVERRO
1467	15368	A	1475	87	433	FGSFFPSDHCYSQRLPLHLVKVSTYRLQ KIRKIHKSPGNNEYFGGFFLFSFLFFF ETGFNVFVPOAGVQGDGL*LOPLPLGFK GFS/CPQPPRTFFFFFLRVGGFQKK KFLFV
1468	15369	A	1476	212	430	SLILMTSNGIHFIYFLFLLLFFFF*DR VSACHPGWRAMS*SYFT*ALTSQVK/QS YLSLSS*NYRHTAIMP
1469	15370	A	1477	493	2	PGAAAHACNPSTLGSQGGWITRSKIPEH PG/TLWNPRSY*KTMCGLEAP
1470	15371	A	1478	454	492	HRVGEEF/CLFETESHSLTQDRVQWHD LGSLOPPPPRFKQFSWHI*PHAW
1471	15372	A	1479	2	213	IDQERERLMEGDRERDTEAEDKMGRE /RNYRERERLRG/RRERRRRDRMT*M PRERERENLSLYRETYRDFETEWMDR ERQRLKRLL*AVIVPSHSLGSRRTKP PQKKR*REGERKSEFLIQRDI
1472	15373	A	1480	77	453	SFGDSLTLSPRLAVQWYLLGSL*PPPE LK/VSPSTASQVIHYLLFFFFFGKKVS FCPCGGGGSPGPPGLLEIFAPGLMPFFCL NPPKGWVR/RPPTMPLFFVFFIKRGF SPGPRGVSPFEPGT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USNN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GGKFGPFKGAPPFFFFFFFQDGVCSVAQ AGVLQ*AEIVP\FPPT*ATEQDPVSKKK PTRPPTRPPTRPPTRP
1485	15386	A	1493	3	428	IKSP*PDRFIAEFYQTFKELVPILLRRF HKI/EEGTLPS*FYE/ACVTLLPKPKGD TTK
1486	15387	A	1494	3	417	ILNNARLKPFLLR*TRQGTILLSLFLN KI*VLEFLAGAISQEKIKVQVRNEEM SKTLFSQTT*S*GRNPFKILPLPKMSV N/NFIKVTEYKVSIIH
1487	15388	A	1495	429	4	PFCLGSKRFPFFFPNPRGGK*KKKKIV GPPRGGPPPLFPLNAKPGGGPPRAGSG PPPKSGNPLFINPKN/PPPGGALFQ SRFLGGVNPKILFLPFGGKFLTDGPFPS LPPGGKKKKRPFQKKKKRKRKVKKKY FL
1488	15389	A	1496	3	433	FSKEDTPMNVKMKD/CCTSLVIREVQI KTTTRYHLMPTRMAMCIYFNYILFLK/ SKNNKC*RYREIGTLIH/AQWKYKMLQ LLW/KTIWQLLRMLNTKLSKDQE\IPLL GI*KKKKKKKKRGGFRFGINFDPGVE RINFYNSAPK
1489	15390	A	1497	3	326	WPACL*AAVAALLVPEATRLTMGNLT VCTPHSIAELLSSG/DLWLTDMR/LLK YQALLLE\DLQRTFTCLNPATP/VPEE TGEPEHDCWVVQGTGKRNNKHCLYSL
1490	15391	A	1498	345	22	KSKWLIDLHGCKTLR*YRKPTK\LG HGNDFLDTSSNAWI/RKIDKLOFI NVCSGKVTVKRMKR*TTDRDKISSGKIS DKRLCKIYIKILTQQ
1491	15392	A	1499	194	432	PVVVCVVCVYVCMCVETQS/HVARAGN Q*HNHSSQL*TPGLKQVSCNLNLSWD YRHTFN*FFFF/CNPLYERGGVS
1492	15393	A	1500	2	417	RD*FMRFK\EKSYSCNKTQREAAANV ETMASY*EDLAKIINSGSYTK\SQIFNV DEVAL/KMPTRTFTIVRKRSPGPKAS KDRILFLG/ANAPONTKWPVLIYHST NPRAFKNDKSIILLVLYLNSKAWRIAH LF
1493	15394	A	1501	414	0	SSSSSSSSSSPKMTTGALQF/LLSRTF LKDSSEESSQ*AEI*AVHLVVHFHWKE KWPDM*LYTDSLAVASGLAGWSGTWKK HDWKICDK/DWGRGMMNLS
1494	15395	A	1502	3	125	RLGLPKC*DYR/RAATTGLH*F*SWKE ORPO*LALGRKPVNRNKNIKYIHIYTY TH/PIPTNVYICITYTHIHTPV*YTHIY IIYLFKVLVFGFLRRSLT/SVAQAGVPW RDHSSNQPRPPYKQLTCH**LASQSARI TGGSHHTWPALILKLERTEAPVISFRT TSK
1495	15396	A	1503	406	172	DIILDR*ROKQRLRLRQKQRETETE/RR DRGRERQRYRQVQRQRQRQRQLRRH Q*QRQIDRLRQ/RAERDRGRGRDRDR GRDRGRDRERQRLRQRQR*RRQRHRQR /RRDRQRQRQRDRGRDRDRDRGLR G*DRGIDRGRCDRGGDRDRGLDGS DR
1496	15397	A	1504	3	420	ITGVSHRAWLPS*FLKFFVVMESHVS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AQAGLK/PSGLKRSSHLDLPKCWDYRHEP\PHLAFFQFF
1497	15398	A	1505	407	1	PISIIYHSDPGSLKSYTKSTLPVF*KCNKNTWLTAYLFTAWPKFKFPTVETVC/SRKKSPPFKMLLLIANAPSHPRALMEMHKEIPVVFMSAVTSILQPMQDGVVLTFSYYLRNTFCKAIAIDNDSGGSGQIQ
1498	15399	A	1506	1	408	PPGFKPFCLSLPSSWNYRHPP/REG*FVFLGGTRFHVGYTASQHLTSRETHAYALQ
1499	15400	A	1507	2	416	EPRSHHCTPAWLKSTLTSQKKKKKKRKR MVFTGRKGLFFGN/LQNLGTLRSREYPLGPGIKNRLAQKKRPLFYKKRF*NINPGGGAHPGGPKSWERGGRKI*TPVGKYASNPEYHICIPPGKRKNQNP/LQKKKKRRAD
1500	15401	A	1508	276	14	SPPPYFLLR*GRKGRGQF**LRLFFIINLRQCL/DSVSAQAGQWNHSSLLQRTPTCPK*PFSFLSPSSWDYSHAPQLLAFYGANCFN
1501	15402	A	1509	1	391	NIFREIMSENFPSLMSSENFPSLQKTESQIQEAQRTPNKMNPKRSTPKQVILKF*VRE/MLKTAREK*IVICKGTTLRPAVDET AETLQIRRE*DTFTFKTLGKKKKKKTLDP AKLTFPSILVFKKTRGGSR
1502	15403	A	1510	2	419	PRVRSRATNVISKYQKHKKNTSK*IKDLNVKPEPIKLL/SEKTKGKLLDIELGNDFLDS/TPKTRAPKANLTP*NYFKLSFLTAKETFN\KTPTKRGANHISDRGLISKIYKELTIQ*QKNNLISK*AKDLKRHFKEKDV
1503	15404	A	1511	392	122	SVSLCVSLQSSGMFRCL/PTIMPLRK*EQENPLTSAGGCGCSEMRSHPTPAWVTQODSVSKK*INK*IK*/Q*LRQNVIKPSPIFCEOGKRRK
1504	15405	A	1512	2	281	GGCSELRSCHCTPAWTT/SETLSQKKKKRKIKCIECNTLKH/ILSFVCGGYHSPVSTCL*WSLGRSLKSLERHQLNDLPYPIFONETNIH
1505	15406	A	1513	242	382	QQPNLG*LHPPGGGLKGFSLTLRLRSWK NRLPPQHPFFYCFFRKNKV
1506	15407	A	1514	1	388	RTRGTERTD/RFRERRRERDRREGRYRW RYRERERHRRERES*V*RDVRDGDVRID RERERQSERERL/RERDWRDITYIYRE TETRERTGEDRD/EREDIVDRYM/RD RDRDILRE*ERDRETDLDSK
1507	15408	A	1515	4	285	TRXQICNGDKTALY*KEMPSRMFARVELMPGFKASKDTLTLRLRPNAVGDVNLKPMMIYSENPRALNKVDKTLCLYSTNGN KAWNTDYRFT
1508	15409	A	1516	415	2	MGDRSLPFSRVFLFLAPCFKGLIFHPV*FGSVRSFIERCYR*QGRNEFWGVPV RVKASSRAG*VVFSSAPPLPF/CFPE TESCSVAQAGGQ*CDFSSRLPLPKFKGFLCPSLPDAD
1509	15410	A	1517	1	324	PTRFEMGFRHAAPAGLELLSSSDLDPTSA SQSGGITGVSHRTWPILASNNY/SMDKLCAI/CERFILFFLKNILLWILIFIFIYFCLIK*CITINFQNSLLPHSHILYI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1510	15411	A	1518	2	163	ACRYFWLNFVLLVEMGL\TMLASDLERS G*FQ/CDLPASASQSAGITAESHGWP
1511	15412	A	1519	425	52	VLRGQFLFQEARLKWDRPGGMAAPPEN EPPLGV*KGPLEKGQGNPPGPPRGNP VFSGKPKITPPGGGAGVPPFWGGGAEK FFYPGGPRVQOTE/RKTPFPFPGKQGT PLPQKQKKKKPWSL
1512	15413	A	1520	3	404	THASGKSNIRGLTLFVFTFYKVAIVR/ TVMP/WLRANTNRQNR/L/DGPEVDPYKC SQMIFDQGAIAQ*RTDNNLLNK*/ES *TSTCQKKKKKNQFR/DPAFLITYKFNS NGRKNLVRIGTK*VKLKKNIQNNQDGLG
1513	15414	A	1521	332	39	TSRETGNFOLDLTAFLNEVGVLFWRKGL KGKIDIGIGTKEMP*FFI*LLMFSYIVI ERERKPE/LSLSPSLECSGMLAHKKNS LPGSSDSDHPASRVAG
1514	15415	A	1522	482	0	RARTSGVLLSCPGWS*TPDLR*SLCLSF PKRWDT*ATVPGLLYSLSRSP/DE LKGCEKSRTPA
1515	15416	A	1523	1	417	NKC*RCCEKGMPPVYYNECK*QGPFWK TKERFFKKNL/NIELPYNTAIALNMRP Q*I*SQ*RVKCSMLCAT/PTPNK*IKT MH*VCLVEYSSPLKKV\LLFSTTWINLE DISSNK/LRHRKSSISRFLILL
1516	15417	A	1524	1	397	RDSTYQGHHTPPVQ*GLRYGVLFITSE VFFVAGFL/WSAFTRSSLAPTLQGGHW PRTGITRLNRLEVPLLNTFVLLASGVS I T*AHSLIESNNKRIQALLITLLGLY FTLLQASEYFESPCITISDGIY
1517	15418	A	1525	2	376	LKARTGQKGLLHQTVSKFVNAKERFWK ELL\KSATPVDI*MIRKRTSLITDMETV *VV*REDQTSHPILPS*SLTQSKALNLF KAMKTRDGGAVE*KSEANRGWFMQFKE RSC/RFCNKKVQG
1518	15419	A	1526	3	386	ESMLKAKTGQKGLLHQVSKFVNAKER FWKELL\KSATPVDI*MIRKRTSLITDM ETV*VV*REDQTSHPILPS*SLTQSKAL NLFKAMKTRDGGAVE*KSEANRGWFMQ FKERSC/RFCNKKVQG
1519	15420	A	1527	127	388	KRKQINNLILLQFKELEK/QEETKPKAS RRNKKKIRVDLLIKKKGPLEGVKKKG GFF*RTNKRDKPLLKLPKKGGGRITKF HKTS
1520	15421	A	1528	3	402	HENHMKTCSTSYVIRELQIKTMK*YYT PVRTTAIQNTDHTKQWQ*REQ/GSLIY CW*QCKMVQ/PLWKRWVQFPTKLHSLN I*SAVVLGLIYP/KSGKFNVHTKTCT*M FLAK*PQCSVDDEERKKN/WYMYGFE
1521	15422	A	1529	2	365	IEKLYRSQAKFFCRDVSLLCCPGWSRTY GLKQSSCFGPPKCDYR/R*AALSGRLL LTISSH/REQIEQETHYPEKSAKLFMQ DGPFRK/HPTTRPQASNIQKFSFLLR QSL/NSLAQAG
1522	15423	A	1530	1	418	GTDTE*ACDKIQKPPFDKRLNKLGI/IRK KHLQDLKYL/WKNPILASILLKSRRLKSV RLRPGDGRQGCSPFPAWLFNIIIEGLARA IR*EKQKQKQKQ\QIGKKEVNLISLFIED IMLYENLKESTKKPIIINEFSKEDF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1523	15424	A	1531	381	3	RP ILQGFVIRKSKIFQKACHTSDLWLTN LSCLMHKGLEPHRLYSSTVLLFLRKPV MRKTTLSCCFLT*DFFLPLPPCFRR*F ILLIF*LYFCKDKVSLCCPSWSKLLP/Q QSSCLSLPKYQDYKA
1524	15425	A	1532	38	479	DEACGPDPLYLTPVVTQWTKD*TRNKG IQPLEENGK\FDGFSSDLLDMTPKTR ATKVKL\NDIRLNFCAKSDTINLSLLC R\KR*PVEWEKISANHISDKGLISGIYR QPFLNSKTSHLI*K*ARDFNRHPSSEDI QSALYRWVL
1525	15426	A	1533	105	447	LIFCRVFEYLSHLHPQELCLSLALFSR FTFCVIIICEVDVWSVIFKVPFCSKRNKV AVHTMLYIQIFVSLFI*PQNWQKPCPA TVERINKMWYIHIV/EYISANKR
1526	15427	A	1534	76	471	VWVCLLSLEGSQSKFNSIEFGVLLSSG GFSAMRLFFVFLRQSL/NSVQAQAGVQ QWRDLSELQPLPSPK*VLKQRGVCLFV CFETESHSAQAQGTQWCLDGLSLQPSPE FKRPSCL/SLSPPPWSG
1527	15428	A	1535	45	338	SNNEPFLDVTN*RVVDFTQPMNTSSV VGRRRSKALPKAKLAPKKVMVTIWS ARLIHCSFLNASETTASECTQQIDMH *KLQRLQALINRK
1528	15429	A	1536	425	1	FFNITFHVSVSFPLSQKCILFL*ILLKS IVIGNMNRNFORSVLRK*AKDMNRHFTDD HVQMAS/KHMKRCSLVIGEMQIN\TVS YHYPPIRMIVKVRNSNTKC*GCGQTGS LMRCWW/NK*NQLLWKTGIPPHGLVSTR SRVF
1529	15430	A	1537	4	443	ETFDVHYQCGGIRFFSDQLQLAGRTTAL FKAVRQGHLSLQRLLSF/VCLCPAPRG GAYRGRQVSLSCGGLHPVRASWLLCLPK *AWTMEGTSTPASLPPCSLISDCCASQ RDSVGIGSEPGAEYNLLVPRFLSPSEK RSIYVGV
1530	15431	A	1538	487	3	TQNGVULLSAPRSVFSPTTLR/CTLQAQ C*AFWGGGTQQAASSTAAMAAMPGLGIW AGGAAGILPKLGFQD/LPLSAEADPAGK ELSIGRQRAWREQPDQSAEPFSPQAPRP GYPSPQPLSMWRGPGGANPLARLPGP VIVRLKASSERQKRSBGSGPLG
1531	15432	A	1539	394	489	TYLYIFETESRSVAHAGQWRDLDSLQ SPFG
1532	15433	A	1540	475	202	PGGWFSPDDNFSLEKNSQGGPPVSHFP PPPGNGEGGKTPGAGHSGI*NPPLKTI N/LEKGRGGPPGLNPPFPKEXPRGG KKKKKKKK
1533	15434	A	1541	14	468	LSMWNNSRLKARRLVLQSVVNA/KERF LKEIKSVIPMNTLMVRERNLIVAVEKV LVA*VKEQTSHTNIPLCQSLVQSKALTL HSVKAKRG*EAEEKLEAGKHWFLRFKG KSRLHNIKVOGEATSDGELQOVITYPDL VKIVGEGDYPKQ
1534	15435	A	1542	479	141	RKTDSDWLK\SFSTAK*AINADGGQT EWEKTFANYASDKGLISRKELQKINKK ANSPIKK*AKDTKKQPTMMKKCRTSLII

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RENQIKTITMRVHLTTESE*LLIKSQGRA L
1535	15436	A	1543	17	474	NPKKKKKKKIDLLDTYYTLYPK/AEYTF SSEIHKNLVYIN*LRANLNKFIN*KIKT ILSDHNRQPEINKCNKTKR/RVT/TQK FKNLILSNYVWKGELQTQIAEFLKRNVN KNIT YLNT*MTIKVLNSGGST/ALNTYI DKNFKKRVPS
1536	15437	A	1544	89	481	ICLVKVISLRQENATSVACIVSCLSESSR ASENLVLHNASPNSCGIGIATPCLCNV SSGNKITDCYD*LSSS/WLGFPPFFFLK KSFLEVAQAQGGGQNLG*EKPLPGLKQ FLPPPRANFCFLEKTGFPLF
1537	15438	A	1545	1	300	PPFPAPXXCRPY*XPXHPVYHSSWRHG SGAAQGAVALAGFGVGVRQGPAAVSIP LCPENQGREFGPGSHVAPSAFLPSLRS LTGGQIGGTRAAQAVG
1538	15439	A	1546	2	436	GAPETKSIITGYND/RLCTIKFYNLDEM DKFLVRHKLPLKI*E*IDNLNRWITSQE TDW*I*QQSSSSSSSSSS/PSSSSSRPN GFTTESYQSFFDKLPIICKLKKIDKE \GHFFPLQL*GITQIKPDIYH/IENYRP ISLM
1539	15440	A	1547	54	419	PATWEDHLSQGGRCDEPRLHHCTPAW RE*DPTSKKKKEK/NDQ*LLIP*S*RL *RSSHQTSHLMDWNSEAGR*EATFLRSY SKL\KELELELLILDNDNDHNSD*YLL SIYSIPGTVLS
1540	15441	A	1548	37	339	KRWKCLRA*LLMRPRHAD*LNPDGVGYS EL*SRHCTPAWVTEQDLVSISTRNKNR HTLEYSHQHSYG*P*TG/EESEYPSAL* QREIIDIYSFIQGMTDQL
1541	15442	A	1549	477	1	PGSHDLGSYT*PQ/VVSSPEVTSRDAPS HPSAPKFCNSNPCRGRWLTSKQPKLRLT SVFGAQPGRGTHLAGAGAAEAGGHS SRPEAALCRPLPLPMTLTSHPLLSGPG RLAWOCNGRR*IKGGG
1542	15443	A	1550	430	8	CWFGSSGTPDLK*STREGLPTCNDYRHE PLCPASKTFLSPQIETFPYPLNNNAHSFR RPALVNYSLSVSMDLPL/AFTNGIT GYVASPAPPVRWGHSHVAQAGVWPNLG SL*PPFPRLK*SSRLSLLSSWDYSHMT LN
1543	15444	A	1551	2	419	ETSPSLOGWLGVLFPKRGAKTSRFLIYR PQGGSKFDGDFNPPGEIKTPPAKKKK KDSARSPPARLQA*GAGLWDARASFRP FQAPVPLSAQPRAGPLAVGTSRDGSSG PTPGQESAV\PWREXHPQQPPQPG
1544	15445	A	1552	2	387	FRHVAQAGLELLG/SSDPVSASQSTGI RGMTYRAQPL*LFNSKNLSLSPKV/L QDYMW
1545	15446	A	1553	393	2	KNPIFFFLKQGFPPFF*LEGRGKFLGPC HLCPFGSKKG/LPHPPOLIGAPPPPS GFFFLKRGFS/LFCPGGSFSLRRKGPP PALPKF/GFLRVTPLAGGNPSFFFF RDGVS LCHPGMSAVAASRLTA
1546	15447	A	1554	1	427	LLLLILYIAVEAVT*TEGAGYPPLP SHRGASGHRATFALHITGGCCI*GMHMC

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FIKYFRPTVEM*CSYKILVLIDTGLDHPRLIETIK\FINLHVCLFNTPIVQPLPR
1560	15461	A	1568	453	39	TALYWKKTPTSPRTIAREEKSVPGKGAHFLPRGHIKFKLVSLKLDHPND/R/ALKNYAKS/TLAYKNNKANMTHLPSF\WFIKYFRPTVEM*CSYKILVLIDTGLDHPRTLIIETIK\FINLHVCLFNTPILQPMPRQ
1561	15462	A	1569	1	352	FGTRRERERERERERERERERERGGGAGHQIPSTIEGQHKIVGAIY\CREC\GRKISGSTSYIKVWDIRDSAKIRTLTSSGQGISGDACAATFTTRITSAQGEH*INQIALRPSGT
1562	15463	A	1570	394	3	TLDWPOSRRGGSTGKPVVYVCCCCCCCCCFNFCQEAENNAEGLIHNQAGRTKDGSFAPSHDH*A/PRGTEV/DLESTLQTSIKQVESKPR\EQARTGAGGQKEKATQNPESVLTSMYTKSQGSEGRLPGRN
1563	15464	A	1571	399	2	KHQLPVFWQYNKKAWTRTLFLDNLHCCFVEVVRKYLASKGLPFKKVLIIDNAPGHPPTPT*VQY\KGIEVIVLPPNTMSLI*FLDQGVIRTYR\SHYTQYSMORTISAMOE NSNKENII KWKDS TDDDAIVA
1564	15465	A	1572	37	400	RGTITGEAASADQBIADKLSDANKIMEKRG\Y*LPEQVFNDESTLFWG\KKRPQRTLLSKEKKRAPGFKTGKDRITLLFC/ANAVKLIIRLTALTYKAENPQALKENVKHQLPVFCITTRGL
1565	15466	A	1573	84	485	AGHKDSRPHQTOEPSRLHLWDPAFGLQVELPAS*GRALLSLSPWVDGTGRGAGCCTRRGSGSPTGAHGAGRLMHGGLQVPSAPAPREGS*GPARYQAQRMWARTAGGSPSTASAGSRVPSPHCPGP
1566	15467	A	1574	3	463	TPAGGLRDPFSNMRKHAYCGCCV/CTILCVGAQNKNRVACGLYSTCPRLCVHEHICVNE*VCEHV CERESVRVCSETH/LPLCA*TCGPIFGCMSEKHVFSYTPCVHRVCVCVHLGCCVC/VCVCVCVCVCVCVCV
1567	15468	A	1575	1	383	FLSFGFAPQAGGQGHNNH*GFF*P/PKAKGIFPHPEKREQRVHATFPGKFLDFPFFWKGGNLNIGPKNLGPGGKKNLVSPPKGGGKKETPGPGGVFFWGGIFFFFPPPCSPG*PLSLLKKPKGG
1568	15469	A	1576	35	469	RIPRCHQPVGLGCRGGAQPGGPDAA DSHFFASPAH*ISTSHRDP IGFGRGPRCRNAGAGPRAHTAGICAPQPNMS*SRHH PWAAAPAGDDSPITSLGSHVFGKSSD GCRQALRTPGSPAPSEAEVGGSPELRS LRPAAW
1569	15470	A	1577	473	62	SLEINPYISGGLIFNQHAKTNH*SMRKE/SFFNKWCLDN*ISTGRRMKLDLYLKP KILNSK/LKDLNIRDTTMINLHDLGFGNGF*IMTTK*AIKEKIN/WDFIKI*NFCASNDIIKKVKRPNVATYCNPSSTLEGPR
1570	15471	A	1578	59	426	LRRRFGAPLSFFAPQPEMKKGFS*KEFFSPKALNFGGCVFPFFPPKKRFPKXNPQEGFI PFELKKKKKTSQFP/YKFGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Value, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PKESFKRAPPPFFPKGGPPFLVSNQWT GKPRLP PPPPKETQNPSSFIQGGQKKGK GGPQSFSPPIKKKKKGHSRSTSPRV
1571	15472	A	1579	2	419	KANKTKNAYFEGINRMDRPQVILKKRY/ REKT*IPSI GEEKGIMSP\NSEDTRKRII KECFQTYAHRFPYSLKE/MDILLES HKL PKLTQ/EETDSLNSPV
1572	15473	A	1580	129	403	YMFPI PINCODHPK*KKKKKKKKKRGG /RPFKTLRGPKLNRAENKFF*KGSI KKKCLLEILKKLFFGGGEKNCKNPPKKK PSREKKK
1573	15474	A	1581	317	76	PRFFFFFPKKGGFSPPPFFFSRPPFF PPFLKPPRRFFFFPFPKKNF\PPPRP LLEFF*ADPPFFFFFPFFFFFV
1574	15475	A	1582	259	377	PREMKTYLTKKLGYSIHYH*WGGCKM VQPVWKTVMQFLKGLNILE*DSAVPLV GM*PREMKTYLTPTKLGYE/MFTLSLLI IANK*KQKCPRMNKH
1575	15476	A	1583	1	415	PIRPTTSSICLRQSYLKLAIYSSISHI ALGV\TAIINPT*SETGAGILIA\HG LTCSLFLCLANSYVETRRRIIILSQGH QTLPLLAF*LLARLANLAPPTINLL GELSELRTTFS*SNITLLLTGNILGT
1576	15477	A	1584	216	406	LNLLPLVLGGSSCLPPFCGN*KPFPEP G/LFLEKKGFSPCGAPG*PPALRGPP PPLPRGLI
1577	15478	A	1585	383	3	KKFGYFFYWG*KILK*PFG*K*SLPHR KSPFFFF*GRVLLCPGWGRTTKGHGS QVT\LPAAAMTFQV\K*SSPLRLPSR*G YRQASPWGNNFF/CLVESLMLPLGLIL NYWALAIKPSGPPKVLG
1578	15479	A	1586	126	413	NPTLKK*MKENRMKNEQSLRDL*DTI KLTRNRCILGPKKEERKGAEGIFGEIMV GNSSNLIR\ENINLNI EIAQ*TLSRIN* KRATLRHVIMKM
1579	15480	A	1587	242	409	GWMTRFRNPPFFFLRGSFTLVTOAG*GG DFG/SLRPPFPLGKRFSCLTLPRSDYR H
1580	15481	A	1588	2	338	ELEKKGKGGKRRG*RSNKKRGGRLGQ KI*SPCFRLSFLVDEKGPVLQDSL GWMKTP/SGCEMTDSSQY/YRAFYVL KN/QRVGSVDVGEIEKDQVEKNQDPS CPRL
1581	15482	A	1589	360	0	MNFLEQLKPPPKKLTITDSYKAPRPF PPPSQKGVPPPTLFFGPPPGFPFPPFLN PPPGFF/CFWAPIKKFFFPYVGG*TNVS LKGPFF/L/RPFFFF*DGVS LCHPGWSS SAQS
1582	15483	A	1590	75	412	VEGQHNCFAAQETINRVKROHTELELT FANWSPDKGLIPRTYKELKHLNRKHSY *KWADDLRHFSKETYTPPKTYSTCYC *P/SITIEN*KLKTSNIKTRLQGGHKRL ER
1583	15484	A	1591	309	1	FSTQGAHMVQCYNDTFHDAEWTSTIEPV TQIVNNMLPNR*FFNCPHFPPFPFCSP/ LVSFLLLRDRVSLCCPGQSRVGF*K/S TCLGLPKRWYKCEPHVA
1584	15485	A	1592	2	415	LSISLSIFSFLP\FSFLLPSLSLSLS

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						FFFLSFPFESFFFFHRAALCHLGSWA MA*SWLTAVSTSQ\VKOSSHL
1585	15486	A	1593	3	396	HS AFLFFL*DRVSLCHLSWKAVAQSOLT ATSTLL/VLKQSSHLNLP
1586	15487	A	1594	300	62	KMTGVLKSSCGKSPKQGVNLVCVCVF/ SPKROGLAS/VAQTGMQWDHSSLOPPA PGLR*SSCISLSSWDYRRVRPRAPG
1587	15488	A	1595	1	412	FDRFAADQKAASALKASGVQQAQKAGT HDSWLQDKVLMWMT*VS\QQEODPTNL YISNLPCLMDELQLENMLKPFQGVISTR ILRDYSGTFRGDGFARMESTDKCDAVIE HNVNLLIMTPPGVSAPTEPLCKFAE
1588	15489	A	1596	428	2	GSESREPENFLPSTSTSSLLLVHCLSR CVVNSTLSCVPHFPHLTFNSHLLTSQP RRVHFC*LSLSIIISWKLNTLPGVPIR ASEIFGLRTIRNPFPLSHSVLPFFSL ESHSTVQQGVQVHGLSLOPLPHGCQWL SCL
1589	15490	A	1597	2	442	QGS L*PHPPMLK*SLTSAF\NYRHVS PH LANYPLFF* KQGLAVLGLALN*AG/C HLPALASQSGITGVSHGAWLFFFLNQ CYLI*FLILIF\ERRNSPVAVHVLVNGD LGLLKPFPPLGMLGFSCLNLLRSGKYKPP ATSPGYIFC
1590	15491	A	1598	419	121	NLGYPRVSPPPFPFLNPPPEFYGP PPKKK FY/PPPPPAQKIDPP*TPPPFFFTGIDG SHYVAQGLELILASSDLPASALQSTGIT KHEPHLAETIELVFL
1591	15492	A	1599	45	397	DRVSLCYPGASAVV* S*LTAASSN V K* SACSFLLSRDGYMCMTHIANIKNF LGRVRGSHL*SYHLKCLCK*RTKEGFL SPFWGKRHPLGQKNILNRLKVFFLPG PPKGLGY
1592	15493	A	1600	3	397	SRPRGRFSIMLTLSWHS*VCRALAAARE EQWSGCGKSHF*LEVNFWVSGIDREV/C GY/LKTVLGEDLDYVSTQI*D*LMKPR CPEKQDESLLKEFGGA*RLNVVRFGA VAHACNPNALGAKGRIRPSG
1593	15494	A	1601	244	2	KTKTSFHSILDSGGLSYNSFQI*KKM IFK/YLHLRAVRHVIRFTNLREQEV LRAAREKG*VMKKGKPIRLTADLSA
1594	15495	A	1602	435	2	PQEAITYPTQHTPTGYAICRIARHGSRD Q/SVEMKWHPLTITPSGP/LGKSLPLPI PVALCFADLEVFIPKGMLS PGVTIISL NWKLRLPWILQ*RIITPLARVIPPYQ RIRLLNNERKKS YVWNTRDPLGHLVVL PCEMVIK
1595	15496	A	1603	288	8	EPFLIREMQIKFTMYRLTFV*MD*R*W *GCGRGTLVHCWN*CKLVQSVCSERSSK NITIELPCDPVLLGMHTKERKLRPCG WTRGVGPGYC
1596	15497	A	1604	411	236	LTPSEHFFSG*F*AFDRSSLAFTPOLR RHRPPTGLPLSLLOQP/LLTPSVLLS* GGRFKGNFTPPGQGGKIFPMGPPKSNP GPGV
1597	15498	A	1605	2	437	KCLRISPCAGRRPWCFSFEPFVCMWEL GVPOVG/PEGP*GEG/GPEGGDVQLAQ GKKKKKNTLGRGVPFPEKRGFSLTP

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						WFGPQQLWEFCNLNPGGFLFLIGGFQKGP KVLIGKGTGPGPKKNNRPRKRGSGLGPP GKDDFFL
1598	15499	A	1606	31	467	EPFGRRFRGGGCSLELRVCTPAWITTEG DSISNNI*LVNEN/HTVNSWKSCDS
1599	15500	A	1607	418	32	VGVGGLLETTSSDPFASAYPK*WDYKR\ DPRAPNPNNILKAQSNRSPPRQR*PASS FSNQNSCMHRCISLP*VLFLIFFKNRP* NNSFGYNSSGWSGLNINLSC*FWFLFG NSDTEIRICRSFHRGREV
1600	15501	A	1608	379	3	FFILSPSYNPSSTELP***SLQSPFLFEP YDFPSVMMFSLFFPNLKSHITVAQAGVQW RNHGSIQFRSPQLK\HPASASAGITGM CHHW/LIYLCVYLFLENRSHCVSQD*V QWNNSSLOPETPK
1601	15502	A	1609	456	99	FFFTFFFPBHSWGLGGLG/L/EPWTFP SGLGLKGSPS*SPPAHRLSGAOLCPVLAR APVLGSPQMPGCRKKPTARGSPWRKGV FVMSQSDPLGFPSSCOELGPRQSTQGTF PGA
1602	15503	A	1610	1	420	FRFDGAAGQKCSSPPRRGGRGAEVLLT SQTGROGRGAPHISDNGQPGRDAP\PS* M*WRPGRGAP\PS*VGWRPGGDAPHF\Q TGQPRGGRAPHIPDDGPRGDAPHFDPGV GAGORLQTRHFGRP\TAANKVKVVTSLR
1603	15504	A	1611	426	3	KNPFLLEAKVSNFKNPALPGEORDS VSQKKKKLLIHKKAHSKH*FFICRE\C ESALLLHQNIHAGGKSYVCNK*GRGRFN KSHFTYQRTSHGKKAFL*KECG*DFL*K AILTAYQKTHSGKSFVCKECCR*DPTQK TK
1604	15505	A	1612	428	273	HHA*LIFKIF/CVETRVSLCPGWS*TP ELK*SSLGCPKCWDYRREPPIRPT
1605	15506	A	1613	311	4	ANKFKNLNEIKFPEAHNLKPKFTQEGGLN NPVSLY*KN*YSRLRFP/KKKKSGPDD FTGEFN*TSKEEVPSLHKLQKI*ERNR LPNLFHKARVTVQVSKSEM
1606	15507	A	1614	338	88	PMPFFPSKGG\GFPPPTGRRKKKTFRFP PFGKFLGP*KKRGFPFFERGGP\NPAPG GPFPFNPCKGCKGKSPSPSEGGVFFFF KKGSTCLYSLGLLRLHSCNLNGGGC RE/PE/SHCTPAAWTE*DSVSEKKVYL
1607	15508	A	1615	2	162	PEVREYLTSLGLFFKVLITLDNAHSHSE PQRENTGCVNVPVLLNPNRSLIQTLDOG VTRTFKSHWTMYSTERIANAMEENPDR S*KSRIMTFL/IDAIVMTEKAMEATMPK TTISCWKLCDDVVDHFTRT
1609	15510	A	1617	390	1	KRNCFGPFLTPFGQRLGGFKFLK\HEF YYRGERGGFFPSFNNKGPFPFPPWGF LGALKF*RGVPPSKPFPFGGKPKFLK FPFKSYGGCFKCFLGFPFFFGPPPOK KKKNFTAADLEPNW
1610	15511	A	1618	468	0	MKLVINWLLLVALL*GKKHLGDRLEKK SFEKAPCGCSHLTKVFSSTVAEY IVAFNGYFTAKARNSFISRAKSSSEVN WRIIPRNSPSSDYPT*NP/VALKKKKK AGV/LPLENYSIITRV
1611	15512	A	1619	421	2	SSRLSLPKCWDYRREPRAQPRLLKKI

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						S* * E P F F L I L K C I * L R T Q G L R G H K G K L N S T Y V L H K F M D * * L G Q L M N G L N M L D E S S F C N V L K H T K Q \ W R D Y Y F V C L F V C F V R Q S L / N P V S Q A G V Q R R D H G S L R A P P P G F A P P S
1612	15513	A	1620	406	2	Q T K K A S S N G P I N G P G A A R K K S Q T F A F L A K P G A F P S I L L D E K N R P Q I K P P A C P F / S I R E S Q T S Y V P F F W S P S C G F F F G K G K P E P L L K E A G V P L F L F L F G L * D V S L C Q P G W N A V L R S Q L T A E S N P H A S A H A S
1613	15514	A	1621	411	0	P F F P K K K F S G P P P F / P S S S S F S P P R K F L G G P R V F P P P F F K P P P F K N F W G P P K K K K F P P P P G G K K P F * R A P P P
1614	15515	A	1622	2	403	T A R C G L N F P C S S S L F F T A S * V A G T G T H H H A Q L I L L I F C G D E L S M \ C P G W S / P N S S H L G L P K C W D Y R
1615	15516	A	1623	298	411	L I I N V C W F G L V A H A C N F S T L G G * G G R I / T M R S G V R D Q P
1616	15517	A	1624	263	2	D S V S K K K N F K E * L I P V L L K L F O N T E E E G I L P N S L Y K A G V \ L I P K P K D T * R K E I Y R P I S L I N I D A K I V S K I L A N K I Q * F I K K I T D A W
1617	15518	A	1625	3	281	P F S C L S L F S C W D Y R R P P P R A N F F / V Y F Y K K N T R T Q C F T V K H G F T V L T R L V L I S * P C D P P S L A S Q S A G I T G V S H R T Q P H T V F L N N P A L P K L Q T
1618	15519	A	1626	300	20	N P G F R G F P P P P G P F K R L D F R G G A P R P G F * Y F L K N F L G F P F W Q K N F L V F L G N K T P F P P Q F F F F / R D R M S L C H P G S E V A Q A W L K A A L T S Q T P A I
1619	15520	A	1627	394	40	P Q E A A A S L F S Q L F F F F P P V F S P P P F F K T P P R I F F F W P P * K N F F F \ P P P A F F F F F L G A P F F F F F F F F F F F F * D R V S L C R P G W S A V A Q S * L T A A L N S Q T
1620	15521	A	1628	386	3	I F F T R C T H L H L G T N K L P C T S F P D Q A K N P F C S \ H S R G V L Q A R L F C E R L T I E G A G T P A C A P * F P G E P R R / P C R V W L T F A I P A L W E A E T G S * V V A R T G L L L V S S N P L S A S Q S A R I T G V S H R T W P
1621	15522	A	1629	401	93	A R G V L P I N P P W G G R G G G S P * G K N S K P P R P R G E N P P P F L K P Q K L P P P G G G P P P L F L G G * S K K T P P P P K G G A P I N Q P P P G L P P P G K G A P F P K K K K K K D K N I R T K K A R R S G L L Q S Q H P G R P R / R G G P P L T K N P P L A S P P O E K R G P P F Q K K K K K T K I
1622	15523	A	1630	417	47	P P P G T I S S E N F / Q N L K K G P G P G G N P R N P P I L G G Q R G / R G L W A K K S R P P G P P R G N P L F K K K K I N G G G P P P V P P P R G A R A G K S L Y P G G G P P Q * P Q M G P P P P P P G A K K G F F P K K K K K P K K P R K T
1623	15524	A	1631	416	54	E Y W C K R G * I D Q W N K M * F K M D Q H L H S Q F I F N * A T K A I Q W G K E S L F N R L C L K N W L T I R D K \ I Y L D A C L T T Y \ * K I N S S W H S G A F L * S Q I L E R L R Q E A S L S P G I * V Q P R Q H S K T P S L K K F F F F F F S
1624	15525	A	1632	2	373	L V F L D N M L K L L R H S A L A S A C F P E D L A K I M D E G G Y T K G Q I F K V H G T A F C W K K M P S R T F V V R E Q S V P G F K / A T D * L L L G A N A A G N \

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						KLKPMPTIYHSENPRVFKNYVXPILPALY TWNSKA/QMAAPLF
1625	15526	A	1633	3	383	NIWN*KAWMTVHL/FIT*FTEYFKSTVE NC*EKKKILFKI/LLLDINTFGHPKALM EIKYKINVIMPANTISIL*PMDQGVIA TLNSYYLRNTPHKTIAFINYDSSDRCGQ SOLKNFWKGSILDAIR
1626	15527	A	1634	2	182	GACTOLIGRLRQENRLN/SGDRGCSEPT LHLCTPPWATE*DPVSKKKKKNCCKLK KGPPP
1627	15528	A	1635	331	1	LFPPPPVLKSGPGFN*N*PFLKGSFGP LKKKFFPPFF/FRDWLLYCLGWSQTSIG LKRSSCWDRCEPHLTNPF/SYF/CRD SVSL*PRLEGSGSIIALCSLKLDDSSP H
1628	15529	A	1636	80	381	KLKCHAHHSRGFYKYSFLQFGASQFPQ VLRITPHKGSWAAPRS*G*SQC/SHFF SPFFTKSHFVQAGGIGNFT*LQPPP DGLKRFSLHLSGSDWS
1629	15530	A	1637	381	38	SKRQSFHHVQAGLELLSSSLPTMALH PTCPKCKWYRC/DATAFNLSSTFFWQ EKCLAFI,PLFSSAPHSL*PKAVIEKD CPGL*IW**VARSQRNMVNFIK
1630	15531	A	1638	3	295	PGPDGFTAEFNQTFKE*LIPLVLKFL*K IQEVR/EFKFSITLTPKSNKD
1631	15532	A	1639	48	380	ILGKATSFTE*KGLKYLGTLYLKEAKG LHTENYKMLLKLKLDNTNIWGLIQC/W TRRLNMVKISV
1632	15533	A	1640	343	23	SWLTAT/FCFLGSSDSPASAGVELLTS DLPALAS*TAGITGVSHRTRPALSINTS TLCSPPYCPHLQSLQGTTPVPFLKA QRTGCLLQGVILTSQAENFCNKH
1633	15534	A	1641	3	397	LELFSSAHCCFSLTVMQYYP/RPTSHD CQREKSPHRTKKKKPLEGVFLG/KIKTN LENPPPLPFFGGGGPPPKGGGPKIV*GG WPPWPGLKIPTLPKGPTRPPWPGLGTF GGEKPLRAPPLQRRFRGPE
1634	15535	A	1642	2	308	NKWR*GNWISVKLDNFNLYMPYTNLS* IRDDLNAKATTIKLVGENIGENLIGKN F*ERTLKA/LRGKKMDKDLFITIGNFCF SKDRKKNKARRGSSRL
1635	15536	A	1643	16	386	EKKKLSLFTENGIPYL*NPKEAKRLLS LINDFSKV*GYKNK/DEKSAFINTNK
1636	15537	A	1644	533	3	PLSLSLSLFLSFFL*DRACFVQAQAGVQ LDLGSLOPPPPGPK*PS/CGHNAVTP RLSPLTLPMTEVRLPSKIGTWKEKNT VMSEIYQSLM*MGWG/M*YENCWKFKP WVDN**VSMGCLLPSPFLPSFLS PSFLSFFPPYFETESCFVAGAQNLDL G*LQPPPPAVP
1637	15538	A	1645	341	19	GIGGRPP*FOLLGLRQKEK/HLERKGF NEPKSRPCISAWATKDCFCQKKKKHMT LQIQIPQSWKTDISOFRDYKTTIKT VGHGIWIDIFINGELSENLNQCS
1638	15539	A	1646	279	3	TFYINERDNNKCLWIT/GKI*MLTGCYW ECKMVQLPWKTAWQFL/R/DVNI*LPYD LAITLLSIYTRKRTYVYTKTCIQMFLA VLFTTAKRWKOP

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1639	15540	A	1647	392	1	QKLEIMLRREGMLKARTGSKGLLQCAV THLVNAKEKFLKIANVLLQOHHK*ESBT AKSLILFNSMKAEKG*AAEEKFAASRG WFM/RFKERNCLHILKVGQEAASAVVEA VANYIEDLVKKIDGGGCIN
1640	15541	A	1648	425	148	SQSLI*SKALTLCNSMKT/ERAEEVAGK KLEASNF/LKFKKRSVCV/RNVNMQGKVA SLDGEAAASSPEDLVNFIDEGGYTKQOI FN*DKTSFFF
1641	15542	A	1649	271	462	RKQKKRRKRCILSPLEFIDVLEVPARTI *QEKKIKGQIGKKEV/KIISLFADVV LYL
1642	15543	A	1650	70	398	RPEASLRHMCINAGOLLSKRAKLGALS SFFFWKKS LAFAPQGGQGNLG* *KPP LPGLRGFSGLTLRN/WE*RPVPPPT/ NFGPLIKTGFPVLVQAGFLRLTLGALR
1643	15544	A	1651	425	3	FEGFVKVGFPLGPRFSPRPVFFGLTPPP PKRGPRCFPPQGPAPPKIWTTPGALPQG GVGPALPG/ALQKFGPKNPGFFSGPQQ MAP\GGFPGGP*RPFRGGAPFFFLRQG FPVAQRVHLPSSDPPISAPQVAGTTD VC
1644	15545	A	1652	385	2	KGNNSPPEIKPFFFFPK*GGLLPLPQGG GQWGYFRSLQPPPSRLKLFSCPNLPSNW EYRGP*\RL*LTGRGTSGSKTKVPTP CGPFMLNLQGLGTQARNFS/RLVFFFFE TESPFVAQGIQLDRDLS
1645	15546	A	1653	242	3	KNKNGINRGFPPTFKVPGFFFLGKVK LEFFERMLKFLKAKPP*VFFYIGPSF FFFFFLDRVLCCPGNNVVQSL
1646	15547	A	1654	3	285	HFITYYTKLNNRRYSKEDI*ITYYKHV/KK CSPSLAVREMQTKTTVRPGTVAGTCNPN TLGGQGRIVQDQLKQKSTSSLQKKIL FRLAERHGGTCP
1647	15548	A	1655	1	373	KVSLFFFFFGGLCCPGMSAVVSSLQPG CPRVKQFSHV/LSN*EYSCPTNTFSL QVCVSIHKYI*YIYIYFKFF/CR/DRT LARLRLVSNWSQAILPWPVKVLQLO
1648	15549	A	1656	189	2	VOPGQOERNYSKTKNKTOKLPTTKK GPD*FKELIPIHLKL/F/HKIDBKGLT HNSFYVVTI
1649	15550	A	1657	385	13	GGPPFWGARSFFKL*NPFPKPKPPGPP PPPGGAPPLGGFFLFFPPPGGPPPGGGK /SPSPRFFFFFLGGGGQIFLSPGPGG PRGVFSPAPPLVFKPAFFSKKKKRGSS GGKEPADGYFIK
1650	15551	A	1658	352	2	HLSSLNSNWDSTRAPP/RPCVIFKNVPLN IFFL*RGVTMLPRLVNDPPISASQVAR IIDVSHWAKLRRSV/CYVFETGSGSLQ AGVORYNHGSVQPPQPSRV*SSHSLWK YRYPPIRR
1651	15552	A	1659	265	3	HSGQRDEGRMRCGEWLESHGVVRARS CM TLKTSFLTMAKI*NLKCLFMDEWIKK MWHIHTMEYSAIKR/DEIPSFVATWME LEVIM
1652	15553	A	1660	1	163	NQGNENKTIETKIIGTK*LPKKIKKFD KPLARWT/RGKKNITNIRN*RRDVI
1653	15554	A	1661	56	320	KFFMYSAGESTKIRCLF/SLCLFLRLR/Q

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						ESRSVSQDGG*SEPRSCYCTPAWATE*D SVSKKQKNKPKKNLNKCFASSLLITLP PARHKA
1654	15553	A	1662	3	421	GIITDTFPNLEKGINIQVKV/RRPPSR FNPKTTTSRDLIILPKIKDKGS*KKKE KTSKSARLPQPHGLLGLGLGKSASSPIK KERKQ/QITYSGAPIFLVTDFSVETLQV RRWHWDVFKLKEK/DFYPRIVVLVKIS F
1655	15556	A	1663	362	2	VIFADEAQILKKEDKLDIFIKMTSVHOK TLSTEYKDNHREKIFVSQISDKELISRV YKGLLKLNNITDKNLILFYF*RLGHSVTO GRVQWCMHSSLHPQTPGLK/NPPTSAS* AAGNTGVHL
1656	15557	A	1664	79	355	IHLPELIGDFNLFTGISLLICLVLFVFI FTGSCSVAQ/S/GVQWNNHGLLQPRFS GLRQSHLSPLSSNNHRHGG*FIYF/C VEIRAHVHP
1657	15558	A	1665	47	384	KEKASGELINFFFPFKLCKLAPFFPLP FLWGGGGGKFSRNPQKHFP*KRVEVNF FFFFFRLHCLTVSLSHCHPQMSAVA*S QLTAGSNFW/VKQSSHLS/LPSSWDHRR APP
1658	15559	A	1666	163	601	IFCKGGVLPCCPGLADLHFTSNTSPFY YSSGLLRMTNKTETPMSTIPKGVGVAHR FGNSECI FOELPRLTLHLLSTMLASFII SHEASANALVGRSLTVGNGCRGVGVSD PAANLWREDLKGF*DKSHSVTQSGGQWC NLSSLQP*APRLKRSCLSLPSSWDHWH VPPFLANF*IFCKGGVLP/FAQGW
1659	15560	A	1667	418	3	SVCLGLPKCWDGKPKLCPAPSPFFY/EG SITLIPKSEMHLPNENYRSGFLN/M/ DAKILNRILANCIS*INH**KVKPT PGKIDWFNNRKPTDIIYPH*QNRREKSL VSSDTMAKVFNKIQPVRLRELTIEIKGNF LNL
1660	15561	A	1668	411	1	LRLHVGRTTTLFKAVSQGHLSLQRFLL PSVEICPAPRGGVYRGRQASLSCGGLHR VRASQLLWFLTQASAMAGPPFVLLPBC SLI*DCCANNGGFIQGVGFECVGYNL LVSHLLPSEKPSIRVGT*PSRC
1661	15562	A	1669	151	1	PLEKEAETGP*SHANLIF/CEFTESR YIAQARKMWHNLCSLOPTPPGK
1662	15563	A	1670	1	389	TFP*KLKMINLSEGLKAKTSQKLGIC TVTSQVUNSEKFLKEIKSATPEST*MI RK*NSSVANTENV*ERSSTSHNLF*S GIQNKDLTFPNSLKAWRGQVEAEKSEA SSGWMRFKERSHLHTIK
1663	15564	A	1671	1	363	ECTGPRIAKIILEKRNNVGGLPI/PNPK I*YKAPVI*FWLKVPVIPSSAILMKTU *Y/YFKDRNQDENYRLRVKINSHIYGQ LI/PSKGTKTION*SLFNK*CWNWLF TCKRMKLD
1664	15565	A	1672	203	2	ALNKRITDMP*IRRCNII/KCLFSPKM N*VFNVIT/IQCPSGHFTETDKSILKP IWKSK*FRLAKRTL
1665	15566	A	1673	15	378	NYHHNNNEHMYHSLPNFFFFFFGKGAP PG/PKGGGRG*REP*IPGKGNNPL*PP

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						KEGGPFGGTPFPFGKFGKIWFDEWKGFGP LSPGGAGTPGPKGDGPPWPPKGGKFGG TKQFGPKKFF
1666	15567	A	1674	2	349	LFLLTVLARKLVNS*PQ/CDPPALASQSA EITGMSHRAQPRGIR*+CGQVTTCHPL LLT\YLETYFSTSHSVIQAGVQVHDL GSLQSQLRRLT/CILTLPSSWD*FHVTL PG*FCFL
1667	15568	A	1675	348	78	LGPWVFFVIPAPIG*GGRSPRFGFLTN PGPKGKPRVPLKIQNLPGV/RGRPPLFP /GSPGSGGPKSP*PLGPSFPLT*NFSPP FWGPPGGPK
1668	15569	A	1676	2	385	TSRRDYRP\GHRNQLIF*/SFCRDGASL CCPCWSOTPGIKKSSCLVFRCDWYRCE PGL*I*MGKNPT\LSNGL*CDCLPLIH SIADIRKKPHS*LQGL*LCHQONSQTES CSVTQAGVQ*CDLGSLOP
1669	15570	A	1677	386	1	KSTRPVLYKWNNA*VTEHLFTA*FTEY FKATIEFCEK*IPLKILLICNVPSH PRALMGMYKEINVSMPTDITCILQPM DQGVISTFKSYLRNTFDKAIAT/DSDDS DGSQNLKLTFWKGFTI
1670	15571	A	1678	2	193	EGGRIFNFSFVEVITLILPKPKRVVER K*SYHPISIMNGDVRIKLAOTLNGIQOY LKRIIHYDS
1671	15572	A	1679	561	830	TLLLT\NAVVDVFKLFNLTYS\HS\ENS RGL*KSWINLGLTVFYKWTNNAGDDR HHLVYRHGFTGIF*GSLKTYCSENIFF KILLFIDN
1672	15573	A	1680	415	2	TSCAWLSLYPVLYPSSSLPRETECHPK ELAYKNITKKAARINTNFCYINRVLLC HLGWS/ATVVSS*LTVSKLLGSRDPT LSLPSS*EGRCITPRLGDLNLSRDGG GIRGSTLTLPQVLNANWPAILLVRIT
1673	15574	A	1681	1	78	RPRIRHEVGAGLKLSTSGQTASVSP*C WDYRPEPPCPALHISYK*NHAMCGLKCL AVSA*RHVLGFIrg/WHVECCPFCS*A GLKLLTSGQTASVP
1674	15575	A	1682	414	162	GGPGGPIFGA/AGLRFPPPLGNPPPP* KAKICPGGGAPPVFPGS*KGGGES*P*PP RGRGPFIGVQPLFGLGHRGLFPKKKK KI
1675	15576	A	1683	378	129	QPFGRPNFYQIFNFPG/PPV*HSPLEGP KFPFPSPGGGQWGLGNPRPPGAKGGST LRGPRTGSGRGGPPGPKFFFLKQSLA L
1676	15577	A	1684	3	374	GISVLFGTAGPNKPELFEEVKLYNNAR EREKYDNMAELF/AVVKIMQALEKAYIK DCVSPSEYTAACSRLLVQYKAVFRVQ SEISSIDEFCRKFRLCDPLAMERIKEDR FITIKDD*GNSLS
1677	15578	A	1685	2	373	PFRFPETIKLLEIIPGKKLLDLGLGNDL LARTPNAKINTWDHIIKLSFCTIKETIN TMKQPTDCSKIFSLRLSDKGLM/SGMC KELVOLN*KK/TDSVKGWAEDLDHRHS KKDIKMANRPGKVL
1678	15579	A	1686	378	201	HATCLANF\CSVG*DRVSPFCFGKS*TP ELKRS*TRLGLPKCDWYRCLGRSLFPGA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1679	15580	A	1687	1	404	PPDH MCVNPGGGACSEPRSCHCTPAWVTERDS V*KTNKKVKRRKKI PHANS / KLKRVGM AVLISDKIYYLKKVRRDKYIIKGSTY QEDISITNTYTLNT*APKYMKDTLTELK EEDIVAIIVGDFNTLLLIICRG
1680	15581	A	1688	307	33	DEGSCDHAGAKLLDSSGLPASASQSA GILGVSHGARPLISSYNGTSHGGLGPAL VTSFNLSHLFKDLLSLQI / HVTF*GMGL GFAGAKLSL
1681	15582	A	1689	11	394	IFILEARTISSRTFFFS* INIHAPYNS AI*LIGIFPREKK / STCPYIYTMFIAS LFVTAQTRKQPKCPSTGE \WSKNLWN
1682	15583	A	1690	20	391	SEGKGYSTCKWQSMKLGITFFFFFPF PKNPPPKSGP / QKGPF*GKGPPWPPK KRGHN \RGFPKQARFPKPVFLIPGK RFLIGPKG*NPGEKRNPPWP*KGK NPGNPKGGPHLT
1683	15584	A	1691	72	392	IKMIGSLFSGFAFFFFFGKKTFFFPQPK R \GGPK*IT*TPPGN*RNPSGPPQVK GIKAPPLPK \NF*FFGNKGVTFPPGG FEPPTPEKSPPVPSKGGKTNPA
1684	15585	A	1692	389	161	HGGACLSQLLGRIRREDCNLGG*GCS EPCTPAWVTE \D / SSQKQKSKIKKSGL DNSFSIG \GILGLSTCDYS
1685	15586	A	1693	286	363	DGIST \PRPFGRLRPSQPS \LLSNWGR STPLCLAGFFVFVETGFLHVAQCLRG FTWVAQS / ASQKIHIT*GAFETIQVLFY WGGVGFQWRFFFFFETESHVTOAGVR GCSLSLQVPPFG
1686	15587	A	1694	1	356	ELLEPRGRGCSERRPCHCFPVVVAEQDS VSKKKRERKYLFLFRFNWRLRIFIYFC * / HPLQHNICNISFTLONSFGFFSROYC PSPLEII FLTPLTENLLGLFMKGI IQNW FFGVGLF
1687	15588	A	1695	3	298	KYFETNENKNIQYQNL \AVKLVERENLT VNVACVKEERFQVNNLALYPKN*EKM LNPKGKII \KVRSEKNDIE*KNDEENQ*N *SWYFEKITYWQTL
1688	15589	A	1696	3	405	RLWCGWRNRHLGS*NRVENPETGLHRYA QLI FLTKVQKQVGEQGFNK*CGSWAP TKT / MEQPPKASSSSSSSSSSSSSSC KM*NIVEFKWENLNDH*AKSYEVTRKA *TIKGVKDLDFKIGHECKN
1689	15590	A	1697	6	392	LQRTLLVGLFNAAGNLKLEMLTCHSEN PRALKNYAKSTLPVFFWKIAMIWIV*T VAANLTEYFKPIFENYCS / EKKIPEKFL LLTNAPGHPTGLMENMYKTTNVGSLPAN TTSVLQPMQORVISTFES
1690	15591	A	1698	390	3	AIIESDFLTTSREVAKLRLVHFFMVLNV LEPIGKVKVKNWGP*KLNK / NKNKNCI EVSSSLFLCNNPFLDGI VTCDEKWIY HNW* \SAQNLNREVAPK \HFLQPNLHOK KVTIVVWSAAGLIQNEH
1691	15592	A	1699	1	245	GGGGEYSKII \AIKALKNTTYLG IYLK \DVPDLYTQNYGTMREIKYLEK \RARP CS*TERFKIVKMSI / L \NL IYRFTII
1692	15593	A	1700	2	324	GTSGTSGTSGTSGT \CRISRVRTSSWTS

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						GRHLQCHVSKAESWFWLSASSCSSTGSP ISLSGS/GSSLSNSSKNLTLPCLFSSLL S*P*ANPVDSAFKIYPGLSSVGSCL
1693	15594	A	1701	183	372	PVLLCWPGNSAVTVHQCCHSALQPRTP RLK*SP\STWDYRYTLPCLPA
1694	15595	A	1702	29	382	GKRFFPCSWEPKFFLTQGGFFPLPHFGQKK KPGSKKKDKSKCW*G/CREA/GLTLTHY RQELMVQSFVK/TVMQVLRKLNVLPY DPAFLLGLHFTSTQKR/UTMFMA/AITL /ISERWQPCRTS
1695	15596	A	1703	1	382	KKVKIGEAAREPDDTKIIEEKVLP L*VYWADESGI.FWKKLOQRTFISKEEK \SMDRLTLIILCKSVVYEQDG*ALKE KGEHLPVF*L*KKKAWTVRTFLD*FH QCVPVEVRKYVASKRL
1696	15597	A	1704	2	330	KLNNLLNNNS*VNTETKAEVSSSLLEIN EYEDTTYQNLDAAKAVLKGKHVAPHP LQEVKK/RLKRFQNNLTLYLKEL/EKE HINKASGRK*MTKIGDLGLYFVLNG
1697	15598	A	1705	100	342	APKWSIVCPGLVGSWSH*/PSRMKFWTL TROGFTMLARLVLS*RRDLPALASQSP GITGMSHRTQPLLLINLMEIFTEILS
1698	15599	A	1706	600	211	SCSVARLEFSDVIKACHL/RTPLGKQS SHLSHLS\WD*GRVPHDLANF*IFCRD RVLPRLQAGLEL/LASSDPPS*ASEKC WNYREPTVPRQNLGLLKTYYGWVFLKK YILT/VSVFLMCLDHLCLM
1699	15600	A	1707	409	1	RGPPFFSPGKAFILKLGNSFFPIKTRTA PKPKIFSPVSP/LNFPKTKGPPVPFPQ MGGFFF/CFPSLFFFLPPPFPFPFP PPPPPPPPPPPPPLFFF*DRVSLCHPG WSAVALSQLTAALTSMDSSNSPTCV
1700	15601	A	1708	154	2	IGKPLAGLTK/RKRENT*INKIRNEKGD MTADNTEIQSIIRDVFS*RTAHQ
1701	15602	A	1709	263	37	SAQLHPLNIQNRKSIILHDBFLLKKQD/ G/WPGAGAHACNPSTLGGQGGWITRSGD QDHQ*HISV
1702	15603	A	1710	390	42	YAGGFRAIEFFELBREGAKNPFVGGP PFGGPPFFFPSPQKKEPGFGKGVF* GGAKGFPNARGPFF/G*KKKGPKNKT PGFFL/MGPPNPGSPPPRGEGGIGAKK KKKSIRL
1703	15604	A	1711	3	167	YTCVFVCLCLDCMC/CVCACMYICVCV CTRVC*VCVCMCVRVQVQALTVLCKSV
1704	15605	A	1712	116	391	KRNFFFGPGGGEGPKFN*RGPPPGVK GIFPPSPPEG/GKKGAPPPPGIIFWFF KKKGVPFCPGGV*TPDGGPPFPKPK GGAPRQGPL
1705	15606	A	1713	401	47	BHYATRFTHAHTCTCIQDTNCTMCQHT QVHT/HTDTHTRKVSVCVLMAEQE RPCPHC*GGEAGACGVCANGLSS*TW RNRKGPAHTVRVVGQSQSAGCAHGLVFP RSYLWT
1706	15607	A	1714	1	400	CVSECEVDIEMVSCCV/CSG*SAVCSGT ASAHCSLPIPGSRDSPASACQVAGTOM PH/LYPGVLPKPREGLQTELPSSGLEI QPTCENK*HVPCAL*VQLTDIRP*RY QFRVAENVHGTRFTAPSKHCS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/51,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1707	15608	A	1715	413	3	LNTFEPQRFSEFFIVNSSEMILLVECLFVT SGWIYHERFLNPGREIDWATCYSETGPC PVTODGVQMSNHGSL*PQTPRLX\HFTT SVFPVA/RQGL/NSVAQAGVQWHDLSL *CRLPSLKGSSHPRLPSSWNRYAPPPC I
1708	15609	A	1716	421	144	RLECSGGITAYCSNLNLPFPSSSPASAS* VAETTGLLHWKKKIVETGSHFIVQTAFK FLDSSDLPALAC/SWDYRSELLCPACFY NFCLFINIPC
1709	15610	A	1717	3	384	YSACVVCVQVVDVSVHRCMSISGH/ARI IRVGPAHKAQSSCRPVFAGCCTSAQTPP WCSAATADPPFR*GESLPGAYPGSHSTC CPGCCLDN*HSLPSTEPACACRAGPGGG H*AWLQCGGRGCRPG
1710	15611	A	1719	3	615	PVGSWAKSSGAGWPFSSPOSVDGEGAGH STPAPRCQCSRHAEORTARVCLSIKCSF SGFRPCLVPIR*SLGRDPAVQAVPDSQ EGRKGTGIAEAAVMFPLGPGQVKGCGNG RLCPSSPPSRCLDLGRRGMPSSSGPAGP RPSGVGSDLGRPGAGAAATSSSSSSSSSS SSSSSSSSSSRDGEGP\TGSVEAPGSL GPWLPSPQS
1711	15612	A	1720	320	3	GLKWLNLKDNSLYLTLAKVDDCDEK* YADKMLQYTKSVWVSRSRGCGQVGEKK QATEAAQEWELRK\RLYWRKCEDALRAA REEQKELRDVRKAKVYVCVRV
1712	15613	A	1721	44	373	KAMGQTLWKTVMQFLTKKEEFGP*QSCP T/DLALVFLGICTIDLKAYIHTETCTOM IIITLLLIAKNRKKASCSSVGE/WNKKL YYIRTMSYSSLR*NELSSYKHWGGGS
1713	15614	A	1722	135	396	AQGLFCTSVKLASEQPLRLIFOLDKRNK \FEIYGTG* L* SIIICQNNLQSKFQMY HHKIMSSLGAVAHACNPSTLGGQQQIT RSGD
1714	15615	A	1723	4	383	LNLRAKAIKLEENIGIHLDPIDGLDDLF LDITPKSQATK/ARIQNGFIKLKHFC AKNIIKKMKROYKWKIIFGNHVSDKKL VFRYK*HLPLIIKNSSS
1715	15616	A	1724	2	405	NRFTSLNLQNLB/IKLSEKGTWKAATG *KGLLQQAISKIANAKELKVEVNSA TSMNM*MMRK*NNFIPENQKVLVW/I* NI/PLCQSLIQNKALTLFNSIKAEERGE A/KLEATKRWFMRFKESCLINVKVQDEG
1716	15617	A	1725	90	400	SOLLRLRLKQNSLNPRESSSTTTTRTKVS HWHKNRHVNO/YNKIENSGINLHYG*L TLNKGDEASQYSS/DILFNKWKQWKKK \YLDPLYTPCTKISSTNTISGFL
1717	15618	A	1726	390	1	TFFFKI\EKKIL*FTWGRPRPKIANVFP *QNKPKIEGIFLPGFKIYYRALVTXTAW F*HGNPPIGQNRKNVENSETNPHPPSELN FFFF\YGAKNIHGEDSLFNKWCWENW ISI*RRMKLGFNLTPYTK
1718	15619	A	1727	3	363	HASAKSNLRWITKLNLRAKTIKLEENM GENLWDLLESRGFLDRT/PKLYSLKLK RK/WNFIKIKNFCFSRDT*KS*MAGKNI LSGKDLSEYLK*CNLIIRQSTST* MFIALLPIIAKH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1719	15620	A	1728	368	2	RVLNSGGCCSEPSRSHCTFAMATEPD SVSKMK*KKKINK*IMFLY*EQQSETEY FKLPLTLA/SRNMKFLGINKSGVQDLE TENYKILLQIEEDLNK*RNKY*WIKL NTVMKMSILSKR
1720	15621	A	1729	326	30	NPFGGPKKGGSGGREIKPPLPPMGKPLF F*TKNKNKVGCGAPPVPPS/SGVLSQKK TFTLEGGGPNKLNPPALP/ARGPKKNF FQKKKKKTQNPQREE
1721	15622	A	1730	1	374	IFNADKIA\FWKKF*FKQGTSGVREEKQ APGFKAGNRNLTTL/L/GASAVGMIRA ALICKAANPQVLKGRDGHQLPVFRLLYN KKAMTTRTLFLDCFHQCFVPEVRKYLAS KGLVFKVLLILDNGFC
1722	15623	A	1731	389	1	FPFKIFFFSTLFFFFPRFFPPFPFL*P/ SPPIYFF/CAPKKKNFFPPPPGKNFFFF KTPPPFFFFF*P*VCLCCPGNSAVAQ SWLTTTSVFRVPVI
1723	15624	A	1732	118	422	DITTHLKFMLKFKK*EKLNLITKEDM QMEKNLKRCLT*FVVKELQIKMRHYFP IQMAKI*KN/STISIAWQGYRTIGTLF/ HC*EQPP*FLSKLNMILPYNPA/IML LSIYPHALKGHVHTKTC*MFIALPII TKNWKPRCPSCISW
1724	15625	A	1733	407	1	NIKGPPRGGLIQWGLLLIWPKDSFPILGY PPFPSPKISFFFLARSCSAPNHFFLPN QSPCPQPSFPLGEEKPLPGIYLAPP FN/RFGGS*RVKKGNGGPIPMGESFLF F*DRVLCCPGNSAVA*SRLTATC
1725	15626	A	1734	322	362	TAIYIYII*LFIDNI PSHRTWIEIYKE INIFVPANTIPVQHNRQGVCTFRKTI TVTDCDPANGSGQSKLTKGFTILDVA KN/IRDSWEKVKIG/TIN/GVRKLIPLSL KNDFKRPKT
1726	15627	A	1735	49	395	RGCGPFFFFFFFSSKKSQILPFGWKGRG EPRVNGTPPPRGKGNPPAQPPQSGGKT PPHKPG*FLCLFKKKGVQKGG*GGPG/A PGPKGAPRPGPPKGGEKREGPPGPTRPN LYYAH
1727	15628	A	1736	417	2	FLFFFFFFLFFFSFASGPEILFTCL*HT HIHFLFFYSKST*PPVFAGMGQDDQW LPETKMVPNFKKRTTLT/YIP*KLCE CDLSNFFCFF*DRLLLCRPGNSAVA*SR LTATSTFOAQNRTG
1728	15629	A	1737	316	338	FFFLSFYFETESYLHHP*GFIVKLSKV DIEN/LKKTARGNVQTYKGASIRLAAD FSAEISQAWRENDNMFVKLEKTNWQPR IYKILFVPHF
1729	15630	A	1738	197	379	QKRAQIDKALFICRDIAL/P*P*EQ/MYYN ATVTKTAN*WYKNRHIEQWNRSN/PPEI KSQSYSL
1730	15631	A	1739	4	401	RGYRHAPPSLANFCISFD/MGFTVVLN S*PQ/CHLPASTS*SGITIGSHCTRCP MATELIGPHKII PWSYLNEL
1731	15632	A	1740	94	117	KDRNVDPVAGAGEOADEPCRGHSLWS QLVSAPTTPIPLPGRDVPSRATPPPAAL AAQQPP*ASPYPLPQLGAGHASAPVT VPFSPISESTGS*ESAL/PAPRPGSGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1732	15633	A	1741	3	390	VDQFLISHDL SKL TEDEVHNLN SSTTIG \EVEFKVKK\)*KKKSSGPDGITGKFY* TVREEVTPIL/SYLF/HEIEKEETLVNS FYEAR IIL/ I PKPKDKPK*TNIDAKTTS KVLPNRIWQYVKI I IQHN*VGVFV
1733	15634	A	1742	3	442	DLSSRVPRVRPSVRRQ*VLLKVLICA SKDTLKRKRQPIGWKFI VNNHMPDKDL IPEYKINMQKSOVFLFTNNSYSTTDND INKWKADLSRHFSEEDIQMANKHM\KR* SVSLVIREIKITKTGR*LFTPKCWQG*G EITTLVH
1734	15635	A	1743	411	2	LPFFKHPPPEIILGAPKKK I TLP PPRPK KCISLKGPPFFFFCR YRVLLCCPGWFST PGLQSSSHLGLPKWWDYRHEPYCTQSSP SLSFPLKQTCR*WELSNFFFY/CYCFI YFSRDRGTLTLP EIVLNSWPAILL
1735	15636	A	1744	1	393	RPGQPFKRSRECCRGEGERSRRRPRAP WAKSHMNCARVSVPRSPDQRPQKCVQ SSYKQQLPARARDGTGNLRGAPLFFF* DGVLLCRPGWSAGFKQFSRLSLPSR*DY RRTPPHPANF*ML/CLRRSLT
1736	15637	A	1745	395	0	PSAFSFFSTRL*LGEPGPGFPFPFLKPP PRN/SIGAPKKKFLFP PPRGKKFVSLK GPPLFFF*DGVL LCCPGWSAGFKQFHS LSLPSS*DYRRTPPHPDNF*MF/CLRRSL T
1737	15638	A	1746	397	1	CGNFLKREKNFEARRFLQK*AAFRNIR *VTPEITAF CPL*HVASFVFLTPNFPPT IPQLYCLEPLGEMGGSGKLFPFPTS KT PNPLISVNLCPF*AIKWFNFFF*DGVL L LHPGWSAVAQSRPTATSTS
1738	15639	A	1747	392	2	FTKKGGRGGNLSF/LPPQKIF*KKKTLK KPFFWQRVWFSP LFPEQKQGGPFFFKK PFF*KRPPDTPQPPPSIFIFFLFFFR /HLVAQAGMCWRHLGSGQPPPPGLTQSS QLELPHTPPFDNFCIFGRDR
1739	15640	A	1749	33	403	IKGFKKRKGKGAAPQKKGGTAKPPPPP PGGF* K*QKRNGSPENVFPFNPGGPPP PPFWGDKRGSP PROGGAPPPRGKRENP FFFTLA/HGKKEKK
1740	15641	A	1750	3	396	KRCITNWKVEFA*KNVADGLISLIRKCK LKVKK/W*R/DNMTQPTDKGLMTNKH M KRSTSLIMEMQHKAGVIFHPSDWQK* STDNTQS*QGHEMYTIKHS*TFDYQQ PF/SESNL
1741	15642	A	1752	30	419	NEGIGAGHEVSPFAANKCRSMRKNVEVLA LNRRLDGLL SGLTSTQALPCWAYLHLL SHHAVRPLFLCFKRGWVLLCHPGWSAVA OSQ/FELGQVILRPHLPS*DYRSIIP CLANFKNFRERARYACR
1742	15643	A	1753	16	410	VGPKKSLQGVAAVQATIPLESYDLAHP IILKSLADRAI*NLWQIPIVAS*YIP LGF/YSKAMPSSVDIYSSFEKKKTHFFL TGGGGPPLYSNYLGRLLGGANHLTPGVKN QPGQFGKPPPLQKVQTLAAGR
1743	15644	A	1754	2	17	NSSLIKRRRIHTGERPYQSCSGRVFNQ NSHLIQKQVHTR*RM YI*SR/CGKDEPT QKSTLI*H

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1744	15645	A	1755	138	380	KPXXXSPKPPPCXPLSSFLTKCSAY*TPAHRPPPPGPFVPPPKCCPPPPPLRPWPPLPLLTPNPPTPLSFHGPALS
1745	15646	A	1756	194	3	WLCIPIRHTTEQQGFFP/LIINSEQPYSPLFCLFVF*DTVSLCGPGWAGVQSGLTAASTSQAPSL
1746	15647	A	1757	2	403	RVLFSPTLAYTYLLFLGATILMGVNIWQPCNCPK/GQQKIKLQIYRMEYYSALKKK*ILLFAIR*VNLGDIMLSEVSQ\SRKKNIVLSHWW
1747	15648	A	1758	398	65	FFFFFPP*TKGLGCIHRCDHGSQPRH\GSSNAPSLAS\VGSTGAFAHHRFTLIQSSSVHVSTHTLHPYPSLSP
1748	15649	A	1759	456	31	FAKRITDKLLSLYLAT*KGETIKALI KO*\LKAQAKNSLKRHTIVLNHMKL/CLILLIIKEMQIK/STLRVHFFITLAK\I*KLGNTPCWQGL*GTLIHCWWECK*HNSYVGGIWQ/FSNKLYVQI*YNSAISNLDRVGRPG
1749	15650	A	1760	3	378	OFQYFYNGSVIKAVWYWSKNRK\IDQ*NRTESPDKNLHKHMLQIFDKGTNPQWRKDDLFPKKWCNN*TSCTQKKKKKGGGP*KEQNLTPGWEDIIPLFGAPKNMPCGAVKTRWGGKNGFPQ
1750	15651	A	1761	69	384	YTSASWGGARYTASAGWKTLLLLFLFI*DRVLLCHPRWSALTQPRIIAASTFQ\VKQSFWMHIGDWDYRRCPPCRANFFNLCKKKKTLRRQEVNOTPALVRV
1751	15652	A	1762	390	1	KFSTFGKNLFFLKAPPPFFFCRGRVLLCCPDWYSTFGLKQSP/CFSLPKCWDYRRESPPQAFFVFEGPLSPFSPAPPSLSQSSSFF*MEFHSFAQAGVKWLN\LFGSLQPPPPGLK*FSCLSLPPTRP
1752	15653	A	1763	2	390	PRVRGFWRKFDVSLVVPYTKSNLWKTIDLHVRAKAINLN*NVRIHLVDRELNCGFLEWKKTKAARTTKLDFIKIKNFCAQQMS/HKVRQSTKWKKCSYHISDKGLVSRKYVKKAYNSSIRTOSH
1753	15654	A	1764	334	3	WSKRSRPFSLKKNQTKKNATKPT*KNWINEIGPII/NTSPSKE*YGSNGTD*FY*TLKEELLSILKLFQ*EKSIVFPKSFYVKDHSSCLSGIHPKDAVMEQHMQINQC
1754	15655	A	1765	259	1	KSTFLMKKYVWKGFLKXHFLETRSLSD/SPG/GVQWRDHSLSQPRTPGLKQSPHLSLLSSWDHR*APCPANFRRLKTRIGRDV
1755	15656	A	1766	402	386	FKKKSRLRKI/KVQDEAASPTDLAKTI/DYEGHYTKQIFHVDERAFYWKMP/RFTIARKKKSMPPRASDKLTLVSGANAAGDLKLPVLTYS/ENPRALK/HYAKSTLPELYKWNTKAWMKIQKPPS*FT*IFM
1756	15657	A	1767	2	406	PRVRPRVRKLITLNVSQWSSSEKKKKKTKTKKKKKKKKRGGRLL*KKKKKPRGRVNLFFWGPKKSTPRVFKHRGGEK/PPPPPKPRERKPSLGVGSTWHGISPIKHSKTKSTK
1757	15658	A	1768	14	409	IASGLFFIYFGVIGRPPKRGVFFFGGCGAPHPPQGGC*KKKRGGGGPPPPPPF

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						SLGGLGRPRPMSKIKTPPSAGGKPF/PF LRNQNTGGGGPPQ*PPLFGPGGKNFS PPRGGGGGGFKTPPPPPGGE
1758	15659	A	1769	305	1	TRKTGPPPSNRKKKKIVFQKKKKKKKIN CFVTAPFKGIKTEATD*EKIFAKHLSVK G/LVYL*YI*ISKIYKELLKLNNEKTTI PIKK*AKDLSRHFRTRYD
1759	15660	A	1770	148	402	FSPVSLG*GRGNIYAGMSNV*EVPPFID PQHEVKRALQTSFOVKLVKIIFFKSTII* KSLAK/WLAVVAHACNPSTLGG*GWIT RSGVKSPPGQHGE
1760	15661	A	1771	250	2	KKKKEKKITCFVTDITFRGIKTEATD*EK IFAKHLSVKG/LVYL*YI*ISKIYKELL KLNNEKTTIPIKK*AKDLSRHFRTRYD
1761	15662	A	1772	407	1	KKIRGGGGPPLPPLIGGGREKKKFFPPG KRGPF*TKAGPPSPSSWAKKKKVFVKKK KEKKICFVTATFKGIKTEATD*EKIFA KHLVKG/LVYL*YI*ISKIYKELLKLN NEKTTIPIKK*AKDLSRHFRTRYD
1762	15663	A	1773	1	406	KKKKKKKTPFGLFFFFELSLPFRVPGA RGPSPSPSKPGLCG*IKXSGVSPAPKK KKPRKTNPNKFRPNPKGGGKFFNLPT HPPGGT*PPFF*RRRENDPGFAPOKG/EV FSPGGRNSRGEPRGGKPKKKKGG
1763	15664	A	1774	2	378	AAGEWLHOGSLQSLPGLKQSAFLGVSK W*NPWHDP PPPAPRFVVVVVGGVVLWS FFLGAQAGIFFF* IEMGSHYVAQAGLE /PFLQGSS*LNLPSWDYRVPV
1764	15665	A	1775	1	431	QQMRDKRNLFENNK*GIRGIYLNITIKAR HEKPTVDTILSGESFSSKIKTMLISPFL FNTVLGVLA*ARKRKDI*VGK*EVKSYM FTNDMI*LDNPKDSTPKKKKTGYFMGGP GSKPPQRGGAFLSLTRDPLEREFPKTA LFTLGQKKIKGPKKFS
1765	15666	A	1776	334	402	KGGGGVGG*QGFWRLAHCTDK/KEERKR ERERKRQKKKKKKKKKKKK*MKNNK KKNDK
1766	15667	A	1777	406	3	SPSSSSSSLSFPSPFFFWGGPRF/SPPP VFKPPPPPPFFLGGPKKKKFFPPPPAV*FF FF/LGPPPPPPFFFWGAGFPFFSPG* GP/SGPMAGFRLSPFGNSLSKKKSG LGSGNSVLTRVLLISSQIPGR
1767	15668	A	1778	70	409	LISPLVSSILVRLYRPLLCPLPDPGKGH CIPCLLPFLWILLHI*FLEWHSFTYCLN DRVLLCLPGWCAVVRPRLTAASATQ*IK RSGSHLSLSPSK*NDHRRCPGFFFFFF FF
1768	15669	A	1779	390	31	SHLSLPKCDY/RL*ATTPSQKILVFTH G*VLSLLSLSFLLPDP*TF*KMSLMRPS LTQKSSIIQHDLKVPITIFLRQSL/D S/VTQARMQWHDLSLQPPFGLKLSQ PQAL/SSWDYR
1769	15670	A	1780	357	1	LFLFWGAQYLPKKGKGPFFLLSLSPSPV WOPLPQKKSPPLCFYFLNRLVLLCHPG WIAVVQSWHSSAHFSL/VLTRFK*SSCL SLLSSWNYRCTLHPNPNLNFWRQGNA VLPLKVL
1770	15671	A	1781	122	254	RKNE\WSGAVAHACNPSTLPGGGGQIR

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1771	15672	A	1782	45	387	SGDQDEFG*HEPPRPPTDSFFLYPSH TQTPKLRRFHFSLKSWHYRCSPL\PO HNGYFLNLDIATSMFFKDRVSL\LAQ AGEQWCDPSSLHPQTGRLRR\PPASASQ EGETTGAHHHTWRNLIIFFYYTYKF*GT YKHA
1772	15673	A	1783	1	401	FATLARLVNS*PE/CPLPASASQSGAI TVSPAHLAISPSFPAMPSSGLGLSYFAY HPGLGLRCHLPVLTSPWTSDDTGPSSVLP DAGALHCPPEPQHICPL\LSGWLQTP
1773	15674	A	1784	432	1	FLFLFFFTKKKTFEFGAKPKNRGF*KFP EFFQIF/S/CPVFLGRPKPKQKEFFPPE REMOFFFLPSPOGGGFARGFP*PPLNQG EAPRAGHKKKGNLGGRTFFFFPFEMES \FSVTQAGVQWHDGSLQLP*PPFKRFS CLTHAS
1774	15675	A	1785	15	434	RLSLSCCGREHSTLPGAPWRCTEIAWA DSFDPAPSPPSALPSLLPHVYRDVCPV LCLRGWP**MVERGRGLGISPTWLLGWPF PGGA/PHIKPE*YFLFAYTILRSVFNKL GGVALLLSILILAIIPILHISKQQSII F
1775	15676	A	1786	1	258	CWPETPVULK*SHDLTKRGEDRREPVA ASTTIIFFFTETGL/NSGAQAGVVRVHLS LEPLPPIPSLFMT*GPCPLGSSWFLR EF
1776	15677	A	1787	399	63	SLHNQVVKSTPTLTKTSKKISHI*STWFG VVAHACNSNTLGHGGRTA*/RSGVODQ PGHSETSSQRLRNPHYIKRCIKYLAHSK CCINDSFTVSVTSRKLIGREVSPNNIT FR
1777	15678	A	1788	3	474	MSISPVARNWNSKEAGRAANROFFSFPWK DSDRDAPPEPASTTIG\PIRLAESW TWGSPCAEHPRARARRKAATDCPWAAG SQWRGPAGQAPRSCLFFQOSTAARAQH PRVAPPPPPAPLNTASALRSQLFRNPL *VMTFRPPAAAPRSPVGP
1778	15679	A	1789	66	395	LVQPLFFDTHWSRLSLWGRDLLWSGKE TMNPCLNHSIGVLQEQGSDVKKRRRLM ESLTGPAADVIRILKSNNPATITAECLK ALEQVFGSDSSRDAQIKFLNTYQNP
1779	15680	A	1790	413	1	PSFRALITDYS*EGGRFQWV\KKKGQF LKPHPLGSGPHQESPRVGP*PKRGYNYPF *KKRAKFFAPGENKPPFWTGRDPTF*G KTKKKTNP*PKGKGKGP*PKGQFFFFF LRRSLWSPRLCCSAIAHAHCKLRL
1780	15681	A	1791	314	1	KTKPFFLKKTPPKKNNKKKGC*DKARY QTRKG/IVNLGH/HPSFLFYFLFFETE SHSVGKAGVRWLRANSLQTPSPGFQQFS RHSKPSRKDYRHP*PKRPOECVQ
1781	15682	A	1792	104	409	EKQSFADWHDLYFDNVK*KEGESKA GEFNASTGWFNGFRKRL/RFKNVRVTGE PASVTQEADEFDPNFKKITEKKGYLHG KFLMYHEAAKYLNFNCP*TK
1782	15683	A	1793	392	2	GERERDRL*REEREREREREGERERAR ERERAROGTSTVESRF/HSYCRDDQVA RPKAKEVAAGRGSPDGLQVGRGQ*PGP SLRPGFWREWGATYLAGGGPIPTGEVE

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1783	15684	A	1794	405	119	SGEEWAQGEWQALGPP I I K M A I V P K A I R I N T I S I K V P M A F T K \\ L K T I I K F I * N * K R A R I A K A I L S K N K A G S I L P D F K L Y K A I V S K P T W C W Y K N R P I V L V H S R T A R K K
1784	15685	A	1795	455	3	CSV T Q A G E Q W C N H S S L Q P Q P G L K W S / C P S O L P K \\ W N Y R H V P P R P A L T A H P A L T A D F * R R K E Y K L M R H R G K K W H D F T L R S K K M K A M R H E Y H S F L T Y P N G H L Y L W Q F F F F D T E S H S Y S Q A G V Q W H D L G S L Q P P P G F K R F E R V G P G N S C A D
1785	15686	A	1796	2	134	P R L Q H C T F A R A T P Q D S V S K R R K D M I T D P A I * K G * * A T T I N I Y I H K F N L D E I D Q P L K K H K L P Q L T W Y E I / D N L N S P I T R A I E F V I L N S K K Y P G S D G T P G E F * D * F C L E T K K R Y D V R P C N L K R I I S D Y N K H L T
1786	15687	A	1797	1	404	P T R P L T G S S A S G M N V E I F F K T Y L I S S A C W V K I S K I D L K L F S F F F F G F L E G G F Y F C P P N S R G G S P G G K F L E P L P P G L K G I P P P P P K R G G E F G P P F P T P A Y F F F F L W G G V / P P / A V G G G K P P I * G N P P P W P Q G
1787	15688	A	1798	2	383	S G W L W A C R S P D S E F L C A P A G P R O * G A Y H P G Q L L M V R * V S Q Q C W P T P A L H S I S \\ P R P * L P P R R A G L G T C S P P / V P E S E L L P W A P A W K P P R R A L P P A / P V P G P I D R P R A E E C R R M V R D W Q A P P A A P
1788	15689	A	1799	35	410	A T G P S L G K V C S * A P S F L * P K L D F W H L Y F Q A S G F L L / C H N S P S Q T N S C S S F G K H Y G M V L R V N S L * P D H P W N E F Y F L N F F I F Y R D S / S L T I L P R L V S N S * A G T I L L P L P / P K V L G L E
1789	15690	A	1800	65	415	K K G V L K G G P P P P L G V * G P P P E K G G P G F F \\ G A P K E P P L A L G E P K G K P F * R G P K G F F F K K G L E P G A P P P P K P R G E K P P V F K G P H P E C K K G G G D K R E K N G L * R K K P T E L G N G P P P G
1790	15691	A	1801	417	3	N L G P N I F P P R A P Q N G S P A P E L F F F L K K N F T W G G G S T P L F P / L N L O L G C P P F G L E V Y A P P S P H G * P R F F F K N Q K L P P V W G A I Y S P F F G G W E N \\ R K A P P G Q T L F F F F F L K * G Q D L F M L L Q L V P N Y W A Q V I L P W P P K V
1791	15692	A	1802	1	431	O P C T P G L K * S S C L S L P S I G D Y R C / R T V P S * F F F F F L E K G V G F I P R G G I K G L D N C * L G P H P P E L K \\ N P P P Q N S O E V C T T G P P R P G * L F F F F E T F F F F * K G G F I L A Q P * M K W G A L K K T P A F S K R G G Y K G G T P M E P T H C F L K E N
1792	15693	A	1803	256	399	A I K N I H D S * E E V K I S T L A G I W K K L I T T L I D D F D G F K T S V E E V T V D V M E
1793	15694	A	1804	407	2	F E K A N L F P P L F K N S G P P N V E R G M A G V P K F C C P S K R K V G P I F F L R L L F L F Y P K C R R P P L F W P A F G P * K P F L P Q V E A P A F * K P S P K I K R A P V F F F F F F / R D K V W L C H P P W S A M A * S O L T V T S V S W A Q A I L L P O R
1794	15695	A	1805	429	116	L L T K K R K K K P L A C G E S G L G G P * G T V I G V * Q A E D T H V I W \\ V L S S A P S L S S E E M T D S M P G H L P S K D S R Y G M E M L T D K K W T W D G G A W D S S P G A N G K R G A R Q A S G F S

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1795	15696	A	1806	2	408	FVIFVFLVETGFLSLARALACAISSN* PRDLPTLASQAGITGVSHRTNPRRSCV F*EAFITMLMLVLIHPPSLLWHSVPTILL ALSS*CFLLFLLRGPNVATQAEQGHDLG SLQPPPLGLKWFSCLSLESS*NYR
1796	15697	A	1807	1	196	FRLGASLDSGGCSGVSWTPAPPLPPPP PPSAAGSIS/SGTSAAGL*SCRTAFF SFLSSFFFFLLKKINPPFLGGI*PFKG GPRLV*GNI*PPPG/DFLGGTRGGKKP WGGGKFGQGNFPLPLKPPGPKNPPP \PPPPPPSAAGISMAAHLQPLACDRAA QLSFLSSHLFFFFFF
1797	15698	A	1808	395	3	LGRKMMNPKFWGQCEATGTL/M/HCWV CKFVQSFWNDSIY*G*AAATHDSAMLL LGMHSMFACTFVHQKT*TKMFIAALFIL PLNWKQV/RCPSVI\DGVIPTMDOSTAM KMNKLHAKTMNLRNLMLEKPR
1798	15699	A	1809	7	454	IPGSTISLQPPPPGGF*FCLLSLLSD RQPAPPR/LANLR*TLQSA*LRW\RG PILDEMKFSMNCNSLTEGVKGRVEMMS QNGRLLTKFCHVGQACLKTPDLK*SARL GLLKCDWDSCEPPCLTQMPPSFFLFF*D RVS/PLSGWS
1799	15700	A	1810	20	355	PQCAAGCAVAPVVCVRCFCVCVCHGV SHMCCGVSACTLLCLCLSTCSGAYA CDWCCG/CYSACVCAVCACVCAQLLTC IGMWE*GQAGQGVLLDLPLCLCSWAP Q
1800	15701	A	1811	3	414	SSKNDNNSLQEPNDKIAGMKNLGNLTE LNNTV*EHIRAITSINRINIHAERISD LENWLSEI\NRQT*KIVTRNEOKREVW DYVKRLNL*IG\VFEREKGKAYLQNI FEDIVHENFPRFARDANSIQEMQRT
1801	15702	A	1812	1	443	AGKSPSPKPKFKGFGGGRWS*PLGAGG GVPPFRPGIQGSNYRFF/SPPPPLGEKK KPPFKKKKTPOKLGNGNHPYFNPVRVH GCREQQPWEKPADATROPHYADKHVEAG EPREPPKPHSEPLFSSPRKRLPTRSST /SGASPP
1802	15703	A	1813	411	66	WKNVFNKECLER*TF/ITQKKLDP\F LTRYIKIKSK*IKDLNIRLEIKTKTPGKE SVTLAKWLIRSPYLSFP*QIQSQ*INS YVLKITKTEERWSTSKEYQKPWERKAM YKIK
1803	15704	A	1814	369	20	QEVRSPIYLSSSNRKYKDSNARFTKEA IQIANIHMKNCPTSLIVGETHIKTSKGY HYVPIRMALIKL\CNRRCGETGTLIHF *WEWKNVQPPQKPF*WPKKRKH*QFD LATRS
1804	15705	A	1815	2	675	GLAILGRRLRGEACTRSPFSSILIFMVS MGEWPGVP/GIKGTRTGAEAVPTRRRKS SIWPGTGGGCESSG/PLRGLPRQKPCS PRGSPCPNCAARNWHPOAALGACCFSS GPEPSRLPPWRCGNWCLPTPSSSA*EG WR/PVLQPGFL*SPSSLASICPGAERCP PGSSRP/GLRGAGG
1805	15706	A	1816	273	2	MESHIMWFTTGFHLVQCLHGPSMLQC IAVLHSSYLFYLYFY*DRVLLCHPGWS

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						AVVQS*LTGASGSW\LRSSFHLSLP*C* DFRHEPR
1806	15707	A	1817	40	404	GLHE\PGVQCSEL*SHDCTPAWVTSET LTLKKLIKKSXXXXXPRGFERPTFG EAGPGGLLKAIISKPRVIQGTQKSGALL GPNSSNGENHPQKQPYLGGLYAKAHSP RGGGPPSPCG
1807	15708	A	1818	392	3	EKYNMSYDIKSTNHRKNCKLDFIKI/RN CCSLKDTINKMKMQASNLKIFAHMFD RGLIFRKNSCNLVR*QPPFFKEAKDL NTQKSQ*TNG/HGSKETSLIIREMQIKT T/MNYTTSIPT*MLKIKKMI
1808	15709	A	1819	311	431	EVVGRANWLTPVTPSLWEAEAGESRDQE *KLCTTVEK*KTISN/HDVPIRSSWTGM VAHACNFTLGGRRG*ITRSVGVDQPD* HGEGL
1809	15710	A	1820	68	410	AKKNQSGPGMVGFGGKIPPPKQKVRG GFALCEKEQVFFFFHRAVVSQSLNHC SLQCPQGLKQKQSSHLSSLSS*GYKH VLFCPANFILFSLVETGS\SIYFPGWSQ TP
1810	15711	A	1821	408	1	TPFFFLRLRLTPPLLGNFFGPGFPPEWG GFSPPGLLKGRPP/CPPIFKPIPDQKWK GLVFFFFPPFFFPDGSR*NLKIKFPNF PFFFPVFF*ILNPPFFFFFFFFFL*D RVSLCRPGWSAVARYRLTASSTGO
1811	15712	A	1822	362	76	SEIAPLHFNVGDRVSLHLETNKQSNKQT KKTILFRDRVLLCPGKNA/VEVO**LP AASN/FLRLKQSSCISLSSNWIYRHAPP HLATVFNFLIFE
1812	15713	A	1823	314	2	VISKPCRELTCITYGVSLTQCSMFGRM KGLLLINPVCEVRASORPPLMGSEEP LCPAATPSGRCTQ/LH*ERAMMTMAVL SNRKGQVVGKR*RNQIVAVS
1813	15714	A	1824	57	389	NLHLQLPTYTDADSTGPTLSGMNVKNL HWSYEYKRSITGVQWNLILGSLQPLPR FKCCLSLFLRRWDYRCAPPRATF*FL VETAFLERLTSCDLPSTASQADITGV
1814	15715	A	1825	410	70	VPIMSATQDYRHEPPRPRAGRFLKLKME PPHPALLVGI*PKNMKSLHKDVCTPM FSGTLFAIAKIQKPKNCPSMDEWINCR NY\MHYDGYCYALKKNEILARRSGTR L
1815	15716	A	1826	2	411	FLVEMGF\SLVTAAGLKLFSTGGADEA SESAGITDVSRAWPPFFLKRCLVLYG RS**A\WPHTNLIPPLPSGIKGDLCNPS AGGWEKAGPPSPGK/CEF*GRGTGTN FARG/WTKTPD
1816	15717	A	1827	276	3	GRPGFADFRVRPOLLQRFLPIYLFTEME SCSVTQAGVQNCNLGSLQPLPGLO*FS CV\K*FSCGLLSSWDYRHMPPHLDNKS IFSRNGVS
1817	15718	A	1828	1	391	LEPRRRFLQCVODCATALOPGQSKTSL QKKKKKKGGPP/S*YQKQGCPSGKKGR GVAGKGAFGPGGGENKTPPGGPTGEG PFPQKGVVGPQSGPTKGNLWGPGGPKL GGKGGPPGPTKGGGPPSF
1818	15719	A	1829	2	134	DHLSFVVWNPQGHSEAPSL/LINIWKL

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						AGCGGAHLSSHL/LREDHLNLEVQGCSE P* LHACTPAWATE* DPVSQTKLN* NIWK LAGCGGAHLSSHLGRIT
1819	15720	A	1830	427	107	VQHQPQQQRESPTIIITQKLARGGARGCL * SOLPGKRLRLNRP/SGSERSHQCTPA WTRDRCLCKRTGITRASSQRLSVGIQS CLNPRTAQLQVSAQSPSTVSTNL
1820	15721	A	1831	3	540	VQPFNFKITYRATAKKTIV\QHKQR* ID E/MNKI* TPETINSYVGYLNFNKDAKAI QWGNDSF\FKKWC*DNWISACKYSQTSV SASSASSSS
1821	15722	A	1832	385	2	AGRSQSETFYHNSTIMKVLQVCVDSLCL LPGSLVQDSFNI PAQRKRFRLRGSFWL PLRSFRSVGWPLPHWGQRSSGFSPLR\ P P* SOTPAFRSPPPAGPVPARSWVCGRPR QTRPLPAERPSPRPRRL
1822	15723	A	1833	7	399	RISRSYLSYEGSGSGKEHFTLGASVARIM VFG/VFIIFY* RQCLA* AQWYSHSSLLP QTPLGKHPP\AQAS* GAGTIGTHHT* L TFAF/IFVLGCFLL* NKISVTQAGGGGC NFGSLQPPPPGLKRVSCLTPLR
1823	15724	A	1834	2	306	LARLVDS* PQ/CDPPASASQSGAGITCV SHRAQPAEILKVGTCLCEPQRTPTDI FIIPYLFC/LFEMESCSVAQGVQWRIL GSLQPLADGVKRVSCLSPP
1824	15725	A	1835	12	400	KKGMVPKQLKVGKKPPFS CWGPNMKKRD SPVFHQDPIFP I P P P F F G N G L F F P P LAGGGGGNLN* PNPLPWGLKEFPPTPR GRGKGGAPPPF INFVFLKGGFPLGR GGLPEPPLGDPPLPPKRG
1825	15726	A	1836	220	401	KGSVFVIFQPESEGFPLG* LKPRFPGLK QFSCLTLRSGNYGPPFPFVIF/CGFL R
1826	15727	A	1837	12	357	GLLGGOMNGSLGTSYEDLMSSS\FKP NSPPPTPS/VRTGHLK* PLESSNGPFP PCVSHSFQCGMARHGPSPPQWNTFSP PQOYTCQSKTDP* PPPSPPYLGQEGSNA PSLA
1827	15728	A	1838	8	380	LMKTHAKLLNKRKAN* IQQYK/HH/NK MGFILGVQIYFNF* KINLLOIINSVKK KN/HSSSSSSSSSSSSSSPPVILKSLC NLGKNRNFCLCTGIYKNKTE\NSMKI ILNGEQLNAFFPLRLGTK
1828	15729	A	1839	2	444	VPGDAKWFSLVHLKDAFFIPLVPESQV PFAFEWENPNTREK\TWAFLP* GFWDSP HFFAQPLERDLRGLQLEDGSLQYVDHL LVYSPTQESDONTIKTLHFADRSYKV SKKKAQITLQQVHCLGYILTPGTCK/LS PERVQAI
1829	15730	A	1840	1	642	ETKGIQIGKEVT/SLFADDIDVLRIDS TKKLEVI CELNKVG* KINM* T* IVFLY IGNEHLEI/ R/ELMPCIKTSSTMKYL EINLKKDV* DLYTENYKVPREIKIT* A NQ* EILCLCSRLNTKM/STFPQVFCVY YAI PVK/ IPSRNFVLVVKLILKFI* KY CRPRTAKTLKKKKVRLTLILPKSY KITVITIGYCFQDRQV* WNE
1830	15731	A	1841	3	423	HRTTSE* DLHLARELITW\SNYGLDHKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YDAELDRMAMPCLCAIAGALPPGYVDAS SSSKAEKKATVDABGNFDP RPVETLSVI IPEKLDLSFINKFAEYTHEKAWFVKIQNN WSYGENIDEELKTRPMKR\PY\KTYSEK D
1831	15732	A	1842	33	179	YMLGGRGCSDLRSHHCTPAWVT/TA*LS KKQYQRQNRQLQYHLQYERKK
1832	15733	A	1843	349	10	LAGGLNSMEGR\LR*EREECTQQQMVH DKYCKDLMGFGTKPRHITPFSFQAVQP QQSNALVLLGYSSHQQLMGFGASPSA KSTLVESRCCRDLMEEKFDQRK\QWVLK CR
1833	15734	A	1844	15	856	AAEQLSFIYKLPQNPSPTSGSSLSGTH GWTMLGSLTHLENLTDMLGPELVQGI SPCCACQGRGCGGREGCCSPGVSPQG \SAVGRGAEGPGGLTRSGSGAASALVR GEKGCWCRTASACGPRRORTRGPSW LSFSQTSEKCPSPAGSACAGPVQRRQ SSFAQCGCTGACAPGST\GDAHPAQGS GGPLRLSPAVGCPRPGPSFLKTSGGGSV PQGVPIWLSLT*RALAAPGSQGPAGLAV SCTGGRGYRDFQAGCTAG*HGNSTRLR GP
1834	15735	A	1845	402	2	SKARRQGRPLRQG*APG/AARIPEQKRY GGP/EERRRPSARGPRATRVAGSGPKPK GQTAMAGGGHDPLPLPPARSQSIGS RSRGSQHSQEQPAPQSGGDPSPQERN LPEGTERPPKLCSTLPGGQPPNIV
1835	15736	A	1846	446	32	TSRKIS*KTGNQFLMKECSNHHKAAF TKKDVLNI\LAUVKHVNTKASETHFFQ SGQAKVQGGFVKEGCELINEALNLFNNV YGAMHVKTCTCMRLLDRLQYIMQYARA LSNQKQAVLM\TERVMGTEHPCIRPL
1836	15737	A	1847	440	4	VDGRHVEVSRKGGQVNVQAG\KTVEIWA DKLGCNMLGTADMVECLKSTRYKSLIQQ AITAGGAPAFGFPVLDGNVIPGDRQILM EGEFLLNYDMLGVNQGGGLKFVDGIH NEDVOTEND*KFSVSNFVDCMRPRRPN YERFO
1837	15738	A	1848	526	0	PRRDFPKRQTPIPTHVSPVMEKGPWGP APLRPDHPSLSGPCPAMG*KVGLRPGCP QTOISPLFNRSFASPLICHHHPPSEP\K PGPEPPPTPSSSIPSLARFTRGPSSPL PPPTQTPSGPP
1838	15739	A	1849	417	31	QATGQECGCHRGPPPGPACETEPQAPL RLPGGTGIWAGGILCPG*LPGGSLSP AAGRG/SGPSAGPGAANFSSP*/PACPS SSRAVPGGAGSFRAGPGLFTTLPAPF WCGRGASNKI IQMPLVC
1839	15740	A	1851	3	285	YTVCECVCVCLCVCLFVSL\SLCSVSV CFFPSLCGFVVCVCPACVSLAECALCAT KRFRV/CMAACLW*ASFVCTVWVRFAVN RFRRGSGALGA
1840	15741	A	1852	128	524	KTPGLGQRSEGVGGKDDLVHTAPVPTH GWGEGAASKPTVLPPPPF\PDAPTVEFF PPFFWEKKYFPGPPPKGAGPQIYLLGN PPGKFPFFPPHPQAAGI*YIKPPWPYK PLKKRGVSTLAP\GFKPPP

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1841	15742	A	1853	1	1648	MTVPLHSGLGKGVKPERKTTVRRPFVSA GKKYACPFKKAETPQWRRLMRPRAPAA SLIATFPISQRLIPITPARKKCPSESET STMVSKAPATPRTRGATPSPPTTRR R*ACSLQKLPAVEEDEFELGAVED AENRFTGSLPVNAGRLRPVSSRPQETVQ AQSSR/PAAVTPHCSLRCPGPARLP/P ASLPPARPVLTA/GPSCIGAAPLRPVST SSSWIGNQRRVTVEVLREPAPQSSAL HPLLTFESQQQVGGFEGPEQDEFDKVL ASMELEEPGMELECGVSSEAIPIIPAQQ REGSVLAKKARVVDLSGSCQKGPVPAIH KAGIMSAQDESDDPVIQCRTP\DPPI*DL VLWVTFLEFQ/PALTVPQTQLHWEVCPQR SPVQALQFLQAAGTIQSSPQNRFPQCP FQSPSSWLSGKAHLRPRTPNSSCSTPS RTSSGLFPRIPLQPAQPVSSIGSPVGT KGPQGALQTPIVTNHLVOLVTAASRTPO QPTHPSSTRAKRRFPFGAGILPHQCSGR SLEDIMVSAPQPTFHGALAKPOTE
1842	15743	A	1854	235	223	IHKFTIQIWLAKITCORTKV*KERSVLL PTSFSPVPSQGHYTCQ\LCSLASDLSQ PDLVYKFMNLAVLHAMNRSRVSICYPT MIYFLHANT
1843	15744	A	1855	373	3	IKDGIYRYFYKALDSFCLCEFPNQFFS CMDRELISQRCFLNSAY*FPSNL*CYLCY LFFF*LKXVFLTFFLPLADRVLLCCPE *SAPVHS*LTVDLDFWVKGSSCHSLLS SWDYRHALLPHY
1844	15745	A	1856	378	1	RQRHSFAGNTGRGPVTPCG*ISWPSITK DRTSMSSVTSAGALGHTAASPHARILLPLA LPSVRTOHGSPFPQGEOPTTICPSNLPT HPSLPLGMHPSVRASPLCK/P/SPPSI PASVHASKHPSPPVY
1845	15746	A	1857	3	379	YMWKRVIEVWFLLLLLLFFFRGGFLGQ GWGPPAPGFSFGKKNPGGLSSNLRGFW *TNP*PVPGGALFLVGPPTPAEPFPKFN SRGFLV/ALADF*TRPRLVSPHGG/RG AKGTAPFLESMPWMP
1846	15747	A	1858	452	1	GTHGLLLSGGPF\QVFKPDNFVFGSG AGNNWAKGHYIEGAKLVDSVVDVVQEE* ESCDCLQGLQLTHSMGSGMGTLPISKIR EECPDCIMNTLSVVPVPKVSOTVVEPYN ITLSIHQSVENTDETYCIDNEALYDICS RTLKLITRCI
1847	15748	A	1859	1	385	NTSSDYIFPPFFFLFRNSIHVSOTAGGQW HNQGSLOQPWPSRLK\CPITASASICLHMP PFLANFLIFVVEIGSPYVAQAGSRDPPA LASQ/SAGITGMGHCTQP*VLFPPFFFF SFRKKCSPPWPPGGGPIF
1848	15749	A	1860	470	17	IEMDSRVRPRDKLACTIKCSKHIFDAIK IT*NEIASAD/DFPPTLYIVLKG/NPP CLQNIQYITFCNPSRLMTGDBGYFT NLRGTHCSWLNMTMTWCFRAKIFSSQ WMSVYLRFRNGITCVSHRAHP
1849	15750	A	1861	3	790	CSRPEFFGRRFVEAVRSKPYLSLFP*SR *SFNVPAE*TSAKDILASSEPKQND VSS\LKQKFMQEVK*LDHIHTA*ADGSW

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						KAELEGRGPDGSAFSPFPQKPAASRQPEL GELATFLGRVDPWYQSNVNTLCFAIHKL AEMPPSLDTSRTVDPFLDVTIYYIRMG TQPIYFQIYTVKIFFSDLSQDPTEDI FL IELKVKIQDSKFPKDGFSRRRGVAEGP GAELSLCYQKALLSHRPREVTVSLRATG LILKAI PAMSY
1850	15751	A	1862	192	3	SSGSHSVTQA/GVQWHERSSLLF/LIT* PPGRK*ASHLTLASS*DYRRAPHPANF *IFCREGV
1851	15752	A	1863	82	370	SLCQKRAFVGEKLVHLLVSPSGGRVPS CPDPWGCRRPRFHAIVAVSFLKLRVVIPE VSILPEDELELYDLFKVRSSGKRGSRP *AGLSRG/DPACP
1852	15753	A	1864	2	325	IQVYSISHSITFL/YIHLRSGSMHVSM SLST*SYPCMDV*MLSNLCMVYIYL FYGSIYRFYLSLISLWLSITLSTYLSI YLI CHPSIFKTVIDEHAI FATWH
1853	15754	A	1865	3	377	YSFPCWKLFRLECKINVFDDLSPLLSGK EFNDTTHNTFDHMMNRTEKHEAGWLLLS SVDKVMKENDELRDSNMLQKV*PLK SAKTALSGSLNSCREKAEIVEKQTOSLT M*VADLQRMHVOP
1854	15755	A	1866	10	378	GWKNGEFIDAL*KVYGHKAPNKSAYYKN IT/*FKQGDDIEDEHSGRASTLRKKI HLVYALIDKD/*RLTAAAIANTIDISIS LAYRILTEKLLSLSTQWVVKQLCPDQ LQRAELPMEILK
1855	15756	A	1867	346	1	DILVVKLQKQPQNGKMLKAERKKKFAF KGVPPVRMNADFSIAAMKA/RRRNISIFS F*KENNCHRLRLYSAKNIFP/EIKTFSD REFVTIRSAVKEILKDVLAERLSHVK SRNV
1856	15757	A	1868	1	377	GTFQRTQCKGKIQ/YVVGLIYKASSDP TCVEKEKVIYIGKLMILAQMLKQWTEH WFAFISDIVGASRTSKSLCQNNMVLKLL VSEEVDFDSSGQITQVSKHVKQDSMCNE FSQI*QVLCQF
1857	15758	A	1869	90	384	QWLLFTEYSSLYHVPVLPFFFFFFGGRTG PWPAPAGENETG/PNGPSTPGGGNPP PLPPGGLGLLMPPPPRQILLMETKKRP PP*TNKCCSPGYSP
1858	15759	A	1870	2	578	FVVHALLGLDPLFGKMAWNSGQCSL GHTEGGTSWDFAVGGASWRLKVVCKGD SHKGPATPIASCKGPIRGPCPLLAQSKA *GS*KRQ/VAPGSP*LAGMGGV/DRLT LISQVHGNQVTOIIPFSTGETKAQRSP SLPPRDLIRGRHSWNLDSTQLLGYCPLL PPPLHPAGPLVPFPFTNGEIQKENSRE
1859	15760	A	1871	1	382	SGQDAGSCLLYAGAGSGANVSGAYNFYE IEQPRQRGMRFYIKCEGRSAGSPWEH STDNNRTYFSIQIMNYGKGKV/RITLV TKNDPYKYPHDLVGVKDCRDGYEEA*FG QERRPLFFPNLGRCA
1860	15761	A	1872	490	1	ADLSLSDKDPGRPLHPNINWDRGRQ*PGE TPQ*HRRSCASQDPGRSQ*PGKILPSPK PGRPPMPTGEDAGPPK/HGNPSPNDQKK NPPPK*/POGNRIHRDGRPPPO*PRKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: In USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end and nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion
						SPFNNLGDSNDQSRKFPVA*KNLPQSSS GTRAGRELYLPPOPGSSAFPNSTT
1861	15762	A	1873	373	1	GGGVPGALFVSHKKKSLFFPPPPPPFRK GL*NF\KIKGCGSPFLPLFFLEKESCF VP\RVCEGGVILGCPKCVLPGSPFSSAS AS*VSGGTGAC/RPRPGKFSPFFFFFYF LVEMRFHRVSQDV
1862	15763	A	1874	3	374	YMLGEIVSKTKIGQELGLLNQ/TSQVV NAKEKFL*ETKSATPMNT*IKRKQNSPI TETEKALLVNIEDQTSNILLTONVI*N MALLTFNSIKAERGEEDTEEKLEGRYW FMRFKKKKAISIT
	15764	A	1875	2	364	IHSKGESLWDJLDTFELDLPSPA*HI KAJNDKLDLIK*NFCSAK/ET*/IRMK TOATHWERIFVNNI*NRLVYKELKLKR N\KKMTIRR*ALDMDRHTK/EKMPMTN *YTKGCSISLVIL
1864	15765	A	1876	41	461	GFLYLCSSEIDPYPPSPKKIKSEWIRTY WMLLSSEWATIMLKSDLSQV\FCVNI P FVQAAKAKTE*DIYLLKWFCSAKAGI* KAKROPTW/N/DRIFANYCYGLITTT CMEFTQLTSLITTTTITLFWNPQCSYH NPT
1865	15766	A	1877	2	185	VRPFTKLDPLERTQYTLPLLYKWNNAKWM TAHL/FTA*FTEYPKS\SVKPE*VREI DYRMLYL
1866	15767	A	1878	1	491	IHRLLWPLLSAARPPSRESGLRCRAFR PASAAAAATAASPS\PTAPQGPPI/RRRL LIQPPPLYPRGLFTPGVPL/APGGSREP S*SLT*DARTLPLPLVLGPRRARLLGACP AVQAEQVDPVGHLSEVLAAPCKQP*TP PPACHCLDGEGRPSGVQAPLHKAKLYP
1867	15768	A	1879	24	449	LQPLLTWALLQPPQPKSRAAFFFFFPP FGKKSQFLFGPPGGGEGEKL*REPPPP GTGKMPPPPPPREGRGKKRGPTGRENLI *RKGVPVPGGRGGGQTPNPGGGGAK\PP KOGK*GGRLPPQPIKGPKRGRPKKRGK RP
1868	15769	A	1880	190	2	PLYCHKVGVGLELLTSGDPPPLSLPKC WDYRY\DHHAQPSF*LFLSVQISGKFN HSVQPCI
1869	15770	A	1881	1	458	PATRAGRNLPDKEFRYDLRTIVIAAVYV GLNSKRLCLTS\LLTFQHRAGVSPYTS FGFA*TCVFAKQLLEFILC/RPCFHRAP LFLKLGHFAP/PP*QCFPR/QALGSP /RSTCVGLRHO
1870	15771	A	1882	3	392	YMRVHYLLIRNAKVKTLSSTNDQT* LKLHC*QECRMVQPLWKV*QFLIKLNI *LP*NLALLWGIYLLTMSYEF/RKI CIQFMFTDLIVIAKYWTQ/PQCSVAGW IKQ/IRSIHTVEYYSAVRNQL
1871	15772	A	1883	2	473	TGGIAAYVRDROERSNGRQGNRRNLGS TNMRNRKQKGLRRCPRN/RSRGMANKV DKPRDAR*KSDDRO/RGETDG*RVSGG LTA*EAYRH\HRGO\EAASQSGRSQAG RQTP*QEQAGNEAIREEEKSRGOERE RE\KRDADRHHK
1872	15773	A	1884	138	444	CYTLTKCRIIYINDKVIDVLTVWY*HK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1873	15774	A	1885	27	470	DRHID*WNRLQSP\LNFSIVQVILLNN AKNTQWVKDILLDKWYV/ENWIYQCMRM PLGSYITPMNQFKMNYGLS TTCCTYTLFFSFFSLPFFFFGKGVSF*S PGGENTG/ANLG*WNPPPPGKGISPA*P PKEPGMEGAGHPGTKS*PGKFGPGGG GPSFFYRGNPKTWGKPGPKWPGGIGY ATIPQKKQPEGKRG\PGGPMSPYNGPP KTPTHGKGG
1874	15775	A	1886	478	1	KNVQENSALQAAAMCRMLIVCQTCQVIL SGESGAGKVAIAKYIMGYISKVGSGGKE VQVRGKQKDKLGRPHLHGSAAPICTP ASV*LLTPPASP\HVKDILLQSNPLL EAFGNAKTVRNNSSRFVSLCRPAWSSC SLRADLETHPPHTRV
1875	15776	A	1887	1	402	HSLEBPHTYG*LFKNLPSRD/VVFAMLA HWSRT*PGLKOSTPLSLPKCWYRCEPH PAGSFFFFFLKNGFWGCSLGGRAGGQQ *LKS*WRPNPLG*GNPPC*PSKEVGTG AHKIANREIRTRACGNTNSL
1876	15777	A	1888	511	124	GTRQHFAGAHVPEPGFS\MLDPKLV DDRPARDMWIREPGLLLPRAPODAGKY YCHRGNTMSFHLKLTARPVLWHCLLRT GGWKVSAVTLAYLI\FCCLSLVGLHLQR GESCPQWVCNPNTPSPG
1877	15778	A	1889	667	310	QLKP*ATKSV*KDTAFGLDVGNDFLAMT PKAQAMKGIDKDWGFYR*SICTAKETI NRVKR*PRK*EKIFAKPTWQKGIS/RI HKEFQQLN/KQKSNLIERQTKDLNRL SKECSKDL
1878	15779	A	1890	462	3	KWFFFLGPPFLPPP/PPPI*NPSFQKNK KLTRGGCARYFPPLKSPRPPIPPFFFEK GEGSPNSKHSAPFPWGPKEITFFRRT PPPPPPPLCSFLKNNLFSYIPKGFGLGK GQNFHSFLSPFFFSIKKKLLGLGVHVR YCRVNSTCGFFVQMY
1879	15780	A	1891	1	455	NTCLFGNGFLDPT*PKA*SMKKIINKLD FNETENCSVKDITVKMGKQATHWK/V RKTHILYKDLIKYVQLLKHRRKKTST IKQ*AKDLNREDIQWINKHMRCSGWR WFTPIIRALWACKVEGSSLESSLGNIV RPHRREREIHCY
1880	15781	A	1892	1	537	RGGIQAPKEVSPGREGEPARKSLI*TA* ETPP*SQ*/DIDEP/TGVPMKKPVSVS LETGKHAVVPKVNKGLEPDNPTIKWFK GKMLELGSKSGARFSKESHNSASNVYP VELHIGKVVLDGRGYRLEVKAQKDTCD CGFNIDVEAPRQDAYQSLESFORTSKR SLYALALEDPGM
1881	15782	A	1893	2	514	VRCQRRCHE*ACGSSLVNAKKLYEDAL MARKVKQSLFSLDVETDEDKQFMMSLQ\ CSLAYGTLTKILSEKRSKASYGMSVVRM RSAGQTSKAHLHPRRVSQVLQVPAVNL LPFRKGGQTKDPALNTSLPKVLGTTEE ISGKKHTEDTISVASSLHSPSPASPGS
1882	15783	A	1894	473	2	VMGESRGSPPPPTTGGNFVFWKGVGS LFCPEGFKTLCSSSPPPPPKAGVLGG SFHARPPPPFFFIQ*IPFFGKIKP/LC

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						SPDP*PL*KKRGI*FVPGKIFCEMESCS VQAQGVQ*YDHGSLQPNPPGF*SSYLN LV*LSS*DYKCVPHPMY
1883	15784	A	1895	613	11	FRPRSFACGLHRAVSVFLPGAQALSSPFG LNLVFTAGSDAG/LRLRSPRANPRVA LPRVHTGPSST/DLSPSCPLGACGFGT SQPACL*SPFLLLAPAPSGCANGLPFP VCSLHLRGWGGADPTGCLDAWAMALAS LRPCLCPALPLSREPPSPLLNDLVLRPM PRRAPVLPLGRTPHSLLLCHVQSPSEQL PSKGPRL
1884	15785	A	1896	20	449	KFGYSSAAARRQQLGWEAWL*YSFPLQL EPSAQTWPGTLRLLENRALLVNVKFEQS EVSPCVACGIAALSMGSTSSVKLLSHF QAPLPQWHQMVFARCLCMGQALNVPP\
1885	15786	A	1897	393	3	ESFTFQVSTKDVPLALMACALRK/KATV FRQL
1886	15787	A	1898	395	217	RPTAGSKGNI*VRVAS*EALSPKLLDFL PGKVLNGEKVDVRPATRQNLQFEAQAR KRECVRVPRGGIIPRAHSRSDSDADR ATPSENLPSSARVDKPPSVLPYFNRP SALPVMGLPPPIPPPPCI
1887	15788	A	1899	1	375	RER/CKSFR/PPA/HLOAKIRGAQ*QVN QAAARQAAAPAAAMVSRDSSLLVSSQK SKVSNYM
1888	15789	A	1900	47	326	NTVIVQ*NNKAMTVHFF/TAMFSEYFK ATVEIYCS/EKIPKILLVFARVHSHPR TLIEI*KRIYAVFIPANTPSILOPMDHG IILSSKPYLLRKASRAQLTPVIPALWE AEAAGSPVCGSSLA
1889	15790	A	1901	181	837	VKSIIQFNSKNEFGKHKDTPSPKGTIV WWLGSELRSYSYGAAGGAEMGRSLESW RSRPPQRAETAPLHSSPGSGSEMLSL*RO HLTPTWAGVQWRGLCSLRPRFPQFK*/ FCPSQHHPQPPSSWDYATRCQATKQFVF FLEMGF\VMFARLILTVELNN
1890	15791	A	1902	1	385	AGRVDREPGMGITGCKLETSGRETRS ASRWGRGRWRLGQACRVQGLPLSTFHL GAQAKARGGTPLACSHLPNSHVGSLKA QRDEAMVQSLAPAVSSTCTRTW*GSEW *GLHIVAARRQOREEFPRTTAAPET LCFOQTSWASSCSLEHSAQPFSEVQVRAL SVPSHSMMV\FQLSLPRDHRKPPGE
1891	15792	A	1903	207	3	YTWGRGKGLPLHCL*EYKLVQLNRAA WRFSK*LRVEL*FNAAISPLGVPEENK LFYQNSTCTCWFITALFITGKT/WNOP
1892	15793	A	1904	2	391	FREMEFLHLGQAGLELSTSGDPTLASQ NVG/HYRREPLRPANTLQS*PLGLQKPS CLSLPSSWEYRHMV
1893	15794	A	1905	3	424	IQPLISQRKYKTLQNSLS/CCAHF/PP HFFFVLDSYFHSLLSQKNAPFT*G*CF YWSKSYSLHSWSSSLLPCLTSSGF PYSFPSPQLFCPSLEL*NSLSTLCLL FSLLSQPSFSNRWPDQYL
						YRAGCLQLLPPFLLL*LLPCDVPFPPS S\LP*VKASCGLIRSQQNVGTIPCLQNR KSNKPLHLKPSLRHSIRAMQNRILPILR IQKFF/IFFS*DGVSLSCHPGWSAGVQLQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1894	15795	A	1906	2	389	PTALHLL/VLKRFFCLSL IQRGDLKSLITDNI PSSQSLIQKKGVN PSPFKSMKADRGKEAAEKESEASRWFMR EKERSHLHN/IK*VQGAACYDPEDLASI IDEGGYTKQ*IFNEDY/MWKKM*FRSFL TREKLTGPGFKASKDRLTPLV
1895	15796	A	1907	458	13	AKEETQSVVDFPM/VPQGVSVPFVPSR NANLSTIKQLLWHRAQYEPFLHMLSGPE AYVFTICINQTAEOQELEDQRRLCDVOP FLFVVRMVDCEGARVNKLSSQISLFIG KGVRELDLSLDPFVSDFSTKMCQPCCKS AAL*QATS
1896	15797	A	1908	409	3	EKIDGLYRASQRGKDLRLRCAQSFPASH KCMALCNLIHRRQDLIGIAKLRKDD PICNLNTAFVAVAKYLDIPKMLDAEDIV TTPKRDEKAIMTYVSWL*IVLAGAEQAE TAASRICKVLAVNREKKKLMEEHV
1897	15798	A	1909	116	379	HSGPRRREGALLKPLCLPHAKRCLLLFKM CSDGATLCCPGWSSAAPS*LTQSF/AS TSQAK*PSHLGLPSCNDYRCIPHPANC LDYYY
1898	15799	A	1910	418	3	QD*YATANRWFCIMLSOACPLPFL*PAH LL*L*QLMLFSFPGTPEVFSYGDIEGLDA SALPGQHMEAPVMLWDESSFPDIPGAVS ALMTIVKGQSEAPGSLLSLFRRLSVQRS KERSLLHGDFLAFSAGPKLSYIRPMY
1899	15800	A	1911	394	3	ILEAYPEVKDPAVKGASSKEMVGH*/A AEQALPVASEQEQQRHERSEKKQPQVKE GNTNINKSEKIOLSENICDSTSSAAAGRL TQQRKIGKITYPQQFPKCLKKEHDRCITLK QENEKTNVNIMSKNREDV
1900	15801	A	1912	499	141	PGLGERDWSRYGGGAGEGSTREWASRC G/IRPGDAGQQQPREP*SVCPRGASHP GPGSWKASPAWHSAPGGRCSGLGVQKE GFGHLLQPGCRTPGPGIRKERFSYGLQ
1901	15802	A	1913	127	387	ISFVFPPTLPKMPQLKPETISMTGLNLF ICHLNCLARLATSAYDGCNSSEV/CDDL L/*AALFLKLDYQIRFPNYFSKYRIYY LCLY
1902	15803	A	1914	504	0	PGFGQRKHSTAPNCLLNIVYQILRFLVLA NQIYKICKRIIHHDQVGFIPMQSWFNI QNO*INLIHHINRLN*KNHMIISFDKT HHLPIKTPIKLGIEGNLLNLINKNIF/S KIPAAINIILNSEKV
1903	15804	A	1915	46	415	YTSNKQLQITILKITVNSTKKYKILINW IKDVKDQYENQKILLREIKDNLN/VRD TSCSW/NIVQMSNFS/KIYRFSPEPNK NLSTL*ILTTSF*FAWKYTGTYKVTM KNRVGRSLPINFQNY
1904	15805	A	1916	420	1	ENADCVARARKSPDSTP*\RGQISVTM VSPNEQEKAGOLAIGVRAVRVNGV/LLA KMWKKLHLTLNLSANLEKIIAIGLFSNF ERKPPENTFLKLTAMATHSESNLSCFAQ EDIAICRHPAIKMPKEAQYKPLTASV
1905	15806	A	1917	384	3	TRITTSGGQYSTHIVRASRVPTRS*VPVF RCSSTNRRFSQAIEPRVMH*KVHIRAST VRYDSGGHVAVYPANDSALVYQLGKILG ANLYVVMNLNLDSESNKGIPIPPCHTS/

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1906	15807	A	1918	405	105	RRTALT*YLDITNPPMY KAAEQRRREITCSGPHSQADSAMHPLVTW WH*PPVVARSSQSPGVHSPVP/HVCRKI LLIRPKMALANEGNYRELWPTPMSRSR +VCLLTTCMCVGLHLCV
1907	15808	A	1919	409	3	GGQEEGVERVLNKSKEFETTERGKD*TPBV KDQETIH\PTKPMHVAHMGPDGKQVLM DLPLSAVPPSQEESPGPAPTINLROPPC RNKPYISWPSGGSEPSVTVPLRSMNDP AQDFDKEPDSDDTKHSTFTSSNSNP
1908	15809	A	1920	9	470	APARNELERFCTNFTGT*CLRARPPFA SACLGGGTWNLALWLCSPGT/PVPLTLP PCS/SCEVQPPASHSVASNSQSKPAKSA AVAHECPGGTGADPGWPGATCPESP GPATPHTLGVVEPGKSSPTIMEEPWAP QGSFCWTVRQMTMM
1909	15810	A	1921	556	1	YQLWALGGLLRRVGRDPFSSHRIKGEFS AMAGQAGNGDGEES\GGLAAPVPHLP *SQAAHPLLITGPGQNLGDSKV*GFP SPRLEENTLENGWGSQKLHGSQSGH GGSWKNGETSLKG/PH*ADGAGRHTMFQ SPSPPPKPHSV*HNPPAS/PPPHGSPA PSGTSPLPMSAVSLPPGSL
1910	15811	A	1922	567	41	GGWGETFSRLGNDLQAH*SRFNAQAQE ETSR\VLAVSLINEALDKGSLKTLAL LLPAAGLDDVSLVPAFHYHLLVAAKRR KAQVTGDPGAVLWLEERQGVVRATQDA NTAQRNALGVAINQAIKEGKAAQTERV LRNARVALRGVVPDCANGYQRDLASAMA KIORPAAV
1911	15812	A	1923	2	405	YGGCGITSSSVLHGMVFKETEGD/VTS VKDAKIAEYSCPPDGMITETKTVLTKT DEELMNLKSKEENLMDA*VKAIADTGAN VVVTGGKVDNMLHYANKYNMMLVKLNS QWDRRLCKTVGATLAKPLTPCL
1912	15813	A	1924	510	37	LLGHAFHVQSSSGRPOLAESGSHLKK GECVQORTGNVGLSPNTARWGTPLGPSI SSAPPPWSFSAFFPGPQSGK*AAKDGP CSLKSGLKR\RSQGLR*TRGSGPSPMP PSPS/ERPPGDEGLLPCTPRGGLPG FKINTACVCAADISPGLEPV
1913	15814	A	1925	74	429	ATIPGHELLLFFFIFFFFLKGAWPL G*GKG/GGPIRG*GNRAPRG*REFPPPT PGKRGNTGGQPGQPIFGFLKKGAPP GPGVPKTRGQIEPPWPWSKRAVGTGWT LPGPKV
1914	15815	A	1926	515	304	ALAASLALALNGVFTNITR*IVGRPP DFFYRCFP/GMG*PHSLMCTGD\VV NEGPKETSPSGHSSPV
1915	15816	A	1927	1	433	NTVGSNNKSKKLYFAETKSYLNFINNL KGPO*VKILKKKSSVTKCTLIHSA*Y KV/LKIVWYQRDTHM/DHWNISIKQHW KQFPGDITKTQWQARDCLYNWCKEK\W ISTSRMKFNITYPTP*ANINCHQDPNSK ELVRYKN
1916	15817	A	1928	316	356	GGT*PPQATPIS*LYLFTSSL/TLPP APSLPLQIAPISDPSPPRYS/TPTPPI SLGLAPPTLLIPVPSLPVSPRLNSTA

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						PP/TELTGSAVTVVSLAVSLSPAFAS AMDKAQNM
1917	15818	A	1929	490	11	PTRLTCPGSHVPGVPVTFPPYETHSMF\ P PCHVHPLVQPPGSSHVPGPVTSSSPSPPS ATHIHPLVQPPGSSQLNTHVWPSQMR TWLQHPPLPAPPQP/PSPGS ICSSMTH LTEYLASFPAFQ/PREQAPQGVPTSLP QW* APOPTAPCRATOSQQLLDG
1918	15819	A	1930	1	552	RNPRKRAFPSPPTIPAPPS* NQENERSRH PQSL\ /PFVKSRKRAFSP/ LSPCSSPV KSRKRAFPSPVPVAPPS* NQENERSRHP QSLLLLEIKEMSVPTPS PCSSFVKSR K* AFPS PVFVLLRHDHFLPLPEPRQPS TVPGCGFGRIPRRWNHTGCAFLLI CH SARLLCDPRVSSCVVRHS
1919	15820	A	1931	414	3	RVPGESK* ERVLDSKHK* EGGRRGNI VSKRVYTT* TVITDVTNLSIDQVGVH RSIAANTFABVTVPFNIDRLQELVRG NSQYPAKYIIRDNDGRIDRLRPHPHKSD LHLQTVGVKVRHMCDDGDIVIFNRQCI
1920	15821	A	1932	521	103	ATEPAGVRLKEGGNITSEFVTGNVISA LADPSQDA/ SRYSS* KKKQVLVPRDSVM TWLLEDSLGNSKAIMMATTSPADVNYG ETLSTLRYANRAKNI INKPTINEDANVK LIRELRAETARLKTLLAQOQIALLDSP
1921	15822	A	1933	1	490	NTGWVVRKGEENGTLMVRRLP CVPCLSS AGGLTEDEGELCAAGFPLLAEDFGQAL QQLQTAHSQAVGAP/ KGGDQVLGGGTGA PPTAYPNHALSIS* IPSVSHWDEGALPA VKIEILGI IHLPERHALLSLVQARSGL LLHGPPATGKILLNKAGTTECLT
1922	15823	A	1934	383	151	EVAFLENLIKDDIERGLPLLLVANAGT AAVGHS\ S* LGRMKELCQCVNRPKMEG YMHVSQHPVPESHKMRKAIF
1923	15824	A	1935	379	1	YVPVSKDKKEYFFNSQ* GLTTHQILPYI DGFRHVQKISAEADVKLNLVRIAIQILL * VGLQSYLGQHPGPKS/ CRGPGCEGNE GMVLR* AQLSLSGTTAL* HWCPSRKL IQFGIINKLIRRLCI
1924	15825	A	1936	376	2	GCLFTYMKFTAMSSSQVARSGEVSPFTA VPA* S* K/ GGHGAVLGCHITSEACFOAC FFFLRPPORTCEFA* SOC* DYKSSSHG GTAHSP/ HGTATHTPMEQHTSHHQHTHS HEQHTSHGTAHMY
1925	15826	A	1937	426	1	KHGEIIBDLKVYRDNASKSKAT/ YSKW ITHNKKRRDDVGEVHSSRRATSCET IHLVCAI* ED* LIAAETIANAVGIPRC SAYTILT/ E/ KLKLSKSTRWPK/ P/ L LPAQLQIREKRSMAILKNKNQDHEAFIH ITTAGLY
1926	15827	A	1938	2	469	KRRKLVSSTAATAHPALSS* TRQRFLL LFLFHIVREDLVQLRIKKHTIQIGNVE VKLL* PTDNIILCGKLYRHRSTQKVQL LI/ NFSIVAAYKINMHISLVFLYSNDE* LENKTQTSSPTIALKRIKYVGSNKSK KPYFAIEKSYLDFIWN
1927	15828	A	1939	468	920	IPLSTHSPMGTSHTLSTRHLSFWTHY ERLNLPGRETDWA/ TMLFRWGLMLPRL

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						VSNS* A Q V I P F T S A S Q S A G I T G M S \ H A S G H L I F N Y \ C S M * W L H L R N S Q * K R C T G Q E T G P C E V T Q D S V G W S N Y S G L * P Q T P R L K Q S I V H S L P S S W D Y S
1928	15829	A	1940	448	474	G I P G C * G S T T R N A L Y H V M G E D V V I L T T C K H G K D W Q H K H S R C R D R N T E Y E \ Y D F G E M L H N A T F C L V H R G R H G S F R F L E A M Q A A C V P V M L S N G W E L F F S E V I N W S Q A V I G D E R L L L Q I P S T I R S I H R D K I A L R Q R S Q F L W E S C I A T A I E D P N L I G V V R
1929	15830	A	1941	1	423	N T T I F A G G M * N V C P G P L C A R L L H R S L T H A T P D P P L L T L P * I P T P T S S R C A P K A P P H L I C P T S C P L C S K P H P W P P / C S S C O
1930	15831	A	1942	48	417	R L T M Y Q V L Y R L H C T A L O P L P R V K * F S C L S L P S T W N Y M H M P Q C P T N F \ C I F T R D E V P P M L P \ S W W R T P
1931	15832	A	1943	450	2	V H R R S N R O N M T S R * R C A M Q S V E S V \ G V P Y \ E Q * T I V D G I \ N S G W E G I A Y A * I E E R Y P E E F A L R D Q E K Y L Y R Y P G G E / A Y K V E T I K L N V E A V N T R D K P T N I F A K N Q A P V R M R R N S F T P L S S N T I R R P R N Y S V G S R P I K P L S F L A Q E C I
1932	15833	A	1944	451	3	G R I T R H L P R A E D D R E R E R E P S P L P S R H P M F P S V T P K A S S D W P / P A S S I P C Q A C H G / P P P V S L P R K P A H R S C \ P V F P P \ A S G G D T S I H S G K T V Y V K R K S Q A W P V L P P G G L * A P S H G A P S P S P P O H R H C P E I \ R * D L L P A P A S P F S I P P L Y
1933	15834	A	1945	402	3	V R L I V S W K V N Y * S R S K A S L / H P Q I T A S L T G S C V N C I V I L L N F F Y E K I S A W I A K M E I P R T Y Q E Y S S L T L K M F L P F V N L Y S S W F Y V A F E K G K F V G V P G K Y T Y L F N E N R S S E C D P G G C L I E L T N Q M T I I M A G D V
1934	15835	A	1947	1	405	N T G W R V F A I L C S L G R F R G I E R V / G G K K K K K K P G G P L G P A G Q K T P K T Q K G G A Q G N R G K P L F S G G N F N G R I F G N P L P A P G P G G G G G P R * K T R \ K R K N G N W D L L K G G G K L V F C P M V G K L S G V P G V * Q K N F K G W
1935	15836	A	1948	443	1	L T P G A A N A S L L G \ C C M E D L S V N G * R Q G L W E A L L T H N M V A G C L E E V D N A Y G H Y E A F S T L A P K A W L S V E L A E P C V P E P L P P V F A N F I Q L L S A / P V V T E G G T A N L E W H V Q P M L A L M E A E L R K S Q V L N R V T * G A H Y S D C I A A A L R I K I T
1936	15837	A	1949	396	2	G N R G G S V P F N S L N E D G I S C A I * / R H I N W L N G * T P T I Y C L * E T H L I C K / D H / H R L R V K G K K I L H P N G N O K P A G V A L L T * G Q T D I K * K A I K S N K E G H Y E I K G S V K Q E N I T V G N I Y A P S T R A P R Y K Q L L D L K G V N
1937	15838	A	1950	419	1	R W Q / P S A R P P T P S G K * G A S L P A R P S S G T * G A L L F G C P V W K V R S A S W P P S R L G S E E P L C P A \ P S H L G S E E R \ P S R P P S H I G S K E R \ P A R P E I A * D V G S A S A P P / L P S G M * E R P A A P F S R * G A S L P G R P S P E M G V L P L R P R W D V R A P S R A F W E V R S V A W P P H L R R E K T L R L A T A R V
1938	15839	A	1951	422	3	Q N H V M S E / D A K I A F G K I Q Y P F M E S L N T L * M K V N F L N L I K I T Q K N P L A N T M E T G E

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						MLE/AFLLRQGGKRS/CSLSPILFIILL EVLPS*VWQEK*/IQG*EREE*NCDFVD DMIVTVEN*KKPLYNLL*IIS*VARFKV ILDTCI
1939	15840	A	1952	2	409	CARYSKNPPQRLRTDARLPAV/DFWSL GAILFMVGGCGPPFQANDSETLTIMD CKYTEPSHVSKEGKDLITRLTQIDPRRR ASLQ* IENHPWLKGVDPSPATKNNIFLV *YK\NLSEEEHNS IHRMALGDTDR
1940	15841	A	1953	2	367	IQCVRL*VHVLCASSCVCTCLVHVHATL CVSTCL*CVAVCM/CLLCACATVSACSL /V/CGCVSTCVCPVCTCDVCMSAC VCT/CLCVCTVSTCVCRRLCVPTCVCR CPCICSSLNGNEWMG
1941	15842	A	1954	374	2	EAPWLLRAGRGALPPCWSKTPPSPPLF\ PPLLPGTLVQWVPLFPWNLACAVTL ST*ARAGTSNPSWHLPPVSTAPQHPSTW QSPGAGTWGDPSPSPWTSHELLPGCCNHP CHCPFPHHKPTRV
1942	15843	A	1955	1	411	NTFSPELHPC*PGL/PPLFSPFQOQPTW APPRTSQQQLPILCLLKPSAHTDAPCT QPGSTLPLHTPTQOAGGTAYOIHHT*A APPPGAKPG*RCPPPPSRQORMQTPA PGNPQPCRLTTLTRVLVFAVPLPI
1943	15844	A	1956	33	451	RGRTFPGQLSPPPRFK*FSCLSLRSW EE\RDYRCMPVHPANTMLASLVLS\CD LPALASQSPGITGVSHPTRPHLS*FLMP LE*GHHHLLLVLSQPPNMPP*FORFST GQLECCSFRNLIVPPSPSLNFHSDRFLPT S
1944	15845	A	1957	3	399	YMQVRTTMSDSSHSISKINDNTRKSK G*GSTESLFHWRWEYKFVQLLWETVMHY VR*FTTILYNPEILLKR/IFRHTYKNVC
1945	15846	A	1958	47	399	AANPTLPAVFFFFLETEPPFGPPGGR GQSRILTETPPSPGVKPIPR/PPPPGEPE KWPD/QGGGGGGDPKPPGPPPP*ATGQN SAGKKKKKI PRPGAGADPLLPKAGG EEWLDP
1946	15847	A	1959	407	238	TQAFALI/KDGGVIGGICFRMFTQGIS EIVF*AVPSNEQVKVSGSPRRQPCQTAH S
1947	15848	A	1960	106	1854	NEAVKSKPNQTRNNHKEKNVYVHLPDQF SQPASAGGSSSACRRSTKATLHKRNVSS PACPGVQPLSWQHPMMMA*GLQGNPSQ AAAPPARPGLVSGNCLT*EMAQAGA/GT GGSLASLGGKRCPIVPVCE/PVL*GLC VPGRSSLGLGGINVTVQSGFPQGAESD PW*GDAECCSLLQASFGDRAGWSIR/RG SVGRPAVGPRGKGRKPTLSGA/SGPGSV LGGFCCEPLSREAESGMVQE**GRFWT GQERTPTGR*GCKVAGYHSSATVGHSG AGAGSGPKTSATLDVGGGLGGT/PSGP AWDRITNGYMEKALPLCNGKVTGNTQCG AQPASGSPSWVWQPLLLRORLRQSTGL *LLFPVGGGLQPGEG/QGPFPSPWGS LTGRKNSNKARPGGNEGTEG*GARNGAS LTVWVTVPNGGYCPQAGRDFWLVDSEFK PSLGLRAMV*NSRKAPLSFEDGRMGTV*

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						PQOQGRASHRRKQDSGLSPHSQKG*DP*G/PGGKERSISPPPLPRGL*GP/VGERGRNGDMWP
1948	15849	A	1961	76	427	QRQEPPTGHTTSGTRHPFGPGGRGPIQT HSHSHLPFWLETSAGSSFPNFLCSLPFY TPLRLRLSPFLCPSTQTTQRMPIADPH SPASPCKVP*DARGAPAGGAPSTL/RGH HPHPH
1949	15850	A	1962	375	131	FLVGRIRLLCYCLREL*FVYLLREOKAKRN SQWVHTLPISRRHVDVAPCSPSINNRNM GRDKRRFPFL/CVDA*LHSPSVVIQ
1950	15851	A	1963	89	538	GLTLLQKWHFPGAVSSMVERG*LLHSGLF FSPDPKVS SVVQAGVQWHDLSLQAPAS GSKRFSLSLGDHRHAPHHLAHCIF/M*T QDFAMLARLGTSTFIYLFGCC*/PETGSH SVAQAEVQWHNHSSLQPHSPRLRRSFHL SIPGSDWDRNAP
1951	15852	A	1964	402	42	CCHYPGTPLQGLRLSASHQAS/SGPQLP APLPLQVLFPFLALGIGVDDVFLAHAF T EALPGTPLQVGPCL/QGSSEAAQLTG*E PLGSSDLGLMNLGASCPL*TGIIIVL CPKGYCLDQ
1952	15853	A	1965	8	14	SSRAAACPPRPALSLPRPVPVTRRMSPQ GSGLPKLPVSAPSSRMGSFPAPSPLLLA SGRHLCPDAAALPLALETGDCS/PPG H*PPSPGGLHPCSPPS*PLIL
1953	15854	A	1966	521	2	YSLYGIIRKRHRKREVSNNQVRYKEHSIP PDVBSVPDTPWGPERRREESSGHFMV DHTGTAAGGCGMILLASPKLGTPLPPE *APA/PPPPPPPPPPPGVCSGHLNIFLI LEELRVLQQRQIRHQMGTQICRQVLLL GSLGQTGAPASPEIHOTGTASSTKPL LPLTV
1954	15855	A	1968	111	395	YLMRGFLLHNNVVKGEDEKRTKGRALI LFFFFFKKESPSPPRVEGRDP/NLGT* NPLPPKVKLSRPTPPEKNEFGAVPHCP NNFLFFKNGGS
1955	15856	A	1969	413	101	DVNRHFSKKNKHCQ*LVTKENQIKTKRR YHFSPTRMKIKIN/KKENKFWQGYGETG IPTHCWECKMVQPIKKTVWQFFLKVK* LLVFGPACKELGYSYSLVTKS
1956	15857	A	1970	411	1	NLTPALCTKVHFKWVMDIKMKGTIRLL ENNTRYKYLHNKIWKGLNRT/KP*TIK KTKDKFDYDTIKNLSSSKNKTQTIDWE NIL/YLQYITDK*IISGIHKAFLKV/YK /KKTNNPVGKWARDLNGHLIKNDIHMAC I
1957	15858	A	1971	3	828	GQACHFIFRSQAQGGSLRLIWRARQLGL WRVCALIMPALEHSFPTRLLQGNSSVPGP SISLDTSC/LCNRCVWEGGRG*TGPLP SLGKVLVEGIPSESPGPTASHPCSPRP DPDQ/LSCISAPSATPTVH*SHLTLPMG WFGPQ*GLHSLDQPGPRKP*PGCSGLGG GDAAPROMCKP*FPFGLP
1958	15859	A	1972	398	3	PGCYFESVRLQCF/RKI*PAKRAVC SAT LTVLGQPSLSAPHVLGLAALVHCSL RSGALPEVDGPPAPGAGLVPVLPALFDSL TCRTRDSLFFCLK*ALLPQSRLLSSLSK

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1959	15860	A	1973	2	433	SDTCSFDKIRDRHADIPPLY QDPTKMTKEELNALKSTGDGTLG/RASE VEVKNEIVANVGKREILHNTKEQHTED TVKDCVDIEVFTAGENTEDQKSSDPTAP FLGTLAGATYEEQVQSQILESASLPENT AQVESNEVMGAPDDRTTRTPELSPNCWSD LNGGS
1960	15861	A	1974	373	580	TTFRSQVLRIGNALSDKPNVSTVYSNNG SELHGTSASV/YHKKLISTEYHKTL
1961	15862	A	1975	47	413	KWKHLRGSSEHWRPQENQVHQTAEALRKA GLWSQRR/PAAEAGGPRKPSHWDYLLLE MQWMTDPAQERWKVASKMKMVRVARQ LQDRTRREAGAREPEPSRLRQTSVPLPE KSSVPLGLVLR
1962	15863	A	1976	444	3	GYEKSRTGTSITHSSRDYDGIQGAATVK WMLDQFRMLSPSCSEVWHPQFYLKRV IMACCEWLIADIQVSSDKVRGRIMSRH SAAIKRRTQQLREELLKPLCPGGLDPS GDAPEVCRAATGAETIMHDQV/QPSS KVLPSDFQ
1963	15864	A	1977	281	567	PRSSLQQLSRPQKGNFPVPPVPP QRMFYDSELSFGISDPSCCF/RSAPTAD QVYGDQDMHEVVRKHCMDYLVLRKWRPLG KGQGGKISSPHRP
1964	15865	A	1978	357	2	KQILGPPHPQAOQPRVFPFPHGPKDAFL WSSRAAPPGRGLGRAGPAAGVEAGATLR DSSPSTWTREGLHVQAQRKRPSSHVHG/ SGPGCLEDEGFPTSLRLQAQLAEIGRGN GLSVRRQ
1965	15866	A	1979	29	434	VQAEAGLFGDTEHPQPLMSRSEGGQS DVTIKHVACGDFPTACTLDRGIIMTFGS GSGNCLGHGSLTDISQPTIVEALLGYEK AQVACGASNVLALATERELFALGRGDSG RTGARTKESH/YLPQQVMP
1966	15867	A	1980	3	2082	SSEGYLRGNMSENEEEISQEGSGDYE VEEIPFGLSEPOSFGFEQSPFEFQSPR FEPSPGFESKSPGLVPPSPFAPRSPFE SDSQSPFESQSPRYEQSPQGYEPRSPF YEPKSPGYESESRYEQNTLKPQSPFE FEAQSSKQFQGAEMLLNPEKSPNLNISV GVHPLDSFTQFQGEQPTDLPICGFEM PTGALLSTPOFEMLQNLPLGLTALRGFG RRGGRRGGQQCPRPNIQICCKSPGRGS TLIQHQRHITGKPKYCEVCSKAFSQSS DLIKHQRHTHTGERPYKCPRCCKAFADSS VLLRHQRHTSGQKPYKCPHCGKAFGDSS YLLRHQRHTSHERPYSCTECGCKYSQNS SLRSHQRVHTGQRPFSQICGKFSQRS ALIPHARSHAREKPFKCPCEGKRGFGSS VLAIHARHTLPQRTYSCPCDCKGTNRSS TLIQHQRSHTERPYRCVACGKFCRSS TLIQHQRHV\SGERPCKDDCGKAFS\R ASDLIRHQRHT
1967	15868	A	1981	2	188	LPETNFAELFLPYISQHNLRKYRK/WP GAVAYACNPSTLGGQGWITRSGDQDHP GLHEEP
1968	15869	A	1982	3	424	EGQAIVERMNLCLKQQLQKQKGENRYR TPHKLNL/ALLTLNLFPLKGRILSAAE

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						QHLQKPAKTEAEQLVWNRDLITESWEI GKIITWGRGYAYVSPGL/NPSRHLKPYH ERMLRKRFPREDPEDPPSCSHVKTDAEED FN
1969	15870	A	1983	3	399	YSKLSFKGT/LTKFRRIYSSSFYKEFGCC ISDLCHP/R/TLTNCLRGELLKENLVWG AFGCHPHFPFCYNNKSQERNLLQALRHPT TVAFGETGFNYSYKCTMPVPEHHKVFKE QLBLAASLEK/PLVILCCQAE
1970	15871	A	1984	1	405	RRHYGGGVRLYYIGGEVFAKSLSSSXI AQTPNCNORVGMHPCTVKIPPGCNLKI FNNQYADLLDQSVNQGLEDY/OLTRM CTILMSLLKCGAGYRRQTATRTFCWIE LHLNGPLQRVDKVLTMQGVPSILM
1971	15872	A	1985	27	452	QGREHAQGGQSFGAGHLGPTPEPQPEPQ PRPSSQAVPAGRMPEAQE/PTRPHPRRL SPASRPLGSPAPLVRSSPGCRLEHT IWSSTVGTSTVEPAPSLGRPQAPLEPGTV TSSVRLQQPHMHTPGKIMPDPSKRNGKF TFT
1972	15873	A	1986	414	220	GAEQEELLSP/GSGGSELRSCHCTPAW ATRAKRLRLTKQNKTKRESYRQGNQNGR ILGELLGRL
1973	15874	A	1987	52	412	TRERLFFACDNVVKHLKRYLRKNSFGE NLWSSRNIKKKKKKKKKKKKTKTNFST PKNTFFPKACQCMGKNKTKDHPHEQNF I EHALLQQLNINFSNTYIEGRV/HPGAP IESLLMCH
1974	15875	A	1988	2	143	EKRGRGLDKRTF/AQAAPFKMQEKRQMER ILKASKIPPPFVCMWSVDS
1975	15876	A	1989	3	163	TEFPQFSEK/WGEDLGDNWTWEYI FAIDLL CCHQKWICHPFLVGVVRAGAEVSGVF
1976	15877	A	1990	1	439	DKTAEDAIRNLNHYKHLGVNINEAST NKSKTSTKLHVGNI/SPPTCNKELRAKFE EYGFQ/I ECDILKDYAFVHMERAEADAE A1KGLDNTEFPQKRMHESQLSTSRRLTAP GMQDQNGCYTGKDGHNKSCSDRSRGR VADLTEQ
1977	15878	A	1991	1	145	VVAASKAMK/MGDKWTKCHFTINEKMNG KVMDLFFPADPVLKRLRESR
1978	15879	A	1992	2	425	NISTLKKTLESECT/KLPSQIGGEQAO AKVURCLSDLAETNFKRDLLQEGITEL NSTAIKPOVPQWINSFFSVSHNIVEEF NDYEANDPNVQQLILNLEQQMAEFKASL SPVIYDSLTLGMLTSLDAVELEKVLKST FN
1979	15880	A	1993	3	449	VAGPAPGAGARPGLDLQFLRFLQILKV LFPSSSSQNALMFLTLLCLTL/LKSF DQFTCNLLYVSWRKDLTEHLHRLYFRGA YYTLNVLRDDIDNDQRTSQDLERFCRQ LSSMASKLIISPFTLVYTYQCFSTGL LGPVSIFGY
1980	15881	A	1995	1	410	SSRRPFTALKTKSMRDLNPDIEQLIYI SGMVIRTYQLIPRMQAEFPQCQVCAHT RVEMDRGRIAEPRVCGCRCHTHSMVLII NRYLFSDKQMIQLPESPEDMPAQQTPT VILVAHNDLDDR/VQPVDRVNDSGFF
1981	15882	A	1996	1	154	LFFFRLLVRYTKKVAQVSTPTLGRVSRN

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1982	15883	A	1997	2	475	LGKVGKKSWKHPEAK\KRPCGKN KKLRRTRRRAQKE\LPDKV\RWGLVTP SETPVGISNLSFPFLGRCL/QNPAELKP PWRFPWAQRPAH\ERANAGPKTPAEQR KVKKIKKLKEDISQGVHISVYVRNLSN PAKKFKIEANAGQLYLTGVVVLHKDVNV VVVEGGPNAPKTI\TRIMPLRI
1983	15884	A	1998	3	431	QLRTRDRGWFSRRPEREKRTSQSARRPT CTESRWKSEEEVESDDEYLALPARLTQV SSLVSYLGSISTLVLTPTGDIKGQ/SPL EVSDDSGPASFPSSSSQSLPPGAALQG SGDPEGQNPCFLRSFVRHDSAGESSLG SSQA
1984	15885	A	1999	1	400	ALDLRGLQILVGFPPKRRVTTCSYPTALO SPIEYQRKERSTAVMRTPEDSAYQASPR PYSAGPADSKKPTKGVCYNPTLP\RIEI MTLEGGTG
1985	15886	A	2000	1	372	QNTDLVTSFSSRLLQAGAELSVERVLE TIKQGVALLPKDR/LRSCAPTLNAGR SSGGQSPCMFGLCVCSFWLTVSWLVCQ KFPCLKKYVEEQPEEFIPYVNSLVN NSAVALYWNQDI
1986	15887	A	2001	393	1	GGTGRGGGAGGAGGAGGAGGVRGRKA GGVIADSGAPGGGVECGVGASGGWRE/G RGTSGGVGSGGAGCGSV/GSGGAGGCV GACGTSDDGVGRSGRTTGGGLSGSAGG GVGACGGASGVVIRGAGGG
1987	15888	A	2002	2	362	WVTFISLLFLFSSAYSFGVFRDANSE VAHRLKDLGEENDKALLIAFAQYLQCC PFEDHVKLNEVTEFAKTCVADESAEDC DK\SL\HTLFGDKLCTVATLRETYGEMA DCCAQOEPE
1988	15889	A	2003	2	358	EANRGWFIRLKEGSQLYNIKVQGEAASA DVEAAASYPEDLAKI\TDEGGCAKQOIFN VDK\QTAFSWMKRCPTLIAREEKSVPK FKL/SKVRALLGANAAGGFKLKSVALI CHSENSRTF
1989	15890	A	2004	190	1	DQTCFLFTVKAFTNGWVWMLTPVIPA LWDYRH\RPANFFVFLVETGFPHVAQAG LKLLGS
1990	15891	A	2005	1	132	GMCHHAQLIPFV/CSRDRVLHGCSQTFC LKQFSCGLGPKCWDR
1991	15892	A	2006	2	134	PHTFTEELSKTTLKFIWNRRIQIAKAI LHNK\WKAIRITHIC
1992	15893	A	2007	315	127	SEIAPFFCSFLKIILDTB/FSPFARAGL KLLASNDLPSSSSQGAGITGVSYGTQPV CFEYNVC
1993	15894	A	2008	3	325	RCSMLAVREM/QKATKRCFLPRTIALY K/ND/GSNCKK\HCWCEKMNQVLWIKI VWQFLKKNLIELPDEPEIPRLDIPKQL KTYVHTKTGCMFIALVILNVHLMNV
1994	15895	A	2009	369	3	VGQAGLEFLTSGDPPASASQSAVITGMS HHTQPIFCIFGFA/GCPDWSQTPBELKS AHLSPSSNDYRCMPHLANFYFCRH/R VCCPGWSQTPGLK\YPPALVSSQVATTG TSPRAWQDTILPV
1995	15896	A	2010	114	287	APLCLCLRHLRLLI\KRLTVLGEATHL\N PITTRGRGGQITWGREFETSLANMVKP

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1996	15897	A	2011	218	346	CF IMKFNLLKFYFIYLFPSRQSL/SSVAQAGVHWRNLGSLQPLPPKF
1997	15898	A	2012	310	1	SSSSSNTHFGIPKYLINPDTCTFLA/KVNNSSLTGLEVTETLKPQIK
1998	15899	A	2013	3	301	SDCCASNQRSTGGVGPSEAPARKHTLCV/CNSLDLIE
1999	15900	A	2014	332	3	LRDPLEEAFCVPSDLQIHAGRTALFKA VROGHLSLQRLLSF/VCLCPAPRGAY RGROAG/SLSCGGHLHPVRSRLCLCPKQ AWAMAGAPPAMFPFPCSLSDCCASNQR
2000	15901	A	2015	2	325	LLLHHAPPVNLFLDRDVS/CCFLCGPGC SOTPLGKQSSCLSLPKFC/WDYR/RATAP GL
2001	15902	A	2016	373	3	WANGLPQPKPKVDLSLKKKKKKKKGLN TFPLRSRTRQACLSPLLSNIVLEVLFPN EIRQ/QKKEIKGHTGREELTSLFTDN MIIVYDIPKQSTKNQGSYSVARFGAVA HACNPSTLGGGG
2002	15903	A	2017	343	1	EFFPVSGSRATGKSSDIRATKIYWRVLE YLRANPRGQRRLKSS/HTSLLSGYHPGA FRGDKWSCCHQKDETGGRGEDEVLLCCP GVLGCSALCRSGVRTKFGIRGRPWKERE R
2003	15904	A	2018	139	2	NSISTKNTKNWSGMVAHAFNPSTLRGSG GOI/RGQDFKTSIANMVKP
2004	15905	A	2019	3	322	ARELVFFFGAYRGKGFPHRDMKPNLLCM GPKLGKIADFLARELRSHPPYTDYGST KWR/YRGNPALLRPTMAKFPYEGWLIH SGSSIWNIKTSDSNFIFFKESKG
2005	15906	A	2020	205	377	NIVENIVFCWFGVCFLOTCTVCINPETS DE/WPGAVAHACNPSTLGGQDQGITRSG DRE
2006	15907	A	2021	3	324	KKWGR/LNRAPNRGRRYPETRWALEEDQ CHICKELHIKTFRPHCTPIFMAKIHITD NPQSNPRCGTGLIHCRGCKTV/R/PL WKTVRQ/FL/RKLNIFLPCDPAVLSLCI Y
2007	15908	A	2022	2	382	RVSQDGLNLLTSRSTRGLPK/CWDYRC EPPSP
2008	15909	A	2023	1	421	RANFGGRGCSSELRLHYCTPTVWTERDSI SKIAKNK/NNKPRNNCR
2009	15910	A	2024	339	3	SWDHRVRLFVFLVQTGFCHVHAGLEL LTSGSQSAGIAGVSHRA/GQKHQFRPEH RFLKPGFVFRDRVSLCCPGWPQTPRLKQ SSRLSLPKSWGPA TALDPDSSYLEEMVL S
2010	15911	A	2025	2	146	NTFGRSRQEDHLGGGQACSELSSHCT PAW/VIEQDPVSKKKKPPK
2011	15912	A	2026	3	380	RLECSGGISIHCLNR/LPGFKRFSCLSL PSRWDTYRLP/PFFVLVETGFHHLGQAG LELLTSGDPKCDWYGC/DHCTWP
2012	15913	A	2027	32	296	DYMSLMYFHSVLVASTDEGLEFKTVST QSAGITGISHCARWPFP/CPFFFKNRK TRFVAQAEQGGNGFGLNPLPGFRGFP CLSLT
2013	15914	A	2028	2	187	FTLLPRELECSG/MILVHCSLNLPLGLRWS SCLSLSSWNYTCVAPFSIFYFIPLTW

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2014	15915	A	2029	197	3	GGTLNC AAGLSQAGMOWGDFGSREHLPSRFORFF CLKVPNNWYDRHGPPRPVGIFFFSF\LV ETGFHHGQ
2015	15916	A	2030	88	362	KFGINLKKKKKKQKQKNNFFPTFLFFF FFETESHITQAGVQWRDLSPLQPLPPG FKSLPSSWYRCLPPCPANFCIP\IPDS VSLCOWGW
2016	15917	A	2031	7	131	GTIMAWAFGEGGCGSEPRSCHCTPANVT SETPSQKKKKGVLL
2017	15918	A	2032	1	343	LECSFRLCHCTPAWV\TGDSVSKKKKK KKKK
2018	15919	A	2033	243	14	OKLAPWPPQSGAGNNRRVPPHPASMAFLT KIERKALFKIQNHRRPQIAK\TILSKNR VGSITLFSNKIHYNTTVIKTI
2019	15920	A	2034	238	3	FLALPKVLGIIGCVPPHPASMAFLTITIE DTALKFIQNHRRPQIA\KPILSKNRAES ITLFSNKIHYMTVIKPLRVST
2020	15921	A	2035	345	2	LVKIQKEMVFWTANFISIPQFMDDQGV SSCKSYFFRNKFLTV\IAAMD\TD/SSNG SQOSEWKTWKGFI\ILDGINKTDSWEE VKIST\LTG\KKKLLPTS\TDGFEFKTLV EDVT
2021	15922	A	2036	1	140	GRCC\HELRSRCHTPAWATRAK\KKKKK KKREKKTQKGNLGFWAF
2022	15923	A	2037	199	348	RSSNEGGRCDCVFCGDRVSLCLPGWSAV AQLMLTATSTSO\VKLSLHGL
2023	15924	A	2038	3	193	NGLNAPIKRLRLANWIKSQDPSVCCIQE AHLTCRDTH\RCYLKG\WYKAF
2024	15925	A	2039	116	337	SKILKILPRLCWGWQAVIPATQOEVEA EDHLNPG\RSRPAWATORTVSIKKKII LRPANGK\CHGPSW
2025	15926	A	2040	368	252	VFFFFFFALFYLEFFFFFFFVFVFVFVFVF QFLGFYFRPF
2026	15927	A	2041	204	399	VSSHKINGLTVCTSTSPFFLSLLPSEES ACFPFAFCHDCKFPEAS\SVMLFVKPVE L
2027	15928	A	2042	103	356	WHFSFPQPLPPP\PLNPPPPPTTFFF\ PPPPPPPPPPSPPPPPPPPPSPPPPPPL PPPPPPPSPPPPPTP/PPPPPPPPPP PLPP
2028	15929	A	2043	3	344	LYKWNKASLAALFAAWFTVYFKPTVE TYC\SGKKIPFKILLIDNTPCYPRAL LEMCEEISIVFAPATTSS/LKPMQDGV IVTFKSNYLRNTFQAGGGEKKEKHERKK NIIS
2029	15930	A	2044	2	349	PRVRKSPGNGFTANFYQTFKELISILL KLFQKKKKIKKGNPPNPFYGAIIPIPI NPNWDLSSK\ETGYVSGRMEAKIFTK FLAGHFQSGFGEIHHDQREIFPGIQGG FNIGN
2030	15931	A	2045	280	462	CXFFLVVVLWVLCVLLFXVVVLLMLCFEG FVVCVVFVXCXGVWVFVVFVVCVLCGVL LGCWC
2031	15932	A	2046	3	284	PSPSFSLLLPPPSLLPPSP/SPPPPS SLLLPPSASLLLPCTSLLIHPTSLQ LPPLPSFYLLLPISISHLPTHNLPTTS IQDPSPTCSIX

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2032	15933	A	2047	95	1	GRVDATLAHCKLR/LPGFTLFSCLSLPS TWDC
2033	15934	A	2048	211	1	EPTTMTGAKWGSSQTTNYHMLQSLRIN VRVDFVFFCTDR/SLSMLPRLVLNSWI PAIILPHPPQVLGLQ
2034	15935	A	2049	35	266	EVRRPSTQPPRLRSEEPRL/QPPRLG NIGFCHVGHAGLKLITSSDLPTLASQSA GIT/GHSYRASEEDKKBSMSS
2035	15936	A	2050	281	3	QSNFKRALLSILLKAIYRSNIPIK/VP MTFFTEI/EKVLPKFIIRKLRLIAKVI LSKNKTRITLSDFKLYYYIAVFVAA WYWKNRSLDOWN
2036	15937	A	2051	251	12	ILRFFLPKPLFGQRPPSLKTHFFLPFAF GNSLFWPPEKLGQKVVFFVFFFLRQG L/NSVSQAGVQVHNLGLQLPLRLR
2037	15938	A	2052	2	325	ADHLRPGVQDQPOPGQNGKTPSPLEKIE LAGCGGHPRLRENCMLNPGRGCEP RSRRCTPAW/VNDSKTLARKKKKKGV KNECGKVMRV/LQGPKAIVKPGENL
2038	15939	A	2053	3	166	SLLLPRVECNAGIAHNCNHLH/NHLHL GSSDSPASASQVAVRGSLEPRSSLA
2039	15940	A	2054	227	3	LNENIGRITGMSHARILLFCE/YRVS ITQAGV/QHDPGSLQPLPRVFKQFSHFS LQSSWDHRCAPILRAIFWVFC
2040	15941	A	2055	301	0	QRKSHMFLTINQLEMIKLSSEGMRSVE TGQKLDLMC/QVSQAVNAKEKFLKIKG DTSVHTQMIRKQSSINVMEKVGIVNIE DQAP/HNHIPLSHLLMRAR
2041	15942	A	2056	1	109	RPLRLRLQENRLNRGSRGYSEPKL/HL CTPAWAT
2042	15943	A	2057	313	250	PQPPPPSPPPQSPSPPPSPSPSPSP/ PPP
2043	15944	A	2058	134	2	EKESRSVA/RLKGSAGISA/HCN/CLP GSSNSPSPASRVAGSSGA
2044	15945	A	2059	120	326	NSLVADME/KVLVVVIEDQTSNIPLSQ S/LIQSKALTLFNSIAKARSEEAEIF EASPDWFMRFKIKQK
2045	15946	A	2060	102	413	ERTGFRHVGSGLFMTISGDPTLASQS VGIT/VHEPRTPG
2046	15947	A	2061	311	1	FFKQRFCKSGCKTPGKPGPKKLGAQ FSGPTPLKNGVSPQWGGFFPPPPGG FPAGRPKWLRILGKQSLRG/RYPKQ GFLPKILGDNSSPORAPKGP
2047	15948	A	2062	229	380	WYDLGSLQWPLRFRKQASRVNLPRSWDY RHPPLSRNLIVFTVDITGLHVG
2048	15949	A	2063	142	383	PQSCFSTHMLQKQDEETAGAVSVCT S/VVCVVCVVCVACAGMVCAGA/CFC VCVCAGA/CLVCVCGA/CLVC
2049	15950	A	2064	408	200	NLTOIKALTHFSSIAKRGDKSTE/EKF EGSRGWVRFKRGHLCNKKVKEAANA YAEACQSLSRSS
2050	15951	A	2065	348	3	WVSPYSPVCVVCVVCVVCVCDRWVSP CCPGVCMVCVVCVCDRW/CFIM/CAQVC VCVCDRWVSPCCPGVVCVCDRWVSPCCTS WSILKLSSGNPPTTVSQSAWITGRSHS AWPARA
2051	15952	A	2066	73	286	NLRIGLLESHILISMRYGYCRSYTLMSR DIPALNKKWS/IMPFCSSRVRLIVSMA

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2052	15953	A	2067	329	0	VLKSLINRFNAKDVOH PSSTFLLFPFPPPPPPPPPPPPPPPP /PSSSSPAPSSPH
2053	15954	A	2068	221	3	ELKVILHCLRDFSLQSSIMKVLILKILI LSVCCVC/VCVVCVAVCSVC/VCSVC /VCSVCVLCVLCVCVCLSC
2054	15955	A	2069	1	167	GTRENFNPGGGGCEPR/SCHCTPAWA TKSETLSQKKKKKINSYKTPFKSYRI
2055	15956	A	2070	2	354	ARACLGLPSSWDF/SVENRFHRVQAGL ELATSGDPPTSASPECWDCRH/DHHTWP LL
2056	15957	A	2071	20	341	CIVTVNTRGENINICWSPEGOTIAVGNK DDVVTIFDAKTHRF/LQNSSSS/SEVN EISWNNNNMLYPDTGNCINILSYPI ESRAIYQRFIFHVHVNDLPHGDVLS
2057	15958	A	2072	353	58	LQLLTTSDPPASARGAGIADGVWFTQ/ SLNGAQAGVQWRDLSSLQPHPPSRL/LL ASQSAEIAASARPPRLGSEERLCIAAH RLGCEELCLLAQSGK
2058	15959	A	2073	1	338	GSLRQRCVINYRLSFPFLLSQGWINF LFCVLCVFLDRVSLCCPGWPSTSGFKR SSCPSSLRWYRHHMFQHLASHTLFGKLL /TLDR
2059	15960	A	2074	1	322	GGREGAEGARGGEGGCGSRRRRRGSG PRYCGAEGRGAGCTPGGARPERQGR GRHSERQGP/RQTKRPKTKTKQLSQNK NT
2060	15961	A	2075	450	225	TPVGRGCSLESGNCTPAWVTD\ETLSQ KEKRGVKGWKRRRTTISLHFGSHE KFNNLETWKNVCNHFCLRLNT
2061	15962	A	2076	2	470	TFQNKPHFTTKNTQPTQK/PTQTP /TTPKPKTKNTTPNPAFNTQKNHTTX PTTQNPHTKQKNTKPNTOQONKPTN QNPKTQQTQKTTTQTKPPKKKKKTADT TSPNPISTKKIKLAEP
2062	15963	A	2077	304	1	NSATPPCSPTA/KPHPTTPTPTPTSFIP TCQHSPTTKICQARPRTPPYAHPDRC RKTIIPKGRHPLAPPQARRDLNYYHPI IWRGRVCVVCVCVCARA
2063	15964	A	2078	167	1	TLQTNSTNSNVLWQGAQAC/NSST LGQGGGRTIRSGDRDHPQHGCTLSRA HETRSRHSCAWSCAALWRAAVASCPSS /IPVTPPOCLYWP/WKVLQCPDDL
2065	15966	A	2080	303	2	SKRGSPSGHECPFLGTSSSRHVASCTI RTPRLCKSQLDRCSPLKERHFKGLSR VLSAMTQSGIY/WOPPPPEFKRCFCLN LLSSWDYRHAPPRARA
2066	15967	A	2081	4	326	AGITGMSHRAWLFLYFLNKAFT/YGLV LNFFLHKICEPSLG/SGSGP/LSCNS
2067	15968	A	2082	1	343	PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP PPSSPSSPPPPHTPH
2068	15969	A	2083	330	88	ACDRSITSRTHKEI/EOLCKOK/SNPI KKWPKDMIYRFSKQDVCTVTNWKCS LIIEMIRSTRMYVLTIVRTHPS
2069	15970	A	2084	1	340	RVKSGTTHLAQLFVLLVQTGFHMDGQ DGPDLL/NLIVRPPQPPKVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2070	15971	A	2085	2	348	ARALSLGANAAGNFKLRPLLRHYSQNPR ALKNYAKYTLPLVLRHWHSESLETAFTFC FTEYFKPTVETCYCEKD/I/SYKALLLI EKALGHPRALMEMYKDISIVFMPVNTTS ILQPM
2071	15972	A	2086	369	2	KGLFSPSANLFFLSVY/MGFPMFTRLIL ISCPYPPSPASPSAGTKLNPFGWPPF SFYQKFRFVFLARNRTRGVDFPSIL YLYGCSNLYRFLSLALYFFSVFVFL TQGIEMVPR
2072	15973	A	2087	314	3	LLESVGPTRNSRPFKGLIGRLLDPEFY PSLVSDDLPASASPNAGRILPFFFFETG SHS\TQAGVQWRHHGSLQ\LRSSYLSL TSSWVYRHTPPHPANICISRA
2073	15974	A	2088	330	16	CPCFFLSALSVLVGWCFAFVVCVGV/VW CVCVFVVVFCVCFGLGCVLCLCFV/VCL VGVCVVVFGGLCCVCC
2074	15975	A	2089	1	337	GTRTFLPPSYKDPCEY/IAWHFDNPGSS SNCNMLNFSTSD/PPVHSSGNWKLSSP NRFPYYYSYATATHTDPTPLHSPNPSPP SPSYPLSDSTICOTTFTTPTITSSHTL LTS
2075	15976	A	2090	350	84	QRKENKTRKRATERRDESEEEKAGRKE GENQEKRNKEQQGRQRSDRT/EEKE EAKRREHKNTKKKKTKPPFKKKKTEKK KTDNLNS
2076	15977	A	2091	1	355	SDPPTSASQSAGITYVSHRTWPLLEFSG TSIRLAGKPAVLVEVTGK/SVCGGVT KTHWNECHTGYPKCCWSSQAGESSLQPP FPGFKRFSCLSLPSSWDYRLLP\QNF IFSRDGL
2077	15978	A	2092	27	345	ASIFCLKKRRKKKKTKGGKPPP/GGPKP KRGOGGPPPTKRTLCPFPQNGTPEGV S/GFPKGGPPFSP\PCORKSPFEKGG KKOPDPWRGVKREKHFLKNGOK
2078	15979	A	2093	3	301	HEHVAQAGLKLGGSSDPLTASPKWCDC KRDYCAWPHIPISGPLVVFPLPRMS PHTHYKTRTFPHYAHKCACTLNLL RAQFOCHFFKGVPDDP
2079	15980	A	2094	76	342	WFXFFFLFVFFVFWFVFCVFCGFF FCFCFCVWVFGCLFLCFLFWCFFV FGFGFWFVFLVCLFLVFCVFCGFF LFCFF
2080	15981	A	2095	115	325	MDERKKIRGGGRQSGKECKIHKCKKLS IRSYPVEN/F/VDTMYDLPAYYKLN LTNADPCAVRYLLFDON
2081	15982	A	2096	80	227	SCLGN/CIHLVSHSPFLSFTHTHTHHT HREREREREREREICMSVYA
2082	15983	A	2097	308	1	NSTVTMNSVNIHRYRRTVFTAQFTIAK SWNPCKPSILEWIKKLWIYIYVCVYI CVCVCICVCVCVCVCVCYIYIMMEYY SAIKRNLAAFAVTWTRA
2083	15984	A	2098	2	361	ARACLGLPSSWDF/SVETRFHRVGGAGL ELATSRDPTASPECRDCRH\DHHTW LL
2084	15985	A	2099	1	221	LLWRLRHNHNLNGRGCSPELHHCTP SWMT/R/GKTPSQKKTKQPMWQNLCLK KVFNGTGVREIFNGIKLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2085	15986	A	2100	186	2	ERVYVCVCVCVCVCVYQCYLPQIRSL/V ASSLKANARVCVCVCVCVCVCVCVCVCV SLWHFLTA
2086	15987	A	2101	305	2	HNILLSQLTQSKALTLENSMKA/E/RG EEAAEEKLEASRGWLMRFKE\RSHLCLN/ TKVQGEVASADTEAAPS YTEDHSKITDE GGYTQQIIFNVDKKASYNMS
2087	15988	A	2102	6	166	EQTALEILARATQKEKTKGTQIRKEEV KLCCFVND\MVLYLENSKDFLKVDAA
2088	15989	A	2103	53	176	EIKNNRPGMVAHAY/NPSTLGGGRQITS WGQEFETS LVNMVK
2089	15990	A	2104	3	267	FRHVQGGGLKVLTS GDDPPALVSQASGIT GVSHCAQPIVGDFNTPSLIL/D/RSTRQ KINKDIQDLSALDEADLLDIYRTLHPK/ SIETYTF
2090	15991	A	2105	268	3	PKSEHGSSPATEQSWMNDFDELREEGF RRSNYS/LREDIQTKGKEVENFEKNLE ECITRTINTKCLKELMELKIKARELRP ECRSLR
2091	15992	A	2106	3	170	GFHHVDOAGLELLTPQVHP\LGLPKCKW DYRREPPCLASPHFQIAISQKHREAK
2092	15993	A	2107	1	398	SARGEFGTAEFYQT\PKSEELVQLLKQF QRITKEILL/KNHVVKPSTLTPKPCQ RDITKLLTRSCVSLCPLVSLPLQSLQS RPSLSMISLHSLVCSFVLSASAHPIVHL CPTCPTLVLSGSHCVCSVSLFFF
2093	15994	A	2108	3	370	HENNNKNGWGDSTTYSMKLYFKPMLRP Y/C/SQKKIIPKILLFQNAFGHPRVLM EIMYKDMFV\MPVNTF/ILQPMQDQV ILTFKSYLNRNTFHKTIAAINS DYSDGS QOSQLKTFWKGFI
2094	15995	A	2109	1	213	HFPVENESAPG/FKAGDGLTLLLGNA AGDFKLKALLVYPSNPCLFGSKFKNL PLVWCSSHKKAWQLG
2095	15996	A	2110	391	3	KKKKNPHRRKTKIKRWRKTFNAERNKQR AGVIIHILDRDLFPKQOTIRDRK/GYVT MINGTQQEVITILNHAANTKAVRYIK QVLLKLTGELGNTIITGDTINTLLSLTL NRSSRQKNQQTLDLICNI
2096	15997	A	2111	188	365	FQNTIHCVCVCVCVCVCVCL/CVCVCF FFFCLLCGGFMCGCWCDFCILECFYGVG FFFL
2097	15998	A	2112	3	340	RHESALDRLKQFTTVVGDGDPHAYDEY KPHDATTNPSSLILAVAMPAYQELSEEA TAYORLQGGQEDQIINADKLSVLLGA EILKMITGRVSTEDARLSFD/SDAMVA TA
2098	15999	A	2113	11	305	FLPFDCLFMTHILGKHINVTN/CRRN VIIT/SYFSPHNRIKLKISIRKISRKSS NTWKLNNRLLHYPOIKDEVSREIRKYLE LNINENTNF/ONLWDIHK
2099	16000	A	2114	3	387	QTNH/NIFLSONLTQSKAITA/NCMKAE RSEEAAGKFEASRGWFMRFKSSSY\IKV QGEAASAGVEAVIYPLAELIDE/GCY TT/QIFSVPQTAFWKKKPSRTFM/REE KLIPGLKASKDSSSLLRVHAAGD
2100	16001	A	2115	152	393	VYCPTCLWLVFFFCFCSVLTLEVMFV/CL CFSFFCLGFVVVSSSYFLFCVFFVIV

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2101	16002	A	2116	2	373	LGCLFLCVFVDFLFLFVLVCLFFVS ARACGLFSSWDF/SVENRPHRVGQAGG ELATSGDPPTSASPECWDCRH/DHHTWPL
2102	16003	A	2117	3	449	HEFDHMLQAHRAHHLAIDAYHEFEETY IPKDKYSLHSDQTSICFSSILPTFEN MEETQKSNLELLRISLLILSNLEFVR VLKSMFANLNVDTSDSDYHFLKDLLE GIQTINAGRAEKRCRTVQNKKOTYRR/F DTNS/HNHDAII
2103	16004	A	2118	146	15	FFFFYFFFLFFFFIPLFFFFFLFFFF FFVFIFILFIYSLLVF
2104	16005	A	2119	406	3	LFSVNETGFVYSKMLSRITFTATETSTPG FKVSKDKLTL/LGANAAGDFLKPMLIY HS/ENPRALKNYAKFTPPVLYKWKAKAL MTTHLFTARYTEYFKPTVETY/ILLIID NAPTHQALRMENYKEINVMFPAINTSI
2105	16006	A	2120	109	396	YVFYFVLVLFYFFFLFLEFFFFFILL FYFFFSFIFFFLFVYFIFLCYFFLEFF FFFFYLFYFSFFFFFIFLFFFFFFFFFF SYLIFFLSYII
2106	16007	A	2121	15	413	IVLARNTNFWLSFLFPVALGILIVLKG KYIFWPLEYQRLKMPVSYSFHY/FFLG SLLFLKYGFMVILL/L/CIFIIMCFP IKYSPFFCCLYHFFFSFYLFYFLYFLP/ CYLVILFFSFLFLFLSSYCF
2107	16008	A	2122	1306	429	SSSSSSSHVLRITKDEDFKILEQRQV LSEKAQALCKEYENEDYFNKLENMTS GPSLALVLLRDNGLQYWKOLLGPRIVE AIEYFPESLCAQFAMDSLPMNOLYGS LETAEREIQHFFPLQSTLCLIKPHATSE /HKRGPSMWXLLTWNAVAEWRKMGPT DPEEAKLLSPDSIRAQFISKLKNIVHG ASNAVEAKEVVNRLFEDPEEN
2108	16009	A	2123	3	206	LRRLEOENHLNWGGGCGSEPRSHQCAA W/VNSNETPQKKKKKKKKKKLNPNS ALKKTYISQKGLF
2109	16010	A	2124	23	401	IASGRPFFFFFFFFFFFWPPPGGYPHFS FLKKKKKRGGGGSLLPPGKGNPPK\ WGFPLFPPLFPQKTPPPPPFFFKTPPI PPQGRGGLKFTPPGGGGGNPTIILLD KKRGVLGPPPPFTWN
2110	16011	A	2125	3	439	MFDSLLTFTHSLPHFSQFHRKCELS LCDGGLRDHILLPTSICTPITR/DKCS PGECC
2111	16012	A	2126	1	213	HFPVENESAPG/FKAAGDLLTLGLGNA AGDFKLKALLVPSENPCFLKGSFKPNL PLVWCSSKKAMVQLG
2112	16013	A	2127	104	419	NSFFFEELYNPFGLGKRTFFGGGEFF GHTIPNEALGGKKNFTGEGGOTFSNN GEEKSVSFWISIEKILHRALL/AHALCK NCVVELNFQKKEEFFFFPPEEF
2113	16014	A	2128	399	140	PPPPKNNFFPPKGFKG/RG/VGPKFPF PKRVSPQKPPRGFFFYPLKKKNPNPDP PGNFGPPRGFKRPPPPPPPPPPPPPP FFFFF
2114	16015	A	2129	10	457	KTSWTCVPVVPVATQKAE/AGGSPEPG RSRL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in: USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2115	16016	A	2130	409	0	PPPPSPSPPPPPSP/PSPPPPPPSP PSSPPSPSPPPSPPP/PPPPSPSPSP PPSPSPPPPPSPPPSPPPSPSSSS SSPPPL
2116	16017	A	2131	317	177	FFFFFFFFFFFFFFFFFLRLQIFFF FLPILILFLFLFFFLFF
2117	16018	A	2132	3	542	EPWSVAQAGVQRDLSPLOPLPRFRERF SRLSLPSSWDYRRLPAHPANF/QFLVET VFRHVQAGLELLTSGHLALTQSAGI TGMSTRS/RPGFLFKV
2118	16019	A	2133	146	439	LKSVTSIAKTWQPK/CPTNSEVDKCES TVKWIKKMWYI/YFTMEYYAAIK
2119	16020	A	2134	95	1	GRVDAILAHCKLR/LPGFTLPSCLSLPS SWDC
2120	16021	A	2135	2	380	THTHHTH/THTHHTHTHTLS
2121	16022	A	2136	4	337	KRNNAKMTVHLFTAWFPEYFRPTVETY CSEKKIPFKIL/LVNDAPGQPRVLVEM HKEMVVRFPANTASLQPMQGGISTF NSYLKANTHFKAIIVADSNSSDGFQNG
2122	16023	A	2137	2	356	PVSSQVRSVTVLKKKKGGPPPEGITN TAGKKPQSGFRGK/PPPLISPKKRPV I/SFLKMFPGCTIGKKKPPHPAKNGGP LQ/RPTQGGGRGKKKGNRPLSLGL GNRSKPFF
2123	16024	A	2138	2	357	FLGSSDPPPSASPVRATG/KVFFFFFL VEVSHYVQNGLELLDTSNPPAVASQS VRITCVSHRTWLSPYLKIQVCVK/S PELEQSEDSKLLK
2124	16025	A	2139	379	16	LLQVRCFVSTVNRGSSCOKTIQVYVQE AIPPSFLLSPFLM/PYTKINSRNKDSN VKPKTIK/TLEENLGMPLNIFTYQLLW LYLHPESQLEICNSFRALQEGNLIIFI GRVGRPGTTGL
2125	16026	A	2140	73	411	NYLLNNLFFFFFFLERGLTFAPRAGSWG NLTSNWLPGPGPNKPPPPPKRP/GTPK PTLKEGLFGPFKTTGFPFGAQKGPGLP LRGPGLAPPROGNKGNPPPGPLKTFN G
2126	16027	A	2141	46	421	AGVSWRDHSSLQPCLTISRARA\SHLSF LSSRDYGPMPPPPKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKK
2127	16028	A	2142	26	479	LAYLLFSFVYMKQGNWRTILQISINSKGL TCRIYKBTILQNMHKTNPNIPFKWVKKS KHFTRGAIQVANK\HKKKGLNISVYGN AQKNTMRVHHTIKMKK/GCALMLTPM CQEAQYILKMYPGWTPYGRVVGRTAP ALPPTGTFPRD
2128	16029	A	2143	9	166	QNRILARLTKKRGKNQAH/TKNDKGD ITADPTEIQASIREVHKH
2129	16030	A	2144	1	328	LEKESRFPFPPPPPPPPPPSP/PHGGS LPKPLGLQPLPRPEVSFTLEYLKLKAC EGGGEVIAAASFRIYLMGMCSSRDRIQ KDIDVVIQKSRADCLFAGVKALKA
2130	16031	A	2145	1	440	KTFLRSLQWLE/CYISSGLIDHRRPM ALTPRHRSGITAPRRPQPPQPVGIE PTALSPSPGPPPPPCSTFGRCQVPSLER RRKREGRPSVGRGCGGHGISPSSDIFF HLNFCLAHPPDLFVFCVINSQLYIFHE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2131	16032	A	2146	23	422	KKKKKGGRR IASGRPPFFFWGAPGGEGGKKNFFWGPR GGKKKIRGAPTPRGKGNPPPKPWGKKGG APPINILGFGKGAQRGGPWFKTPGKK KSPPPGPKKKGNRGR\GPPPPQIFFKP FFSTGEKNPLGKKT\PNWRLLPW
2132	16033	A	2147	3	372	KKNTFFFLTPRGPPPPPRGLSPPPKKRA TPPPPPFKKKKPGFPKKKNFFPPPGGG PPPP/LPGKKGGYF/WW
2133	16034	A	2148	363	1	FNCRWFFETKSHSVQAGSEQWHSFGPLQP LPQGFK\BFSCLSL
2134	16035	A	2149	2	361	FFFLVETGFHQVGQGGLEHLTSDDDPTTF GLP\GGWNYR
2135	16036	A	2150	387	2	KKSEFLVSPARVQWGDFFNPPIGSMNF PFSTPKTGVIIRGPPPARKI\VFVFIKTG \FPOLGRGVLSLPQ/CDSPPAPPKGG VSGGNPPAPPPFFFFFEMESHVSQVGV QWRNLGSLQPPSPGGKGF
2136	16037	A	2151	23	421	IASGRPPFFFFFFFFFLGGRGVFFYP PGGGGGPNFFKKTFFPGKKKFFPPSP KGGFLTTPPPPPFFFLKKGVIINGGG GGVKISPPGGTTPPLPGKG/NKKGPP PPRKKIFLFFPGAIKQRP
2137	16038	A	2152	3	366	VIWAHCIFHLLGYTDRCLKKKKGGPFG GEKMLKNFFPPLGKPPPPQINPWSV IEKPPRGVILGGAAPPKFFLLKP\GPP FFKEPPPPKKGGASPLKKKPKGKKS PPFFSDPTS
2138	16039	A	2153	423	253	FFWGGGAPIFFPPKKGFFFKNPPGVFFS PPKKKIKFFFF/HPVNFPPPKDFFKRPP P
2139	16040	A	2154	287	1	KEMNKKRNPKKKKVSKKISTAFYNKTLN NINFF\FAFFFFFFFFFFIFFFFFFFF FFFFFFFRRFLFLFNKQTA QLMQHSAPTRP
2140	16041	A	2155	433	2	RRVLFIFFPL/HPPSPPLPSPSPPPPP PKFSSPPTEFYKSPHP/HPPQV VFSPTPPMPEITPPPPHSSPSPSFF FFPPPPPPPPSFFFFFFFF FFFFFFFFFPHIISIKGIGRSSVVR VMSRTRG
2141	16042	A	2156	69	606	LWVPLSRHAAYRWQPTAPRGLGHKV KGPASPA\PCGAAGSTAQ\GGGAAC LPGPAAGAVTVVPAGPGGRATGPVLGR PAGAGOPTQGOHDAHGRVLOHIGR GAHRPGCAP/DSAPRAGGRC
2142	16043	A	2157	449	0	SSPGSSSSSPPPGGGVGFLL/YKPPQ KKPPPPPVGGGFPPOKKLSFFFLPP FFLGGGGPPPPPKISFYPPKKVSF PPPPKAFLLPPPLPPPPSPQPP LF
2143	16044	A	2158	241	5	KKFSFFPPGSGGGFGSLQNPFPGF FFCLNLGKKWQGRPPPRPNF/SFFFF FFFLVETGFHHISQDGLDLTS
2144	16045	A	2159	434	2	LGSASQLGSGVRDPLEEAVCPFSDLQ CARRTALFAVRGHLSLQRLLSF\V CLCPVPRSGAYRGQASLSCGHLHPVQA SRLLCLPKQAWAMAGAP/PPASLQPCSL

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						ISDCCASNQRDSVGVGPSEPRAGYNLLVRCFLSP
2145	16046	A	2160	448	84	FLGGFFFFFWPPPPSPQKEAL\QKRIFFVFFSPESNQKNFFSFSERGGPPNFLFKGGGR\FSPWFLFFFFFWFFLVVFFFFFFFFFFFFF
2146	16047	A	2161	3	156	RGCSEPLRLHCTPAWVT\KETVSQKKKKKFLTLGGKTFKNFFFNRAFGTTP
2147	16048	A	2162	412	37	FFHSPPPPPPAGAVFPKKKKKKSPPTPLLL\RGGGGPPPPPPPKRGPQPKPKRGFFSPKKKKKFFPGGGPGPPQPKTPPPPPPPPPPPPPPPPPPPPPPSLFFFLRTLWRKGRGRGI
2148	16049	A	2163	5	370	QSSCVQWLVPVVPTIQEAEGGFLEPRSERLQ\CSHCTPAWA
2149	16050	A	2164	437	36	PPPPFSEAESCSVAQAGVQWHARSLFQPLPFGVSSDSCLSLLSSYMCLSPPKTRGS
2150	16051	A	2165	3	623	RQGFLLVANAGVQVYDLGSLQPPPPGFKRSCLSLPSQWNYRHAPCPANFVLEE TGFLLVQOAGLELTSGLDPASASQAGITGMSHCA/RPKVCSYHLEF
2151	16052	A	2166	337	0	PPPPPPPPPPPS/PSPPPPPPSPS\PSPPP
2152	16053	A	2167	350	156	AEATSKIRCKQCYIMAGHSOTRLOFOLQRLRQENHLNRA/RGCNEPRSHRTWFTWYISKSFLA
2153	16054	A	2168	1	337	DERSLQSRSRWSYNGYYSDLSTARHSGHHKGRKTKKKK/IKKKKKKKRGPFKKKGPLKTRKKPRGGLLKAHPFGWGGPPPGFFLTGEGAPPVPVFFKKKKKPLGKGKGFLLWG
2154	16055	A	2169	2	606	RVLRAVAAHEEPDKESKEKPHAGVSPRGVKRRRSSSGGSGQKRRGPSQEPPLAPP HRRRSQPP\HPGLPPTNAAPTVPGPVE PLLLP PPPPSLAPAGPAVAAPLPAPST SALFTFSLPTVSAAGPKHKHGRKHHHH\ PAMPVIPAPEPI
2155	16056	A	2170	311	2	GLQPLGLSGVKCMDLACVPEVVCVVCVCVCARAHTPVCTQGCVPSTOCVCMHVC/VCVWACTCVPVCMHTCVGVGASVCMQRNELGRWAWENDAI RQRC
2156	16057	A	2171	78	337	NPNSIYKAMSLRGPITGTFLPNYPGHKVCVCDTYLCVYQHTHTHTHTHTQAFFHI/HIYHTT
2157	16058	A	2172	2	278	KRLNPGGGGSKLRSCHCTLAWAT\SETPSQKKKKRKRKRKRKKKIIVTKIEKGNAKMTGESFIHFCKSSSVQVALSAEYRCST
2158	16059	A	2173	2	365	FVHVGORGKLLTSDPPALGLPKCDWYRRE\DAQPNVKS
2159	16060	A	2174	195	389	PRVFSKLYYVDFFRGRISLSCFGWSTTPGFKRLSCLSLPSSWDYRRPPCPAN\FCIFSRDGVSP
2160	16061	A	2175	23	374	IASGRPLIFFFFFFFFFLFCRGGGPPFNPRGKERGGFLIKGPPPPGKKNFWAPP GGGEIKRTPPPPGVFFFLKKKGFSGGGGKK/PPPGPEPPPPPGKGGKKKK

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2161	16062	A	2176	2	158	TRGPLF FFFLKQSLSVTQAGVQ\PVDSLOPLPP RFRKFSCLSLPSSWDYRCVPQCPAN
2162	16063	A	2177	340	120	PRFHFLASPSSENSQTVKAKTTVPASEC AYPKIEPPFF\DPGRSES\FDKLGVHH HPLFLPSOEPLMILHYNTH
2163	16064	A	2178	3	256	YLKLDLNVNOKTLTLL\EKQK/HLHD MRLCKEFLNKTSKAOYLKKISY/LIK VQNFNAVDKPKRMKQASD/WENIFT
2164	16065	A	2179	95	1	GRVDA\LAHCKLR/LFGFTLFSCLSLPS SWDC
2165	16066	A	2180	1	143	ARGERERERERERERERERERERERE RERVVF/RERAALSREGRDKCERSGLF
2166	16067	A	2181	1	304	ARGQGHLSLORLLSF\VLCPGPTGGA YRGRQASLSCGLHPVRASWLLCLPNOA WAIAGAPPAALLPPCSLISDCCASNORD SVGVGSPKPCVGNLLVW
2167	16068	A	2182	3	163	FORRESTESCGWDKARSQSRSPPRQAH GHHS/HTHHTHAHTHTHAHTHATRP
2168	16069	A	2183	3	205	NFKLFCGQFFFLKQSL/DSVQAGVQRH NLGSLQPLPAGFQLFLQPPPPGSKDTHP GVQRHDHNSLQP
2169	16070	A	2184	228	88	WFRFYDSFFLFLVFVFFFFFFF FFCVTFPPVYFIQVYVI
2170	16071	A	2185	287	3	SLFLATPQWFORKTYLRQKIVLLACQ PSKGLSIVQVRGQLNSPVLKSQDPTP\ PRFKRFLCINFLSRMSYRVPPRDSFV FLVETGFLHLV
2171	16072	A	2186	252	105	VSISCHPQ\FCLITYTCY/HIDGYSNIHL CTHTHTHTHTHTRVELQGPA
2172	16073	A	2187	267	459	KHVPGSSYTNL/IFFFRGNFLKGANFV PQGVLKGNLSSLYPPPRLKQYSCLTL LRIGNYKHA
2173	16074	A	2188	170	15	RSVMKDLNSHFSKENIQMANKRTECSA LVVFREIK/TMRCHLTPIRMAIKK
2174	16075	A	2189	2	504	DVTISTCHASAKVGTRLVFDHYGKIQK TPVPHRGMVSVQKLFSTLPVRHKEFO RNKKGL\RSFCFDF
2175	16076	A	2190	1	565	FFETESLPRLESCGATSAHNCNLHPS SDSPASASRVAGTTGACHHTWV/IFVF PVETRFHHVSQDGLDFL/NLVIIRPPRP KVLG
2176	16077	A	2191	142	382	NTPTLLFFVIRDRVSLCCPRNSGVQAF WLSATYASRV\KRFSCLSLP/SNWDYRC VP
2177	16078	A	2192	138	365	KHQYHCC/LKKKKKKKKKKKKKKKKK KKKKIKNKKKGFPKKNF/EGQPRNWA GGV
2178	16079	A	2193	385	21	RGEIFFFKTRKKFSPOGGGGVFPFSP PKNFFPPQGGKFFGG/EGPKVPPPKKG GFFKKPQGGFKVPPKKKKIISPVGIG GPPGNFLKGAPPPPPPPPPPPPPPP FFFLVRAVKLS
2179	16080	A	2194	415	56	PPPTTAPVFSPPPPRPFSSPPPPVFF FRSFPAPPPPLFFPPPSPP\PSFPP PPPTRCPPPPTIPPPPPPSPPPPPP FFFFFFFFFFSLPFFFFFFFFFFFFSPL FLFFPSRLW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2180	16081	A	2195	35	369	MKRPSPPPTPTPPPPPPHLLPFFFEK KTGPP/RSFFKGGGRGPPPPKKKDDPP QKQKKKKKWGGGGGGGQKKKKPQKNP PPPPGRGGGNFLWGRFRGPPPPQGGGK K
2181	16082	A	2196	2	266	SKFRSCHCTPAWATQ\ETPSYKKKKKKK KGLPLGGPGEKTI\FFSLKPGQKAQPKNK IPFKKKIPFFSTPGKKKKNFQGGPKKK KKEI
2182	16083	A	2197	1	277	ARGERERERERERERERERERERERE RERERRHP/RPERERE
2183	16084	A	2198	1	285	ARGERERERERERERERERERERERE RERERERERERERERERERGGAPP RFLYRERVLKQGRFLPPVREKK/RS PVQ\TLFGY
2184	16085	A	2199	346	1	VPRHGLPCFCFPHQLPPKKKKFNKKR ALTSHTQFFVFTSSCSVA/RPSSGATS AHCHL\CIMRSSNSPASGGAGSELFR HCTPVGQQTETWSPKNKPIKKEGCPYC QLFSC
2185	16086	A	2200	3	389	HEGMILAHCSLNLPGSGD/ASHVARTTC VHHVQLLFI\FIVETK/FSHYAQAG/L ELLSSSDP/PTSQSSRTGMSHH
2186	16087	A	2201	3	204	HECHCTPAWAT\SETLSQKKKKKKKKK IFPGEKTTGGWNKKKFLPLNKKFVLGKG LFHLKRGPLKLF
2187	16088	A	2202	69	379	KKKRVFVFWGPGGSKPPT/SGNPPPPWPK GGGLRGLPPPPGPRGVIFKNFGKRGPP PPGLKSWGPRDFFGLALQGGISGLNNG APPPFFGVILKKLPLPFFVSKG
2188	16089	A	2203	81	379	KKKKKPPPPKKKNPGPKKQEGFLRGPF TFSGGGGGKKTCPQLKAAGG/SKKAPG PPPGAEEKNPALGGEKKTLPNGRGPKR LRGLAKKNPSSFGGK
2189	16090	A	2204	1	341	GQSLPVSRLQLSNGNRTLTLSSVTRND VGPIECEIQNPASANFSDPVTLNVLCEY LLF\PVAQATSPNFRSQRPGLSVPLSSK NNDSPPTPRNPARHDLQANMGRPSLD QE
2190	16091	A	2205	2	370	DAPPRANFVFLVKTGFPPVQAGFKLP PGDPPLASQITCKG/HCAQPPF
2191	16092	A	2206	362	24	PRGSSSSSSSSSSSSSSSSSSSSSSSS SSSPF\PPPPVLKPPPPPKKPPPKK NPPPPKKKTFPPPPFFFLRRLGLCPFGR GKRAKPPFQKKKKRRSSFYQQVIH M
2192	16093	A	2207	357	3	AGQALWLARVIVLWNEARSYYRISWYR NIVAMDSDSLQSGHSKIKFRKGPPVL YAIKKTTHDSWEGVS\MSALIVWKSILPS CVDFAELTSSAEVAAQVVGVLATLDEL LVGCARA
2193	16094	A	2208	280	411	GNDVYFLVFLF/CLFEKESCSVAQAGVQ WHDLSLQALPPRRMA
2194	16095	A	2209	3	392	PTTYERYTQINEMPRKQLHQQDALVSR NGPILLHDNAQLHI\TQC/LQKLNELGYR VLPHLPYSLDLSPTDYFFKHLDNF/LQ GKHFNQEDAENVSKQFVKSQSMDFYAT /GNKLISHWPNVCVDN

SEQ ID NO: of nucleotide sequence.	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2195	16096	A	2210	248	417	GILANCASTKDLISRTYKKLQKIN/KOK TNDPLKKWAKDMNRYPSQEEIQGVNKH KK
2196	16097	A	2211	213	493	GKRPYFACPGKIGALQGFFKGGGPPFF FFFLTPPNTNYLTNKLKIKSPCLCTFYF SNILGFPYSITHRTIPDAWVTA/QSGGP VLMRSIS
2197	16098	A	2212	159	413	LAPRVIFGPPKKPPERPLPFFFFFETES SSVTOAGVQVHNLSA/PFRFKRFY/CLS LPENRDYKRP/PPHPANECTPSRDGVS
2198	16099	A	2213	455	60	NPRREVGPICPFKLIRVQGNFQVGVYS PPLKKEKTTSPAPVNLGPPRDPFKGPP FFFFFLDFFFEYETIYKTSAAACRSP AQPRVARRPLVPSS/PPLPCLAPAPR GPGSLCPRGSLGDNSSPG
2199	16100	A	2214	2	243	LTLSPRLKCNMGVSAHNCFLLSSSDS/ RLR/QENCNLGGGCSLRLRHCPTAM TTERDSVSKTNKKSILKIFTCFFVDA
2200	16101	A	2215	1	286	FSQLRLRFIC/QSGGRLLCCSCFASFH PECLSIEMPEGCWNCDCKAGKGLHYKQ IVWVKGNYRQVFPRTKRYKSIIVQTSF ILWIQSDLEIDR
2201	16102	A	2216	173	2	YITFFFRQGLTQAGVQWR/DLSGETLV ILFPLEAPCSLQSSWDYRRVPLPLNFC IV
2202	16103	A	2217	216	4	VYFPSFMVFSQVFLSSSTHISLSPF FWN YLFYLYFIYLYRWSL/DSVTOAGVK WHNLSGLQLPLPGFK
2203	16104	A	2218	14	228	KRSSHLFTDITLYMENTKHSTK/NLLE LIKEISKVTG/YQKSVAFYVNNKQAIK KTIPLTIASKRIKNSGQA
2204	16105	A	2219	244	3	EVLNQNGLFRWPNILRAKASLRVPRQ SRGVVFSANGAGTTRYLYAKEWGGLGG GCSKLRSCHCTPVNAT/SETLSQKK
2205	16106	A	2220	162	2	INWVGNLFFFGDRVSLCHAGNSAVAF SW PTVASTSL/VKQGSFLSLPSSWNHRH
2206	16107	A	2221	146	3	GRVDGVWRNFGSLQPPSP/GSSDPTTS ASQESGTTGAHHHTRLIFVF
2207	16108	A	2222	239	2	SYISKPKFPFHSPELKFVYVNNRNSF SEIFPFFFLPEKRSVTOAGVQWNLN GVSSYWP/AGLKLITSGDPPALAS
2208	16109	A	2223	2	159	LNRLDGGGCSLRSCHCTPFAWT/SES PSQKKKKKKKKKKKKGRGRNSKI
2209	16110	A	2224	3	345	RFKLFESCLSPSSWDYRRVPRPA/NFF VFLIET/GFAILTSSKTERQSRLEICIFG FYGLPCREKRASERRSVG/HERKILFS FDFFFLGGTESCFVTOAGVQCCTYLSPO PPPPG
2210	16111	A	2225	103	319	FSEERYNVNFMMLTMSCSCLTIVE/C/ WSEGYMATPCTILLLLFFQRHCLTSPG GVQWCSHSLQPTPGIK
2211	16112	A	2226	2	110	FHHVQAGLELLTQWSIHLSPKCDWF/ RHEPPHPA
2212	16113	A	2227	2	178	IFLIPTFLEMSSHYVAQGLEFFG/FKL TSRLSLSSWDYRRPPPLANFPAFLAK GDAA
2213	16114	A	2228	173	3	YFIFISLFFIFFLRQSVLSPSAVQSR LQPPPPRFKQFS/CLSLSSWDYKRVPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2214	16115	A	2229	333	1	C HTFPFPFTFHSCLTEGAPPPFNT/PNP PRNPFIIPLSRSHTRANEPSLSTPRTHP HSPPRPPLLTHPHNPRASAPPGGRYPFR ARHRERPRERPTQERERERESVUCVUC
2215	16116	A	2230	350	3	KKKDTIPFVNTYAPNTGAHKYIKQILLDL NRDGP\HTITAGDFTTPLSVLNSAER CSRPFIIISPSLVGLRE
2216	16117	A	2231	277	1	QMHPARGHLPQALIPVQKPAISQGM SGSTQVSPFLSPCFVNEVNCSTKVL PFCGAGTGSHSFAQAGAHWCNRSGLPH PPGFKRL
2217	16118	A	2232	3	335	ETRFHHVGGAGLEPLTSDPPASASQSV /GITGVSRLRARGES/GSWKTVCCNMS EPT
2218	16119	A	2233	29	448	CPSLRQAWHEAAIDEVTRGTYRQLFHE QLITGKEDAAANNYARGHYTIGKEIIDLV LDRIRKLADQCTGLQ/GFLVPHSFGGGT QSGFTSLMLERLSVDYGGKSKLFSIYP APCVFTAVVEYFNFLTTHTTLEHSDCA GARLLVFEETGTFHYVQAGLELLTSS DPPASA/PPKCV
2219	16120	A	2234	1	365	DRLLTDHISKCTRGLOGLFVHSCGNLG /TGQFTSLMLERLSLDYGGKAKLEFSI YPAPQVSTAGVEPYNSILTTHTTLEHSD CAFVMDNEAIYDICRNLDTERPTYTNL NRVISQIVSSITASLRFDGALNVDLTF QTNLV
2221	16122	A	2236	614	84	LAASLAACAQLSALAASHRMWALQRLRK LLTTEFGQININRLGENDGETRALS TGSALAALVKGLEALQRFYEYDPIV RGGKQLLH/SPHFFKVLVASRLVLEAG HFCPCCAETHKW\AWFRRYCMASRVAVA LDKRTPLPRVFLDEVAARVCGHILQLG DTELOQHICHL
2222	16123	A	2237	1	393	GPMLAQLSVFRCGSTSAENDLWYHFI PYHGESTIMLIALPTESTPLSAIIPHM STKTIDRNMIMVPPKQVILPKFTAVA QTDLKEPLKDLGITDIVDSQGHFCQIT KAENLLV/SHILOKQK
2223	16124	A	2238	3	402	HVGQAGVQIGKACWELYWLEHGIQPEQ MPSDKITGGGNDSPNTFSETGAGHVP RAVEVLEPTVIDEGRGTGYRQLFHPQ LITGKEDAAANNYARGHYTIGKEIIDLV LDRIRKLADQCTGSGGLFP
2224	16125	A	2239	2	478	GRGSLHRTFVVTPLTFSEARGLVPSLAR GVEARNGAGPTKSPRPGSLKMGNGSK GSLQNKQTFHWEICDAHVNSKIQKQVH ISSRRHKDRVAGKPLPKYRFPYKLRSS PSILAAKLAFQKMMNPLAPFLSSPLA AAEAVSALTLPFRPFCCV
2225	16126	A	2240	255	2	FLFVKPHQTSCTPKKGKISFLVLCPLNF FLFWRQDLAHFGWSAVTQSLTAASNYP GLKQSSYFSLSSWDYRCIEPHLGGKRP L
2226	16127	A	2241	365	11	EPFFPGGEKKRGKPPPKTKPKKDGPK KSAAPFGG\GKIKKKGAFRKKKKGGG PPPKKKPPPRKKKKKNFSLPFPKHTP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USNN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleo- tide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, = possible nucleotide insertion
						SLFQKPPTKIFLFSPLLFLNLIFFPPL SPFIF
2227	16128	A	2242	3	143	PNFLSPRLDCRGITRGHGLYLPSCDP S/CLSPSSSNWYRSTPP
2228	16129	A	2243	132	2	MSAHCNHLPGSSDSPASVSQVAGIMGA CHIF/VFLVQTKPHHI
2229	16130	A	2244	334	43	TSKHKMRCISLSTREMKNKTTIGGHFV PTRLANIQKPEKAYRGCLMC/WCWC NLASPLMKTIWHYLVKCLFYSSAIFTLG /IYPEVLASSVPGT
2230	16131	A	2245	312	2	FPSSLPKKNFFFFFLRQSL/SSVAHS VVGWRDLCPKPPRESKQFSCPTLLSI WETQTLSDQCATALHPGGQRETLSHKI CVCVCVCVCVCVCAVCYIN
2231	16132	A	2246	3	230	RAQAMVETSEKELLRPQITRTHVAQ AGLLKLASSDPPTASQSGITGVSHHT WPQLTFCPHAKSLPFINQI
2232	16133	A	2247	2	214	GRVLDVIAQAGVQWHDLSLHPPFL/GSS DL/ASDSQVAGTAGRTHYANLIFVVF FVETGS/HTQVSNYSYDL
2233	16134	A	2248	3	139	EGVQCGHNSLOPPTPG/SSDPPTASAI EAGTAGSHYHVWLIFLLF
2234	16135	A	2249	3	160	EGVQCGHNSLOPPTPG/SSDPPTASAI VAGTAGSHYHVWLIFLLFCFEGDAA
2235	16136	A	2250	319	3	GQKRYKIFLCFFLFGNLVFLRWLTLSP RLERESVKKPKSKQKPKPKFTPREF KEVLAKYGTKFFVFQGLVWFFLRWNL /NSVAQAGVQWRDPGSLQASRP
2236	16137	A	2251	15	394	FVSFFFPSPFSLHFFSSSSFPFLFSP HFSFLPSDRPSVVPVS/FLPSFLP
2237	16138	A	2252	60	306	GRERILEITMAEDFLNLMKDLNISTQVA QQIPSKMNSKRPHRYQHFRSQSRIILKA TREXOLATYKSSVT/VSPSPGQTVNS
2238	16139	A	2253	3	351	GPHHVDQNLKLLTSSDLPASTQSSTGI TGI/DHCTQPNFI
2239	16140	A	2254	150	2	RPRRPDHSRLGADQPGQHSKTPS/HQK KTKTSQAWRHAFAPAGTRQAEA
2240	16141	A	2255	357	1	LNLNLSLTLYAKINLKWITGTVNKHKT KFLGGKNGANLMDTRLDNAFLDLTSKAQ LTKEIKDLNFIKIQTF/CSIKDLLGNL KQAPBEKKILRNHISNKLVSRIHKEV KPLANKK
2241	16142	A	2256	397	1	FSLFFPVGGGGFFSSCKSPPPRRFAFF CPNPPKGNRGPDPHPKCTGLGFFFF FQSPFALSPEVEYHLCLOSSDPPRAS QVGGAPGLPPPAWNGIFIFF/CFFLRQ SRSVAAQRMQRHLGSLQAMP
2242	16143	A	2257	2	132	TLTLTPRELCSTGTS/AHCKLHLPGSR HSPASAPRVAGCGGHL
2243	16144	A	2258	214	347	KISLILGVHKICCF/CFEMKRSRVTO AGVQCHDLSLQPPPPGL
2244	16145	A	2259	347	2	FFSFFFFSEAESRVA/RLECSDTVSA HCTLHLPGS
2245	16146	A	2260	333	1	SDQRWTENAFVLEDEGGFACPSFEL/R STPSTSGEEVENFEKKLDECIITRINTE KCLKELMELKAKAREPREECRSIRSRHN OLEERVSVMEDQNMENKREGKFKREKT
2246	16147	A	2261	2	357	SPRSCSVYGIALLFLYFLYKALFALLY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2247	16148	A	2262	355	0	GLALNSPLHEIQEP/SLASGSGPLSRNS PFLPSPFLSPFLSLSFSLPPFFPPFFPPF PLF/CPSFSFFFFSPPFF
2248	16149	A	2263	348	35	YFLKKGFSFFPRGEGRGKDSRLKQLTF GFKKP/SCPSFLRKW\ETRLCPAQKIF FFFFFLLEMGFCYIAQDGLKGSQSSGI TGVSYHWPTFIGHLTMCLAKC
2249	16150	A	2264	270	92	DREARRKMFFTYSSRLFFFFFFPPFF FFFFR\PPFFPPFFPKFFFLFSRWSLM IFIS
2250	16151	A	2265	1	417	FRPPAGVQWRNLSLQSLPFGFRFLYL SLPSS/WDYRCMPQLA/NFFVVFVVDV VVVVVVVLEMRHLRVLARLDIVLICI SLMANGMEYFLCSFAIHLPSLLKCRFT YFAHCLFLYYFLETGSHSVTETGWQWCI I
2251	16152	A	2266	344	427	LIGLCEOTNLGATHAKRVTLIAQDLQLA
2252	16153	A	2267	310	417	RVYGTGLSGSLATMAGFDDILKPHMEG AAPILVR
2253	16154	A	2268	186	464	NSCLSHNQRLFLRLEKMGPIISAQEK VLHTLSGFSGLV/VGWLVPFMECSVVG AQVQRVHPFPRFKQSFLSPSSWDVG HVPZCPANE
2254	16155	A	2269	1	427	PEPFSLPFGAKKQTKSKKKWRICFLR KKKKKKKKKKKKKKKKGGGSKSR GPKLTETETNIILIKGGLKMMYRETEK KLLFGGGGVIGTPTQDIKGREINYLE AVGREKQRFISLVK/TNVA/HEATRDTI FRGYL
2255	16156	A	2270	399	44	ISFOLLPIITVLPGHVRLMEMYKEVHV VFVP/STTFMLQSMGGVTLTFKSY\Y LRNTFNKAVALTSDSSEESGSQLKPV WAAFSLSNASKNI/RDSWEAVKIPALKG VWKWNSLKM
2256	16157	A	2271	19	420	AAGTRHEERERERERERE/QRERERERE RERERERARRNIYHTYRPRPRVPPFF FFFFKKRRGFLVPTPPGGGGAQKKTS LEGGKGVFFKGGGKKTPLKNFGWGGEPP QKNGGGGPPPRDPPPPPLF
2257	16158	A	2272	463	20	SYNIPLSQSLIQ/SRALTFDSTKAERN RRGK/RSGLQWESRGWLMRFKERSHL HNIKVDQEAVSYPEDLDMDALNTKQOI FSVHKIALYSKMPSPRIFAVERESMPG FQASKDR/L/LLG/ATAAGDLKLFMLI YNSKNPRVPRAEF
2258	16159	A	2273	474	82	VGVWADFLKNTSQAQATKAKMDKWDPIK LKSFTAKETISAKRQPTGEKIFANY TSDKGL/SRIDELKQYRKFNPNVPL KWAKNAQWLTPTVLLALNEAKAGRTQQQ ETEATLAFSGSLFCOWFLC
2259	16160	A	2274	152	3	AEGRNGDGIQKSTVRLTSLNDKNPQN IHRRPTFLITMLYQOMLCHLGL
2260	16161	A	2275	32	361	LGASARYEKPTVNLINERLINFPPIR/ SKTRGLYLLSLFLFNIGLAILASAINOK KEIQIQIVKKKIKTRQKKKKNKTKKKK ALFKFGGGEKEGPKNPKFPKTPPVVF
2261	16162	A	2276	329	487	EFVNITTIKIATSLHYKAIVIK/AMVW YWHKNRHIOWNRISLEINPHICNKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2262	16163	A	2277	2	466	AHHSCSHLLTTAAHYSCSPQLLTTTAAH TYSPPQLLTPAHHSCSHLLTTAAHHS CSPQVLTPAAH\GAHTCSPPQLLTPAHH SSPQLLTPAHHSCPHLLTTTAAHSCSP QLANSTRG\SPYCSWSQTGFRKSSH VGLPEPWIFHGLQVV
2263	16164	A	2278	4	467	KNTVQGGKTHIRDLDEMCGNTSVFCTN HMKGTNPAKIKCVKECG\TACNPFQ LTOYQISHANQKPYECQICGKPFKRAH LTOHNRHTGGKPYECKGCGKVPICCT LIQHKRHTTSEKPYECLCKRTFRSAH LIRHQRIHTGKPYK
2264	16165	A	2279	383	3	FLCVCACVCVYVCMCMCACAC\CMCMCG CVCVCVCVCGVLRGLGWAGVVCRSWGP LCFLLGLILPLKSRLLWLPRTISICTL PSAQGPLPAPGFGYASNTTGVGSSSV FSLLSRITALSHLW
2265	16166	A	2280	47	219	VCSLKSCHCTFANAT\SVTILSQKQNT KORRTLGSIFFQHTFMHLKESLILQK W
2266	16167	A	2281	294	160	NRTFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLFLF
2267	16168	A	2282	68	490	RTFAYPKPPVFGSHSGKTIKPNARGSP PS/PPLPFPSPSPSPGSPVSLPRLP SPSPSPSLSPISRLPSP/SRSPSPSL
2268	16169	A	2283	3	454	CQSAPLGGASQLGYSVGRDLEEAVCPE SDIWLCAGRITTLFKAVRQGHLSLQRF LPFVWLCPAPRGVYRGRQASLSCGGLH QVRASRPLCLPTQASAMAGAPPPASLPP CSLISDCCASNERSGTGMGP/SEPGTG
2269	16170	A	2285	1	452	LKDSGRDYVSQFEGCALGQNLNKLDDN WDSSTSPSKLREGLPVTFEFDNLEK DTFGLRQMSKDLSEKAKVQVYLDQF KKWQEMELYRQKEEPLRAELQCARQK LHEL/QEELSP/LQQEMLDARAHVDAL RTHMAPYSDELRO
2270	16171	A	2286	3	266	NSSPPSSGHSTPLRLAPPSAREGTOKAV SALKSPQPNRMGMRQR/PGLPS/DTAT ITPHTSFGFKPQQLSKVQTORAKRGLS HWDLEP
2271	16172	A	2287	274	453	IYTFVKSSTKTLPRRIIDOWNRIENPEI KP/EYSOLIFDKANKNIKWEKDTLLNKW CWDN
2272	16173	A	2288	81	487	TVYFKPTVETY\CWDKKKIPFKGLLRD NTPCYPKSLLEMECKINIVFAPATTSS /LKPMDDQGVIVTFKSNYLKNTF\RLGEG RKKKKKKGRKKSFKALAAINSDSDGA GQSKQT/FWKGSFIPNAIKNIQDPWE
2273	16174	A	2289	75	469	SRGVAGAPFKSPSPSPSGPLDVTGPH SSHHAASPGP\PPPEPTASSMASAP/P PAPQPTPL\PPATILGPSAGPE/PSPGS CTSTGWGYSFCCPRCRRNMRWQPPQOQP AMHWWPREFP/PPPRVSGS
2274	16175	A	2290	256	55	PTQPLRVELTIVTLRCDINKWDYIKLS FCTA\KKROPTEREKIPFNHVSNNKLIS KIYKELIHR
2275	16176	A	2291	497	29	SLTHRVAGGAIVTPLARAGARQIFFLGD PHPTSSLLGWGPAWDPACAFQVSDHPASS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RVGKFTLLSCPGGGRLPWVTCPPGGQLSC LTQMHLTPAGMCSPCVVCVCVCVCVCPN GMCPRCMCVVCPCRDVY/ICVVCVCVCV CVMCMCLPCWDVFTL
2276	16177	A	2292	141	392	SCSTEVKQPKIGVREVDVFAAFGIAPFS PQKKQTTSLSLKLRLSKVRPLFNIV LDVLAREIRQKEIKGIQ/LGKEE
2277	16178	A	2293	14	291	YVGTGEGISIFMRVINYMTKLATLRE S\CYSR\VYPRFIEFLRFDIQSTGQ/R TSRQHPPR/DLRDALLYNRRITLVRTR CKSVAKRPPGPS
2278	16179	A	2294	110	293	LLSNRSLATASLCGGCNELRSCHWTPA/ WRQRETVKKKKKKKKPGWGFLNPPQOR GKLCF
2279	16180	A	2295	96	313	WNGCYLLSNRSLATASLCGGCNELRSCH WTEA/WRQRETVKKKKKKKKPGWGFLN PTPQREKLGFLKRGPGF
2280	16181	A	2296	234	2	CCLETTSLSFLDKGTRENQWKGDSFSNK RCWNWISCKRMLDPYLIP/VTNINV KV/IKDNLRFETIKLEENLRK
2281	16182	A	2297	334	6	KLFSPPGGGGPPDPDPKKGWDPETN KRGGGAPNPPPKGGGAPKPPPGQKQSP PKKKKIKFCPPPKKKGPGVFLRGPRGP YRVFLKGPPLPFFFFLKKSWRPLAMVA
2282	16183	A	2298	467	8	LPGFKASTDORN/VAGDEKQLKMLIYHS ESSALKNDTKSTLPVLYRNKEAF/VTA HLLIPWCTEYFKLIAETCCSERKISFKI LLLI/DNAPSYPRALMKMKINVFMSDN TTSIVYSTDQGVILTCNSGYLRNTFYKA ITAIDSDSCRMPOEQEN
2283	16184	A	2299	1	449	STYLSIF/FNLSINLSIYLSIPIYLSIY /HISVYIYL/SIYLSIHLSAIICLSIF QSISLSLSINLSIYLSIYLSLSIIYS SIIYHLSIH/LSYYS
2284	16185	A	2300	1	445	QAGLQLLTSGDPRTSGLPQCWDYRC/DH RSWQT
2285	16186	A	2301	241	22	KWVLGTCACVHVFICVYMCLYVCAWV/C VSMCLYVCAVCVMQC/VTCMCMVCVCV CRFCVCGVPPHSSKWSIG
2286	16187	A	2302	3	478	GGQTETLLTSQRKGWPEALLTSQMGEP GRGAPHIPDDEQPGRDAPHPDGAAGQ/ SAPHLPDGE/PGRGAPHIPDGAAGQRRS PLPFWGG/ELGRGAPHIPDGAAGQRRSS HPR/PSRPGRGAPHFPDGAATG/Q/DGAP HFGIPDDGT
2287	16188	A	2303	440	41	KSHLSFLSFLFFFP/TKSHSVAQ/CW SAISAHCNCLPGSSSHSALASRVAVTT GVYRI
2288	16189	A	2304	2	395	FFLVKTRFLHVGAGLKLFTSGGFPALA SQ/SL/RTGMSHRTQPE
2289	16190	A	2305	184	2	SIKKPKPLVNLNRNH/NTWQAVTPACN SSTLGGRGGRITRSVGQDQSGQRSEF LRIGYGLD
2290	16191	A	2306	86	472	IYKCKWQNK/REFAGSLVPEMGFFYVT QAGLELLFSRDPHTSASQASAGITGAAFH QRWSVGTVLLQVDRGTPPVGDGSGRTPO WPGQAFRLTALKSEAPPHSSDVTVPVL WSEGSFCLLSPPLSLFTG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2291	16192	A	2307	133	2	RVIHVVVRSHPAIP\TTREAEAGESPEP GGGGCNEPRSCHCTPAW
2292	16193	A	2308	3	369	LTATFPDFGGSTHPLTASQVAVATGAH HHSWLI\FVFFVETGFHL\SELLSSSSPL ASASQASGITG/REPCLTSPFFF
2293	16194	A	2309	253	365	TFYFYLFITYLRQSL/SSVAQAGVQWQDL GSLQPPPSGFK
2294	16195	A	2310	362	0	TKAQCCVHENHFKLDKANTLNKVKWRNI CHSSPNQKKYGLAILNLNLDKSGFRSRKDT GDDE/HFKIKKSVIQEAI I I I N I Y A
2295	16196	A	2311	167	2	LCYCV\FVFFIFWKGSTLSQGGQWQCD HGSLQPLPP/GLKRSLSHLPSNWDYR
2296	16197	A	2312	67	482	DHLIFGGGCSSELGHPTPAWTA/ET LSQKKKKKKREK
2297	16198	A	2313	188	437	AGFFPENQITNMKVRKANESDPWGVK ESDESETHGSLSLSLPLFTFLRQSL /NSVLAQGVQWNRNLSLQKISD
2298	16199	A	2314	41	325	TTLEKXVRGGYSLINFLPLPVCCLCPA RGGVYRGQSSLSCSRLLHPVRASRPLC LPTQASALAGAPPALPPLPCSLISVCCA SNEQGSVG*DP
2299	16200	A	2315	417	0	SPPRNNDYRCVPPRPAFNVFLVNGF/Y HVARPEFGLLEPTSGEPTLA/FSKCWD YR
2300	16201	A	2316	98	288	LMAVVPATWEAAQESLEPGWGSGEEG CSELRSCHCTPAWVT\SETLSHTHTKKK KKNGAAL
2301	16202	A	2317	1	410	LNHINLSLTKRKFSPHSLNLKKKKKKK KKKKKKKKKKRGGGVKKKPRGGQKKK GGKKKNFSPKGGKKKRGEGPKKNFFG GKKREKTPOKKSPGKKKQNL/BERG EKNPKRGGEKKRSSPRNNLNLRGEKK
2302	16203	A	2318	249	3	PLKASSPPKAFNFCREVGPTCPPPKKV P\PKIPKLVIPPIPIRKLLPCPPPLTL APRPVPLKRP
2303	16204	A	2319	2	393	AHLGLPKCWDYRHEPPRAPFLNLSYF GLDLLT/S/GDPPALASQAETITGVSHC AQ/PEVY
2304	16205	A	2320	389	2	RGNINIGGPGPLRGKKFSPPPPLKNWGT KLGPPIPPPPPPPPF/GKPGFSIFPKPI LKFGPKKKPPRAPKNGGSPGPGWFFFF FLSNFTQLPGILSKGGKNFASPPPPF FFVHYKTSYPSATPDW
2305	16206	A	2321	389	206	FWNRGE/NHVCQANLELTSNDOPASA RSAGCTGMSHHAQLKNYFLMVRMRNW IAGM
2306	16207	A	2322	371	42	SFFPGSGFFSPPPHHEFFPPPSFFSW VGVRQIPPPPKIFSSPPPGGFSPPPE R/VDFFSPPPPPPPPPSFFLSPPPPPF FFFFFFFFFFFPPPPFFSFGVKKRK
2307	16208	A	2323	82	386	PFLTQKYFFTPPEGGLKPNRREGPS PITDPTLWNNMKGI VPKAP I IFMG INMTFSGFVTKAPFPRLRNPMRLQG FDLLTLKAS\WGSSASWY
2308	16209	A	2324	1	413	RGSNDNRHGPFCRVNVLVETGFLHVG RSGLELTPSPALASQSGVITGVSC/RP PQASY
2309	16210	A	2325	58	400	SETLVSKKKKKKKTPPPKNPKKKKNP

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						PPPPGAKKGGGGK/FPPPIFQKKRGG FKK/SPPKKPKKKKTPPPLGKGGFPP RGGPLGGFPPPPQKNGPPPKKKPPF FFPPK
2310	16211	A	2326	462	306	AHHNLRLLFGSSDSPAAGVAGTT/GMC HHARPILYLSGDASALLHCFSSAQLF
2311	16212	A	2327	1	393	SRPSPRTKIRNFFVETGSCYVAQAAL KLLDSSDPTSAQAG/ITGMSHRAQPL TS
2312	16213	A	2328	391	2	AWFKETKAGWIIPRSWDRGSWVSQPYSA LTSSPESGFSHVTVNGDSMTCLDGHSL VAPHGIPQSGSLQDGVSCFAPMTKPY LASTRM/LRHEARELGGFFSLRLRQGLA LSPQLECSGAILAHCSLNI
2313	16214	A	2329	2	115	GCSELRSRFCTPAWAT/STASQKKRGG KKKKGGVYFF
2314	16215	A	2330	2	406	AAAPSAALALRDGAWVRPELDLLPPCGEE VAFGAHCLGCGSPCLFLSPSHTRQSP APTSPLGLSTSPVLVTHVAPSSKGP PSIPGAGALRGCGLGGWDR/PSSPSLP/ PDVSPKLNFAI
2315	16216	A	2332	226	377	KRKSHTITFLFTLSWEDVAHACNFST LGGQGGRI/TPRSQVRDQPDQHG
2316	16217	A	2333	3	191	CLSFQGGGCGGLRLCTYCPANV/VNETV SQERKKERREREKEIKERKKRKKERK KEKKKK
2317	16218	A	2334	295	81	FFKFFPPPKKTCPEFS/FFWEKRGFFPP PLRSFFONPPPKGGPILLKGPPPPPSL GWPPPPPLFFFFFLR
2318	16219	A	2335	375	8	TQIVPLPSNLGNKTRLRLLKKRNEQGN IPTDTIDNRKIQIIQ/TYYEOLCANK/N LDKMDKALESHNPKLKQRESLNI/HS KEIHFI/ILNISTKTPDPTGTGTFKLQ IPKEKMGHSGSHL
2319	16220	A	2336	399	97	FFFFFFFQKQNL/SVTVQGVGGQYFRSL QPLP/PRVKPFPSPNPLSNRGYRGPPPLR VRQENCPKLKSKRFQNLNKLRLGKKKKL RFPKKKKKEKEKIVKT
2320	16221	A	2337	411	57	KKPRSFSSCSSPPFFFFFSPPPKKKIF PPPQIFWGGPPPPPPPPKPPPPPPFFS PQKKKI/SPPPPKKKFFFTPPPPPPFF FFFFFFFFFFFFFFFFFFFFFFF
2321	16222	A	2338	97	354	AKAPSLSLVLSFSTFFLGIQGLALLPM LECRGAIATYCSLNLDPSSGPPPTSAPS TPY/RIAGATGTHNALLFKFSSDGL PL
2322	16223	A	2339	391	45	LMEFHLSHKHSRGEAPSIHWSIYLSIHP SIHPSLYHSSHLISINITYSTCLSIH /CISIHPSIYPSICPSVILLASFIHST ICPSMHLPIHVSQHFSLAQILPVSFVG EVS DI
2323	16224	A	2340	506	0	RDEHGLIVRADKKKKKKKKKKKKKK KKKSSSSSSSGTFFRC/VPLKDPVG
2324	16225	A	2341	203	1	VELRVATEPGFNFLGIGYCTSMWDWIK KMWYIYIMEYHAAIKG/DRMSFVATWM ELEAIFLSKLMO
2325	16226	A	2342	402	40	FYPKKKASPTDA/PSSSSSSPPPPFF SPPPKKGGFSPKPPFFSPRFFSPPFLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Methad	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						PPPPPPPPGLKKNNFFPPPALKEFFFK SPPPPPPPPPPPPPPPPPVAGVLLCYSG
2326	16227	A	2343	181	1	QLKDDQASDLGLKNGDEVKRTIPSPFLPSS LPFF\LPFLHQFLPSFLPSFFPSPLLP FLS
2327	16228	A	2344	2	407	FVASQLGCSGV\VRVDRPLEEAVCPFFSD QLRAGRTTALPKAVRGHLSLQRLLSF \VFLCPAPRGAGYRGQATFLSCGGLHPV GASRLCLPKQAWAMAGAPPASLPFCS LISDCCASNORDSVGARPSPEPAGH
2328	16229	A	2345	405	178	ITKFIYEKATA/LING/EKLAFFLKL TRGQCLHSLLVNCTVLEVITGTLRQKE IKGIIEKKEVELSLFADRL
2329	16230	A	2346	2	412	FKASKASLSPLLGANTAGDFLKLPGLIY HSLH\LKNYADSILLVLCQWNNKAMMIA HLFTAWTEYFSPPLRPQAQKISFKMLL FIDSAPSQPGVLMEMYKEINVVFMPANT TSILOPMDQGVILTLKSYWLRDTFH
2330	16231	A	2347	2	397	ESLEPGRRRLQGARIMPLHSSLDNRVL CLKKERKKEIGVLRCWQECKIVQPLWE IVWYFLKKLN\ESPYPEPAVPLINITYPRE MKIHVYNTCTQIFIVALEFTIAKSGKW GTVCACACKPSSE/WLRWDYL
2331	16232	A	2348	3	423	EGCSSELGSHHCTPAWAT/AESVSQKKK PKKK
2332	16233	A	2349	49	262	QMKCGSNRRRGKRVGRSQISKKKTNAPI KKWAKDMNREF/DIQMANKHMEKCTSL IIREMQIKSTMRYHLY
2333	16234	A	2350	356	2	FVTAPLHSSLGNRARSYCKEKKKQVAA KAVLRGKFI IAYTVFKKKRISNIMLSIS LKILEKEHTETKADGAQVTKI\RAKI NKIETANETKSRSLKTSKTVEGKCLRD ILLSAQI
2334	16235	A	2351	360	19	LDQGLFVGLGELLFRSTVPTLQPPGG ASFPVLNLTPLF\SLSPSSSSSPASLVR PWVAPPLCPHGEPPDGGPDSTSLPFFG PAATGPAARLIQHSPASRQRPASHTCG V
2335	16236	A	2352	360	0	NTFLAAPRLVFCQMTSYSLALLSHKIAL MPLNLSDLLTRWTHCMGELFFLDILAIO NPFTVFFLGHPEWGMESRFVQAVQW PDLRLQPS\PPGSMRPSCLSPNSWNS PSYGR
2336	16237	A	2353	34	474	EGWRPCKELAAQOVGCHPSCFSPHWQLL QKQKTAGAVSVCVCTSLCVCVCVCVC VCAQAMCVCAQA/CFCVCVCAGA/CLCV CVGA/CLVCVCAEAVSVCVQ/VAVSMCVC RS/VSLCVCVQGSCLVCAGA/CLVCVC CGIPPPVLCIN
2337	16238	A	2354	297	16	KFFFLKSSFFSFFFLTPPRFFFFPKK KKIFFPPPRKIFFFLIPPPPKFFFF FFFFFFFFFFFFFFFFFFFFFXRHGG WFEEITLTV
2338	16239	A	2355	3	315	PVTFATRETAGETL/HDLGEPGGRGCG ELRSCHCTPAWTEQDSVSKKKKRGGA RPKESMTTGLQORNFFGLALLISGA GVLRKRDGKTLGFQGNRWG
2339	16240	A	2356	399	154	PGURGEI\SLPKIQ/ELAGCG/GHLNPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						GRIFGEPRSRHCTPAWATEQDSICKSHS RSGLWCYKSSSVYLSTRGVVIRGASV
2340	16241	A	2357	416	2	FFFFFSETESRSVAQAGRLTQWRNLGS LQAPPPGFTTF
2341	16242	A	2358	209	2	KKNLVPNPRGGYFKSLQPPFGV/SCFN PPKKLEYRVLFPQSPNPPFFCIFS RDG VSPCCPGWSRTPD
2342	16243	A	2359	279	380	RGYNF/WPGA VHA CTNFSTLGGGRQIT RSGDQDH
2343	16244	A	2360	415	224	FFFFVFFFLITFTYLMNLPLCHKFLFL QFLGLYLFLLYL/CAFFLLVALNIFITS FOOLDYTF
2344	16245	A	2361	278	2	ISDPFRFNWYRIHTGLISLIQISENCV SCQKFOLEHFRFOIRDAQSVLRK/RKA WTGAVAHACNPSPILGGRGWISRSGLDV HPGQHSPT
2345	16246	A	2362	139	282	KKKKGGRGGGGGGGGGGXXWGTGKKKK GGEKKNLWGGGKGGGKGGGS
2346	16247	A	2363	19	409	PKPPSVLGGGGPARYPSPGLGPNRPVPL GPGVGAPPGPGKTPFFLKIKIYPARG GPFVIPASPGSGKSLPLPRPRVLPTQ IFP/PPPGGNG
2347	16248	A	2364	159	383	HSHEKNLSLTKLHANNITFEHFSLS SLNQCFNLITVPSHLGNFNKN/SWFG AVAHTCNPTNLGGRGQITR
2348	16249	A	2365	400	221	GRLEQENCLNSGGRECEPFR/HLICAF AWATEQDSVSKNKQKQKQTHITVTL LCARH
2349	16250	A	2366	383	14	GGRGCNAPRSCHCTPAWTERASPOKTK KQKNTHTKKRISSCCYKMDPLRQA/TF LOCPRAEGPSQKARMELMEKQKKNQGP ARHRRQQLPSTRPCDHLCVLVSVSS TPAQLSLSLICK
2350	16251	A	2367	274	1	PRKILKARGKEHLASRGTIMRTSDFVL QTMQARREWSKIL/NVLEEKIHQRIL/ PVKSSPKSEEEIKTFSQKQLRGLVTSR SDLGKDVK
2351	16252	A	2368	161	2	PPFFFFSETESCCVTQARVOWRHGLSLP GSSDSPASASQVAVITGRHYAWLIF
2352	16253	A	2369	361	198	NGRLIFVFLVEMGF/VMLARLASCDPPA SASQSTGIRGSMHNSQLKCFTEFDSFC
2353	16254	A	2370	116	300	HLNGDAVEERDFPKCTVSGIIVAHNLE FLG/SSDPSASAPRVATTGMCHITWILI FVILVEM
2354	16255	A	2371	2	192	MKLDPHLSPYTKVNSRWIKDLNLRPKTI KILEPNIR/ITLLGIGLKDSMTNRNPKA IAIKTKLAR
2355	16256	A	2372	1	133	AGELLEPGVGRGCSKPSCHCTTAWATE QDSSPEKKKKKKGGF
2356	16257	A	2373	43	403	LHDSPALASGAGTTGVSHHARPAAGIN SRIGQARDRISELDWLETRARQSGRN MDKMKMNKNQLQERDRTVETKSM/NTR LTGVBERVGENSNLENIFQDLIHENYK GKPIRLMVDL
2357	16258	A	2374	404	215	GQGGRIITRAQKFETSLGNVVRGSEAGE LLEVPDRGCSEPRSCHSTPAWTEQDS VSKRRKRC
2358	16259	A	2375	3	397	SKOLEFTQLYTKLNQLNRTKISDLKKEK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						YPIRLFSKENTQMASRYTRKYSTWLIIR EMQIKTTFRHKLAALASSRCLLGLG\AT SAHCCTVGAPLW
2359	16260	A	2376	413	1	PKKGLFPKPII\WVTPGFFPPFRFKKPP KKIFGAPKKKKKSPPPAKKFFFKGAP PPFFPPFFPPFFPPFFSGDSQER\REAM FVAGGP\FRPHSLSA\HAPGGTAMTFMI FVQTHKAQSKPLPASEC\PPPTPLS
2360	16261	A	2377	398	247	RRFHAGAGLELLTSSDLPALASQ\SA CIRGSHHAGPSATHPKHLVS
2361	16262	A	2378	2	143	CENRLNPGCGGCSLRSCHCTS\AMVTT AKLCLKKKKKKKPKCGGG
2362	16263	A	2379	417	90	FFFFFPFGGRLQVCPFPGLLELCEFLY KGGSPGGSTIFPPPPPGVGP\PPGPP GGFFFFLE/OGGVSPDGPFFVLTPK KPPPPAPKGGEPKPKQVWGPWPPTF
2363	16264	A	2380	36	427	VHPLNHHQDQGASSTQKKKKKKKKK KKKKKKKG/WKGGGAF
2364	16265	A	2381	402	2	NFFLKGRGWPLPFP\LRGPPPPRGSPK /RGGLGGPPFFFFSGKTPPAGGSRTFMG QKKKGPLPEGLPFGGAGAPFLPPVP RGVSPKKKKG/APPPFFPPFFPPPP PPFFFFFLRYNLALLRLGCSGT
2365	16266	A	2382	166	5	THGHVYVDQEMQMNIENM/WPTGVAHA CNRSTLGSRGWITRSODLMVKPRLY
2366	16267	A	2383	2	457	TSQPSLLSSWDYRSTSPRIANP\ILPYF IYFFAFSVETGFHRVSQDGLNLLTS/S /IPSIPRI\PKHWDYRHDP\RTWP
2367	16268	A	2384	2	417	GRVGSQSGNPNSSLSFTLLVD\FEVTT PGEQKDRIFKVS\IKWLAIVSRMLHEAL VSGQIPVPLESV/QALDVAMRH\ASMR
2368	16269	A	2385	318	32	TMEINLDKQIQVIF/FEFKMGREAVET THINITYSGPETVOWMFKKCKXGDESLE DEBCSGRPEVGN\DLRAIIAHASADAWV DRDSGRCCACAP
2369	16270	A	2386	409	3	ISQAPSTPFRKRGFR/PPQKTSF\LGPPF YAAFYQEKKFLFFSSDPPRETGD\KGKQK GPPFPKVA\PKKKGFKKGPPPGKKKDP SFFKKSQETRP\RA\PALEGRSR/SA LPGDRRR/PPSQKKTETPPPPPTP
2370	16271	A	2387	415	10	KKGFFPFGGFTPLFPEGLP\DDPPPI WFSGFCPPPPPLP\FFFFRGGX/HILVF PLFLPPPPFFFFFP\FAKESPKKGPG LNFFFFGPKGN/SPPPFFFFFC\EMEFT SCRPGWSAKNHDLGSLQPPPPVFK
2371	16272	A	2388	410	95	KATMDKSDH\IKLSFYFAKETPT\TKVKTQ PPEWEKV\FANYPSDKGLIP\IYKELQ YG/KKSNN\SIKKWADLNRYFSKD\QMA NRCMKRCSRPGAV\HTYNPST
2372	16273	A	2389	362	92	RFLFFSPPPKGGFFPKFFFFFPSPVFF PPFFFLNPPKLI\FGPPKKI\FPPAGG KKIFFLKGPPPPFFFFFFFFFFFF PV\ENTFY
2373	16274	A	2390	131	487	ATEHEKTEKSSLSFFSISKKKKKMEKLH DIGPSSN\FLG\RPKAQATKGKT\DWTS LKI\SSRDTISRMRQPK\EWAKTFANKS CNNKKPEKIDNKKKKKKKFLGALLKK TNLKPRG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, =possible nucleotide insertion)
2374	16275	A	2391	408	145	RWSLALSPRLCESGVSSAPCKVPFPGVT PFSCLSLPSNWEDRCESPPPAQ/IVFIG EGFYILHGFF/RRGPKRCFISGCPFV LSFFT
2375	16276	A	2392	1	203	LFFFAFSVETGFLVHGAGLEPPTSGBP PVSA/FPMCDYRHD
2376	16277	A	2393	386	16	TPSAGGRHIELSLSTCPSCAQHGKHEHL EGGEGGAQSLTTPASSATSSQDPISAH AVEDKLSIRLETIDLTKTS/WPGAUGHT CNPSLTGRRRQANHLRPGVRDQGLVIC RFRPPKVMGLQA
2377	16278	A	2394	3	396	QLLERLKQEDRLSTGSGQCSLRSRHCT PAWATEP/DSVSK
2378	16279	A	2395	273	416	FFYSFLIKRWKKQPGMVAQACNPSTLG QGQGGRI/TLRTGVRDQPGQHG
2379	16280	A	2396	329	76	FIPFESACSOECLKPNLRQEW/YIFGTL KLIFFETESHPTQ/DWSAGELL/DPGR GCSLRSCHCTPAWATRAKLCCKHCHK IKK
2380	16281	A	2397	210	7	GGKKHYCKRPGGGFFAAVWSPKGLFS/ RIWKAPILSPQKKKKNTNPIKKWAND ANRHSFKETQO
2381	16282	A	2398	48	393	SILTKRKPFLKRGGRKKKESKSVTHV FFSYQSNAPFSKPLNSMTLGRLLSFSP FLVHFHYTDDGILLCCPGWSTPGLKGS SHLSFPKCDWYIHEPPHAYHS/LFCR
2382	16283	A	2399	128	383	EEAPKHFFKPNLH/QKKVLVTANWAAAG LIHCSFLNPWETITPEKYAQQTENMHQK LQCLQLALVNRKGPIILLHNVRHITTH AS
2383	16284	A	2400	54	384	LFTFYLSNVFHTYMLFYFWTLFFSVNPF VSMPIPOCLDDSSFIISLDSINPNIYS QLIFDKKTORGKNSLDRWCNENCIFTY KRMKWDPYL/SPYTKIISNWMKDLNIK
2384	16285	A	2401	393	1	HRGENTHQGGGLSRWRHRQRGTSRW IRHTRQNGPSRWITPSSRGSSRWKRS RAGDIEVKTSQSEGALEVRIRSRQGT SRWRSFSRQVSPFRWICSRQRCSS/KV RRRSRQGTSRWRHRSROR
2385	16286	A	2402	1	330	RPPPPPHKCDYR/HEPPR/QPTLWVIFK LSVETRLCYVAQIGLELLGSSKSSRLD LPKCDYRHLLCWMVIFQEKLV/SGFL PKIPRPFKAGMEIFKQIEGWSSHELAT
2386	16287	A	2403	3	407	ADAMGLRGTHGPWEQAGTSGISPSNPL VCFRQSVVALVSQAGEQNRRLGSLQPPP FGGREGSCPSFGGGITPCFFVFLEKM GLHRVQAGQLLMSGEPPLCSQRGGI TGVSHHARPPSKGPIWHGTAPAM
2387	16288	A	2404	239	573	VCFGVFSLSHFESEFSSITQAGVQWLN LGSLOPPSRGFKQPLCLSLSS/YWFTG TPFLVGGGAGLRGG
2388	16289	A	2405	1	122	PTRPGRCGGLRSCHSTLAW/VNSETTS QKKQKKEKKLLPL
2389	16290	A	2406	417	130	QALRVKHVQLVSSDFLAKTRAQSVNNL LRHSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS LRGAFGRFCPIRR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, =possible nucleotide insertion)
2390	16291	A	2407	327	3	RQSQSLRYMAHQVCCPTCSILIRAEIN EI/ETKKNKIEKINET/RKSWFFPEKINK MGAITPDATERQNI IQGYIEQLYMQNLE NLEYMDKFLGRFKPPSLNQEELDTLNR
2391	16292	A	2408	178	404	AAYRINSLQEVQHPTRKRHSQPRQSKLR EGNAQRNNIRRGPGMVAAHACNPSTLGGQ GGQV/TLRSGVRDQPGQHG
2392	16293	A	2409	94	386	TSFALVALGGRCESEPKSCCHFPAAWVS SETLSQWKRTPTLNNAKVWGRFLRFPF FLTRGGQRFFFGTKTKSLGAGFKKG GGGKGGPGPPMKGLG
2393	16294	A	2410	1	384	PTTROVRILKFPRIYVHTKRKLNTYQNT ETFTTQPPKMHSHVWQILRNNRANKQZEN VAHNEEKNKKQSIETN/QKYTHKNLDT TKKKKKKKKKGGGPKKTI/KARGSEN NFFFLGPKLNSGAGF
2394	16295	A	2411	423	2	FFFFPPPOKSLFFPPFFCGPKIFSSPP VFLLTPPQKIFCPCPKKKKYFPFPRGKIF FFLK\PPPPFFFFFFFFFFF FIFFFFFLGFLLSLLIGVPLLNNAN IMILLQKKILKDEVOIISFFPSTKNRV L
2395	16296	A	2412	218	112	LKKENNTKCYCQWGTGTGLIHC/WW/KL IQVLNKT
2396	16297	A	2413	64	403	LKNFFFFFPPKKGGPPGAPGGSKPRGLG EPPPPPPQRRGGNTGGGPGARPKKNGGGF FFWWRGEP/PPPAKGGGDLGPGPG REETNNFPAPAPPGPKNNLGPRAQKIL CF
2397	16298	A	2414	217	409	VKLSYSVLLTITCTVQACQYQELRPGAM AHTCNPSTLGGHGGRI/TLRSGVRDQPD QH
2398	16299	A	2415	416	0	ERPPSSFFPPPLAPGQVQGFYFGKGPWP ERSKKKNRFWGTKEFPFEGGGPPPPNS PFGGEEKSLFFFGGKGNFTWSGGKFL KKRVIKGRLHPCGGKYKTRFSLKPGF PPKFFLQCG/PGQWKEPQ
2399	16300	A	2416	277	0	PFVLLSSSSSSSSSSSSSSSSSSSSCS LLVRYLCKVHKHSSLCARHPTGVFLELI HDTDSFAH/VFPADLL
2400	16301	A	2417	205	486	RHGYGFGFKNCTNQHRHSYRRYYLHRH IHLTFLAYVHRESPEAMSAITQILFF KLLSFLRRCIA/SVTQAVVQCISLGLR PRPPGFKRFLWC
2401	16302	A	2418	364	1	KESLGDVPKDTVILFATRNPMQGSNYQ FFIYLCIHLTHLSRSYCWFGCKMLQ/PLW KITVWQFLKKLNAEPFYDPAIPL/DICIP VFTASLFIIAQRWQPKCASTDEWINQM WHMHTIEHYPR
2402	16303	A	2419	281	492	LFPPSLPASHPKLSTQQPERSHSVTHCG /VDRRSGDLGLLQPRPRLKPFSSRLSLW SSWDYRAPP RPANSC
2403	16304	A	2420	63	465	RLQRFLLSF/VCLCPAIPGGAYRGRQAS LSCGRLRPVRSLLLCLPKQAWAMAGAP PPASLPSCSLISDCASNORDSVGVGPS NPGAGYYLVARRFLSPLEKRSIQGVVTL FSRCRLSPSLTRKGNLSLTPCAS
2404	16305	A	2421	61	482	QRARTYGVSHHAQ/LRFLCLPMRSHSVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 95/151,26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						QAGVQWCDNSLQPPPSGLKML/STSAF QSL/WDYRCEPQHP IHY
2405	16306	A	2422	90	444	YCFSSCESEKCRCPGHDLQLSPLGCHHG VSGLAKPLLCFWFIWKPPCLCSPTTSL PFLPLPPFSQCPQGPAMLEGRPSLWK QGGLQSLAIKR/REGSRAQWLTPVIAL WEAEAGG
2406	16307	A	2423	1	444	FGPGGCGPVATLGSFSRPARTDSPSLP PHSQLEAEARNRDIEAHVRLQERMEL LOAEGATGESLMCLPLRRT/WEVGRLL
2407		A	2424	189	418	SRRAEPGSFRGLRVRGVSCTCV/SLWV CVVCVWG/VCVCVVCVCARA/CLCLCA NFSL/CSHVSCLCLSLSL
2408	16309	A	2425	30	895	LDEQCTSEIHRRGATARPRAPEHPAPP ATAVRGRDAASONLKRRPGSGTDGLRLQ GAEPKRLRLRTYAGGAVIPRGTPERAQPP PQDPLGRRRLWSRNTWGPWGTTPQPPS PQLLENDMGSCQFVPEARAGKVFQDSQ EQAHIRRETVSSKVCBEPHQRARDA PTNFP LKCKQKRGASTSSQHQHGRNLY FFIDDVSPPSKR/PKTNPPQPPVPEP ANAGERKMRFPNFGPHNVEETKLICLC PSGHASCQVHLWTGAMLLGFQSNRKLPG SGLKARILQ
2409	16310	A	2426	494	154	SSRVRCCQA/LLGASQLGCSGVRRDPLE EAVCFPSDLQPRAGRTTALFKAQMEMQK SPVFCVAHAGSCRLEFLFGHLGSSLHG LWN
2410	16311	A	2427	416	1	PORGFLALEPGRGAAPVEDLPQPGPD KPPPPPLPQPFRARTVVTAAVPRHPPPV ACHPPQPLAASKWP/SVAGGDLPLPG PERPVHAFFIGFIFVHLGLGGVSGRGAV APARSQVPVPPRPPSSSTRFSLFHLHE
2411	16312	A	2428	84	409	DYKHATMPRTQNFVYHSPQOPCENRI NFTPKKKKKKKKKKKKKKKKKKKKI F WGG
2412	16313	A	2429	1	389	LRDLSSDRSNPGRFLSTNSSLY/EKDK RNKAYFTK/RPSVNDIIST
2413	16314	A	2430	456	0	PGWPGRGAP/PSQTGWPGRGAPHIDDG QPGRGAP/PSQTGWPGRGAP/PSQTGWPGRGAPHLPDNGWPGRGAPYIPDDGQPGR GTP/PSQTGWPGRGAPHIDDGQPGRD/ GSLLPRGGSRAEALLTSQTGWPGRGAP P
2414	16315	A	2431	3	344	CRERRSCHCTPAWAT/SETPSQKKKKK FFGNGPPGPQAGLKLRAWGFQKRGTM GPGTKNHPQGRGEPPLQKKKKTTPGG GGGAPPPQGGGAGKSNFNGGGMFQGG E IP
2415	16316	A	2432	1	109	RPLRLRLQENRLNRSRGCEPKLC/HL CTPAWAT
2416	16317	A	2433	1	239	QSFVFLPRLVNSWAKVICL/PSVSQNA EIT
2417	16318	A	2434	3	464	DWLQLEMQGEI VALVSHHGGLPWLSES ARRLQVQSDLEPWLVCRGTHKFRFCVH LTGRREFHGVTDCTLFRDAYHLAGIEM PDFHRENDWNRGNQLYLDLQAPGLYYP VPLSAAQPGDVIMCGGSSVPHAAI/Y

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2418	16319	A	2435	3	427	CODGELLPHIFK EGARTSSSRHPNCKYLLLSLAHLFINA LNLVLKGLSPSPFPALPISFPFFFFPH FLGTPTLEGGADLPFLQPGAGC/QPA PLNYGPGPYRNPC/RLPQLKPMGPHG LLKSPPNPGRNWPLLGSLDFDFKKRTS TLP
2419	16320	A	2436	238	400	QFRWKRKAIFFFFLRQSPSVTHAGMQ WSNLSSVQPPDPGKFOFL\PSVSS
2420	16321	A	2437	11	442	LGTFRRTATGWVRLLESWACPVLGHPAK HPRPQRMCNVFSYSPQADELKLQAGE IVEMIKEA/CGNPDMPSPVPGPQRPKPT TEDKGWEGECQGRGVFPDNFVLPPPP IKDAQPLLFGIDQEAQGESGISGRIR RRLSC
2421	16322	A	2438	411	80	PQAEAGAPTSGSENFNPPPRGGGAPPP PQKNFFPPRGVNPGGGGGKRPMPKXGG /SPKKNPGGDKNPPKKNKINIGEGGFI GAPRGTPKTTPPPRDGYQVFFFIIVSLK
2422	16323	A	2439	290	1	QLNKIKKTLPLFLPWANEKVPKIFPNYP PGPKKKGYPSPISFFFLRQGL/NSVTR AGVQWRDLSSLQPPPGFGRFSQCKFNS AFPHASADAWVP
2423	16324	A	2440	440	213	PFSRPLFFFSPPPKKRASPPFFFCFPR VFPPPPFF/SKPPPKFFPPPPKKKIS PPPPKKIFFFSPPP
2424	16325	A	2441	131	408	GCVPPEPAFLCFVLEIVSSVAQAGVQR NLSSLPSPPGPKRFYRPLPSS/QDYR RAPPLA
2425	16326	A	2442	102	351	QASSSVLKLCCVCRARLCV/CACVQACV CVC/VCVCEVCVC
2426	16327	A	2443	190	3	PQAREKSHRFGPIGRRLKL/DPPFLSP HVKINPRWIKDLNWKTTIKTLEGLNG TLDDTCG
2427	16328	A	2444	410	30	VCVAPFLCVCGIGTLCVHTQTQCVCVHT HSLCVCR/CQFLCVCG/VAVSCVCRA SLCVCRA\ALCVCVCRA\TVCVCVHTVCV CVCRDSPCMCVCAVCCVCVCVCV\C LCVVCVSAQLLGRGFCSSVNIKGAGP
2428	16329	A	2445	243	1	KVMQNKQPFNSLFFGPTTNFTFPQK QGGGONPNPPLFFFFFMROGL/DSVTQA GMQWCHAGSLQHLPLGLKQFSCLLP
2429	16330	A	2446	276	408	MLKNCAPWPGTVAHACNFTSLGGQGGRI /TLRSGVRDQDDHG
2430	16331	A	2447	24	405	LGDVCAFFFFFYLNQNLNPGGKILFVPG PAGENQRNEQFDKLGKGIKNPLRGGI SVPLTKKKNQ/WARGE
2431	16332	A	2448	239	3	SPLCGNNVYKPSVTEKTNQVEKMPFSKQ IWELCVELLWQ/SNRGIAGSGAHACNPG TLGGQGWIRMSGRDHPQGHETP
2432	16333	A	2449	406	144	GCSEPRSRPCTPAWVTSETLS/RKKRKR RKKKSCLLRAILSTSPELTHFTLTPLF SRYNDYPHFRDEKTEARRVYATCSGSHS WKRLG
2433	16334	A	2450	349	1	GGAIFLTPRPVPLTPTPLAFNPGHQE EILPLKKKKIVRAIYDKPTANILHGO KVEVFLKTSITROGCLPSLLYQHKTRM PSL\PLLFNTVLVDVLARAIKQEKIKGI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2434	16335	A	2451	382	19	OIR DLGRMTAGSGDORCAVGVKLLSFLGAA KGKPKHSEAEASLPRNPGSYNRQAQWQP SSLHLKGTIPDPTSLNTPWKLSSLKVP SWQGAVAHDCNHSITLGG\RGGWITRSRV RDQPGQHG
2435	16336	A	2452	3	396	FKLKLMLIYHSENPRLKNYTKSTLSML YKWNKAWMMAHVETTWTEYFPPIAET YFWGKKKI TLKILPLVDNAPGHPRALME MYKEINV\VOICILQPMQGVISTLRSY R\KNTFCKDIAAIDGSSSDRT
2436	16337	A	2453	115	411	KGGNFPPGGGGGKKIWP\PNNGPPFRGK RKPPPPPPGGGGGGGHHPPPGPIFFFEK KKKGLFGG\PGGAPNSHPKRNPPFPFPE GGELTNPTTFFFEFGAF
2437	16338	A	2454	3	114	HHV\GQAGLELLTSDDDPFAVSFQSAGIT GVSHRIRSVS
2438	16339	A	2455	397	1	WSWQK\NRRIDQRSNIESPEMNNPRMYGQ VDFDKIAKNTIEWEKDSLPNKWCNKNWI/ LKRMKLDHPLTP\KQSKWKKDLIRPE TEKLPEETGKNPHIGLSDP\LDLTPK AQAKVNTDKNDN\KIKNFPTPR
2439	16340	A	2456	424	3	PKKKKIFPPGGPKIFFFLKAPFFFPFL CLSHFLNRSRSLSCITTSVCVSTIPTSL CNKSSGV\CGLHCSLLAI\CSLIHLTL PFCVLLVCMCDTVCCVCCVCDTVCVC PCPYGLDIAFKHFFSRNSLTLVAQAGV QR
2440	16341	A	2457	266	379	HWFGAMAHTCPNSTLRGSGRI\TLRSG VRDQPDQHG
2441	16342	A	2458	10	409	SRTGPNFRAQTDPRPVVCFACFELPLW RSVDSATREAEAGGLL\DPGGRGCSLQ LCHCTPAWV\TSETL
2442	16343	A	2459	184	387	IVHFOMHKMINVAYITPCFVSFILEIQS HSVTQAQVQWHSLSLLPLPPGLKQSSH /LSLPSSWDY
2443	16344	A	2460	110	1	KNRVSFFF\CSFETESRSVTOAGVQWCN LGSLLQPPPT
2444	16345	A	2461	380	2	FFFFSETESRSVAQAGRLT\QWCNLS LQAPLPG
2445	16346	A	2462	382	29	NGPGHGGPPVIEGTWGGGGGPPFR\GS KPGFTWGNPPFLKNHKNYPGGGPPVPI NFLGGKPGNFFYPGGGGGQ\SGPGAVFP PPPGQRRSIFLPPKKKKERKILFFSLEQ RLQNCDA
2446	16347	A	2463	228	1	KKGITLKKPPPPGGRFFFFFETQTSRSA VIQTATVQ\WMPRLTANPTFRTQGILLP PCLKGSSCLSLPSSWDYRHV
2447	16348	A	2464	395	1	RLREHNLNPGGGGCSSEPR\HPAWQGS ETTSQKTKTKKXALASDTVLSRQSS ERRFHLSLFHSSEVTPFGIFSLTSPH PILPVWLAPQLPAICYGDSVKSFNQL WLSKELQESLSRLNLTQAFS
2448	16349	A	2465	29	299	ETPNEASPKTSWDYRHVLPCLANFFIF VKTGL\HRAGLELLTSSDLLCPKCMWDY RH\DRSTNPLSSVFGSIFLVVWLYLI ETNMLTTL
2449	16350	A	2466	1266	1473	YFVPEQSTQNHAHVFRVGSLLQEGCGKIS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						KLYGDLKHLKT\FDRGMVWNTDLVETLE LQNLMLCALQTUNG
2450	16351	A	2467	49	356	VQVILLPQLRLRLQENCLNPGGGGCSE PRWSHCCP/PAWVTEQDSISKTKK
2451	16352	A	2468	115	3	LSHTKWSAWFGAVA/STLGGGRQITRS GVCDDQPDQAGE
2452	16353	A	2469	3	404	FVAPGGGGGTFPGSLQPMPPRCPGASGS PSRAELIFGFPGKQVSPVGGGLLPGLPG SRD/SGPGGPBKQWGC/CLQAPQCP
2453	16354	A	2470	404	218	FAGVYIKWGLSSFKPFFFGKLFSSRPS PPSYWDYR/RPRPRPLFFFFLRLQSLA LLRLLE
2454	16355	A	2471	386	258	AGGLLSPGVGVGNKLLSCPCPAWTT\S ETLSQKKKKKKLPFY
2455	16356	A	2472	2	364	HTQTIIFFVLIVETGFHHVQAGVELLTS GDPPASWDYGR/GHRTWPYSHIFNNL
2456	16357	A	2473	1	292	DRGCSEPTSCHTCPVWAT\SETVTSQKKK KKKKKTPLLACPEKKNQNPFRGFFRKN PGFKRKKGGAPPPLFKIGRKKSPVGGH RHTFILGGPLPRF
2457	16358	A	2474	1	307	SLSCSSIVRRACFPFTFYHDCCKPFEA/S PVMLPVKPVLEL
2458	16359	A	2475	2	596	MKNADILTMELVLTSMKQLEAA/CQR HSLWELLRIPIKICRI CFLSFVSSSSSS SSSSSSSSSSSSSSSSSSTKITAW/LP PLEASFYRSTCLMPARALLFASTIPFWG LTLHLQHLGNVFLQTLFGAVTLLANC VAPWALNHSRRLSQMLLFLLATCLLA IIFVPQEKSSQVEERKCLSLFSQGLPW SHLS
2459	16360	A	2476	367	44	YQEDITIMN/TYALNIGVPTYLANI/DL NREIESNIIIVEYFNTSLSKMDRYRSSR QNIDKETVDLKYSI/HINQMDLTDYRT FHPTATERDSISKRIKIKIKINSKLT
2460	16361	A	2477	12	362	HHEPG/GGGCSELRLCHCTPAWVTELD S VSKKKKKKSKKK
2461	16362	A	2478	401	1	VFFFSETRSHFVA/RLCESGATSAHCN QCI
2462	16363	A	2479	3	353	YMCVCVCVCVCV/CVLPWMLCVC/CVCV CVCVLCVCLVSLQGHQHLAVGKRSG PPSHESFKTSLLLWVFENLPPLLCWVP QVSNQMPDQRTLRNNVSLPDEKVDHLL LPLTAA
2463	16364	A	2480	57	361	MNESLLSKRWSLLAFSHI/CVCLICGS TDIALCVTVACAMHVCGRVCVCMCLCV CLCLCVCRMVGRVCAPMCLCVVHCVL ARMCACGCGVCVYKAECP I
2464	16365	A	2481	3	381	YMCACGYICMHA/CVPMCMVCVCLCAH VCL/CMCVCTFVPMVCMVCVCLCVCV TPIITLPLFSQERISFCTDLRSFRATAK RSHEEVENCVYLQTIWNQYLIIFYLQNP NFGNAQWMLMVPVAVE
2465	16366	A	2482	2	380	THVLGNCLYFSEPFPHNQQRITRSFLE GYGENLMRLHMSYIHMCLHICAYICI/C /LCVYICVLLCAYICVVCVLCVICMCI FVYLCIHCVFCVCLVCIYICV/CVVCV CVCVCI
2466	16367	A	2483	296	1	NGTITRRMLPIFSRYRFGMPGLVQCTIQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SCTANSVPVPSHGFIYFFIYLLRDRVWLC YSGWSAVAPSWLTITSN\YRLKPSSCLD LLGSWNYRQMPPCI
2467	16368	A	2484	1	319	NTVGLCVCV/CLFVCVLSCV/CLSLCV /CLCVCVVSLCVC/VSLCN/CVSHCVCL CVYLWLCVSVCSVSLCVCVCVYECVIS STKRSLGAPSRAAKLPRNWAQKQSH
2468	16369	A	2485	3	334	NHFIISIDI/DKHKRIHQPFVPAIKTK LGIKGNFLNLLRGTSVKSTGNINM\NGE KFNPLRLVITQGDVLFHLLLEVLASAV KKKKKKKKKKKKKKKKKKKKKKKKKKK KK
2469	16370	A	2486	17	409	CLDNKKPKKEYCQKTHLTKKNPLLSTIC KELLKLYDKRMNPIKKHAEALYCLSK GDV/HEMASKHMKRCIS/L/SIRKMQM KMTL
2470	16371	A	2487	410	165	LECNVTIMAHCNLNLGSSDDPPTSA\Q TAGIHSLQHFFFFIFVETGFCVYQAGL ELGSSDLP\TASQSVGVGTGTGHGTVP
2471	16372	A	2488	142	417	VEQLLEGYRTKSLYLRSFFLVCMFLRW SL/DSVSPGLTNCIHGLSLYPPPGFKQ FSCIS\LWAWRRTP
2472	16373	A	2489	1	404	KAGAQMGIKHPQHSLSRLRRLRPSLPS SQKPLNTHYFPSPFCAHRHTHTHTHTH THTHTHTGV/HLHPHT
2473	16374	A	2490	373	146	YGLERKISFKIL/LFVGKSPSPYRALME MCKINNVFMHANTTPTLOPIDQEVILGP GTVAHACNPNGLRQSGRNA
2474	16375	A	2491	427	85	KTFPPF\RGFFFFFFFFFFFKAKNFPP PPTPPLGKKKN\PPPEKKISPPPGFPP PPFFKGGPPKTLFXTPLKKKGGAQPKK PFFFFTPPPFFFFFFF
2475	16376	A	2492	443	240	FLFFFFFFXKXFFFFFFFXXFFFFFFXFF FFFFFFFXXXXXXXXXXXXXFFFFFFF FFXGCLFIYLF
2476	16377	A	2493	3	135	ISAHCNR\LLLPGSSNSTASAPVAEIT GACNNRQDPSFIILQI
2477	16378	A	2494	37	420	AHVCVCTCVVCVICLSRRVVCAHSHVC AGIFLHLINQITFTTHL/CVKVMALRV PPSCLQGAQTGLAGQCMARVCMNFMY IFIEGHIQCTQSCGSEPIRGGLSLVC IC/MCAGFFVSFC
2478	16379	A	2495	402	178	RQNKTFPGVKQITGGGGGRGVSVFLRG VSQENPLNPGGGCSEP\RPWGQTKNP LPQKKKKSSKQCGEGED
2479	16380	A	2496	138	439	RTFILGDHHSHPSAVHFLPRKLCTHE TGAAPPPPALGATVPSVSCLTGGGPO ITPPPPALGARDLPSVSVRLTMGGQPIT PPHPDQPL/SPPSVSVC
2480	16381	A	2497	118	382	VKSFCASMRACVCECYMCSVMCVCV CVSACLICVCLCQ/CDLINKCV
2481	16382	A	2498	164	439	VKSFCASMRACVCECYMCSVMCVCV CVSACLICVCLCQ/CDLINKCV
2482	16383	A	2499	1	411	ISTSFYTDITNRTALHFAVGRNHLASVD FLLKHKARVDVADKGMNALHFATQSNH VRIVEYLIQDLHLKDLNPDEPKESPLH LVVINNHITVNSLSAQHDIDIL\IRS SKPLHVAADRGVNLVE/LLLKAGCD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2483	16384	A	2500	80	404	RTAAVSVSFQDPBEGQSPKCTQGVRE ALRQIK/PLVPTCSLRH/WPACSLA/LC QPLSEKDLTQLFHFARNAPTALAMMDY PYPTDFLGPLPANPVKGRRLRRRRRP
2484	16385	A	2501	215	1	AAIQQSLACSISVFPATTPRAYTFVP QLLVNRFVYKPTLELRSLRCARRFPRE TGADCRHAGAGROTK
2485	16386	A	2502	423	214	WQAVGGGLEP/GGRCCELRSCHTPA WVT/GEILSONNPKRQNKTKQKMGPCV PGSWGSPRAGGLTV
2486	16387	A	2503	294	1	LHNNQRQRCPPPPPPPLPPPPPLPPL PLR/HRIAGAGOTAKIRVVGVVVGAA GLGVAAA/DSRESCPDGAAAGGEGGGD SAATAGPGGGGGGGTGK
2487	16388	A	2504	331	411	PFLKTKNGKAPFPPTKIFFLFKKGG/W PGVAHAHCNPSFLGGRGRITRSGDRER
2488	16389	A	2505	407	195	GGRCSELRSCPTPAWVT/GEVLSQKK RKSSNKKSRCLDEQAEVGERQLVQVSV PSTCQRRVGAWFYL
2489	16390	A	2506	1	468	RQGSNMKLETERQIKKAPARNPERERER ERESKKGEDRHTDRCR/RETERQNYRD RQ
2490	16391	A	2507	27	380	FVCLCPAPRGGAYRGRQASLSCGGLHPV RASWLLCLPNQAWAMAGAPPASLLPCS LISDCASNQDSDVGVGPSEPGVGYNLM VRRFLSRSEKRNIRVGVTRFSRCVCHFP L* LGKG
2491	16392	A	2508	396	234	RQENCLNPGGGASSEPRSLCTPAWATE RDSISN/QNKQTNKSHLRAAFSPKSCY
2492	16393	A	2509	1	421	AKKIKPPFPLKKKKKPGRGPPPPPPF/ AKFGRETPLNPGGKGSIKPLGPPPPPP GGPMLPKKKKKKAPX/PLVPSHVKS TGPFPSCS/RSALLRAFTQ
2493	16394	A	2510	197	3	TGPFDFNFFFLMKSHSVAQAGVQWRD LGSLOPPSPQFKQFYWGLQGA/LPCL NKICIFSRGGV
2494	16395	A	2511	114	454	QGFLEKKGAPFNKFFKTVLPFGSGNI PPWWFKGFSRTPEFIKKKNPPGILGGS PKKFFFFFFFEMVLLHHHPGALAAQSLL TTASDF/LRLKQSSHLSLS
2495	16396	A	2512	3	495	FFLSRGLFHLESAPAFCLLLFVVFVLV FVATGSHYVQAGIKLLASNEPPASNSP KCWVYRHEYDALKCLCFGLCLF/AFPL
2496	16397	A	2513	25	437	PLLFSYPAGHAMEEDILPPAPSLFYVFF FYVLVWVKIILYVLAQAATTNTHRLSG LNNKHLFLTILEPRMP/SIKVPA
2497	16398	A	2514	2	256	QAPSAEGEMTSVLLAYLTAQAPTSDE LTSATNIAKWIHKIS/NAQGGFYYNQDN LPYSLCSGRNESTAFGTNGQDIHPVHS S
2498	16399	A	2515	2	284	KCCQDELCSYYSQCTDYTAECKPQVTR GDVFTMPEDEYTDYDGEENNAIRHEQ A/GFTSVISDLQAQIWIWSEQHAMS FV EEMTVLEVL
2499	16400	A	2516	2	432	RDCERESRAAEYATSLKASCWGDLAE SPSLDPQVAMGTPPAGPCGWSVGTGRSP FPRGPRSGPCCVSPSPSWTPEPTGQ/CG EGGGWSPQVFP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,511,26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
2500	16401	A	2517	401	2	GGGAATRGQTKEFQLEKRAPECSECEKRI VRS/PRLIIRRRORTPTGKPYECECGKS FSRRLAQRH/TRAQKTYECNECGR GFERSDLINHYRVHTGERPYKCDCEGK NFSQNSDLVRHHRHTGKPK
2501	16402	A	2518	398	1	ETFGK/SGGRSIVPGQFLAVGPKGRVAM ISAIEKQKLVYILNRDAAARLTSSPVE AHKASALVYHVVDVGFENPMFACLEM DYEEADNGSTGEAAGNTQOTLTLYELDL GLNHVVRYKKEPLEHGNCI
2502	16403	A	2519	384	3	GGGID/SDASLVIAGVRLDEGRYRCCL INGIEDESVALTSLLEGALPLPPHSCV AAGPFRGLGLPGLPSISSAALPTGTPAPSP RPRRPPSPSAPIRWPSPGSPPPPRCGVS VPTQGPVPVQLLRGVY
2503	16404	A	2520	1	426	GDRQMITALLRKLKQSRSESVENRPLR LKALKELGDFYLELHWDQSWVPLLSRI LPSDACTIKQGINRLDTLIDFTDMK CQRDLSFTPNGDAESSEVVLDNEPK VYQRLRHEES/QEINRTQVDCCLTP
2504	16405	A	2521	2	425	ALFIGRMFIMVRSR/CVLTKGTAEFA KLNCEPLDPGGYFIVKGVKRVILTOEL SKNRIIVEADRKGAAGVASVISTHEKKS RTNMAVQKGRFYLRHNTLSEDPITVIIS KPMGVESAQEKIQTVSPQPEWR
2505	16406	A	2522	2	376	IOSFSVVYGYHLCSQGISLSESVASGKFP LLFFFFFKGGPPMP/QGKTKGPKLP GDQPSGPIKGFPLAPPNKKGKGGPPPP RGNFLGFKKKKRFPPQVGGGSKFPREGK PPPLAPQGGGNGRG
2506	16407	A	2523	403	3	GAPRSLSEKEROLMGMINQLSSSFREQLL HAHYEQKLAASQIEKQRQHMKGKQ/Q QEQIARQQORLIQQHKINLQQQIQVQ GHLPPLMIPVFPDRQQLDALAQGQFLL PPGFSYKAGCSDFYPVQVILY
2507	16408	A	2524	2	369	NARCLILRAAEVMAACVYVCTSVFACMC FCVRVCVPCVSGCLCVCVSMNVHLSLC /VEQCACLWMCVSLHVCLYICACLCVSV CEAVCLHLESHCRGSRFPFPVVGPAFSL SSCLILAPPSVT
2508	16409	A	2525	59	380	RNRNFKNNSFFFFFKGPGWGGPGGK GKQKRGGE/NIHQKNGFPQTKRPRKP TPGPPPKPIFFKPLEKSPGQPGQG QKPGGQKPPGGAPQKCKTGET
2509	16410	A	2526	1	371	VNPLSRKHFHGGFSSNHTLVILVARSMD KERVFCATRKSSP/CFVPLLPWPT
2510	16411	A	2527	445	3	RWLGLALTKRELKKGDTAEMRWNSD STIPNG/FDLTEETPKREDYFGIANLVE HPAQLNPVDNDTPVTGLGVLTKEKQK LRRQTRREAQKELQKVRGLGLMPPPEK VRISNLMRVLGTAEVQDPTKVEAHVRAQ MAKROKAHV
2511	16412	A	2528	1	478	RPTPRKRLKSHRLSROESKRVVL/T NAEDNEMEEETDDGGLLPRVKVAEDGS IILDEESLTVEVLRTKGPCVVEENDPIF ERGSTTTYSFRKNYSKPSWNETDMF FLAISMVGTDFSMIGQLFPHRAIETKN KFKREYVASAIEDQATSVHT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2512	16413	A	2529	385	1	QRKCEDLK\QGDNP\VRPFPTPGSCGSGGVNISKPYVUVQWNRGFFYLQAWGRNDYSQPHNKGLYWVAPLNTDGRLLLEYRLCNTLDDPLLYINAREIRITITYVQSGGIADVNNXKYVSMYNTVNV
2513	16414	A	2530	1	1228	FRATLEPFTMEGQTCNCRVFDPMKYIGFETVNGDIFCTQKAARNMSYQGFTKDNQGVVPVVKELMGEEILGASLAPLTSYKVIYVLPMLTIKEDKGTGVVTSVPSDSDDDIAALRDLKKQALRAKYGIRDDMLPFPEFVPVIEIPGFGNLSAVTICDELKIQSONDERKLAEEAKEIYLGKGYEIGMLVDGFKGQKVQDVKKTIOKKMIDAGDALIYM\EPKQVMSRSSDECVVVALCDQWYLDYGEENWKQTSQCLQNLETFCEETRNFEATLGWLQEHACSRITYGLGTHLPWDEQWLIIESLSDSTIYMAFYTVAHLLQGGNHLGQAESPLGIRPQMQTKFVWG\YVFFKEAPFPKQTQIAKEKLDQLKQEFEFVYFPVDRVSGKDLVPNHLSYLLYNHVMWPEQR
2514	16415	A	2531	335	2	KKKALFFFIHPPFVNGRPHKNPKIKSLGSPTPFSLIIFLKKKFCFVQDQWRVLYFGSLQSLPSRFPFFFCNLNLLSSWYRGLPFRPGKYFFFPFFIFYFLVEM\GFTVLARMY
2515	16416	A	2532	3	380	AINSYIRGDDPSSTYFVQVQSAKSSK\WSP\PRALLLTDKAK
2516	16417	A	2533	3	2083	SSSEYLRGNWSENEEETISQQEGSGDYVEELIPGLEPQSPGFEPQSPFEPQSPRFEPEPSPGFESRSPGLVPPSPFEAPRSPESDSQSPFEFESQSPRYEPQSPGVYPRSPGYEPRSPGVYESRSESSRYESQNTLKTQSPFEAQSSKFQEGAEMLLNPEKSPINISVGVHPLDSFTQGFQEQPTGDLPIGPFFEMFTGALLSTPQFEMLQNPLGLTGALRGPGRRGGRARGGQGPFRPNICGICGKSGFRGSSLIQHQRIHTGEKPYKCEVCKAFSPQSSDLIKHQRTHTGERPYKPCPCGKAFADSSYLLRHQRTHSQKPYKPCPCGKAFADSSYLLRHQRTHSHERPYSCTECGKCYSQNSLRSHQRVHTGQRPFFSCGICGKSFQSRSLIPHARSHAREKPFKPCPCGKFRGQSSVLAIHARTHLPGRTYSCPCGKTFNRSSTLIQHQRSHTGERPYRCAVCGKGFCSRSSLTQHHRVH\SGERPYKCDPCGKAFS\RASDLIRHQRTH
2517	16418	A	2534	434	3	APLHSGKRSPTKCN\ECG\GAWNRSLLDRHKIIHSEENPKKCECGKAFQKASRLTHIKIIHAGEKPYKYECGKVFQSSHLTTQKILHSGENLYKCECGKACNLFSNLTHKKIIHAGEKPYKCECGKAFNISNLNKOECI
2518	16419	A	2535	46	454	PETFSSKVMKGTLCSSQATSNTRSYAAALYRQSGIYFKEMKTCVHTKKYTVHSSIFMIAKKWKQPRCPSPASDSWRNRMSIHAMGCYLTMEKNEAVMLPRR\WSLENIVLSESSH
2519	16420	A	2536	13	476	ALKTYKYSHKKAFFNPKKVVYKCSQKDFFPINHLCTPEKHLCDKIGGVFGKVFQT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in US 9,515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						IADHTPVAIKTIAIEGFDLVNGSHQKTF EELPEIIISKELSLSGVCNRTGFI GLNSVHCQGSYPPLLLKAWDHYNSTKG SANDRP/DFPKDDQLY
2520	16421	A	2537	162	296	YVCQRYKL\NPF\PSYTKINCKNVTDIN VKPTS VKLLQEKRRKSL
2521	16422	A	2538	495	348	FGW\HAFIVKEPRVEKCKCASARAKPQ PATIAKTFKAGITGQYQAAL
2522	16423	A	2539	480	63	ARSEAWISADAYMASFGDRITAOQLLLP YIKVGNSEIKRTGGFGSDTPTGKAAYWA SRVSEWRPACAKITQGRQFESLVDGTG VSLIALNQW/PKWPKLKAATGVSIGT ASEVYQSTVILHCLGPNDRDSTSHYSKT R
2523	16424	A	2540	2	509	NVDADDVRLAIOCRADQSTSPPPRDFL LDIARQXNQTPPLIKPYAGPRLEPDRY CLTAPNYRLKSLIKGPNQGRVLRPSV GAVSSKPTTPTIATPCTVSVPNKVATPM SVTSQRFTVQIPPSQSTPVKVPATTAV QNVLINP SMIGHKNILI/TTNMVSSONT A
2524	16425	A	2541	501	1	QWQVVEDPGGPRPREBASSYKCELEQ \LPQYVRDFRKAKE\SGMDSRNLEKL AERFLAKTCTSDKQDFKDNVLSFVNC CHLLLTQVKRESRAHTTSLDIYLNIIIP RFVQVSEDSGSLFKKQVRYFFTEVRGWS NDTIFKILLDINMLITVWTQLSVHQTFV
2525	16426	A	2542	473	287	EKDFNLFPKDLRL/KTSDV/TSTKRENEF EDYCLKRELLMGICEMGWKPSIQVC
2526	16427	A	2543	268	482	KKKKAWLQRRGKNFPKAKELPTHGIQI NSCSYRL/VDIKKEKPFSLIKVGGQAQ RTHLNRAFDIIVLTGCG
2527	16428	A	2544	407	1	CKKICYLHYHWEYKMIQPLNKTVQWFL \KGLNIIYDPVAVILYDIPEELY
2528	16429	A	2545	28	399	FRHSSPQSRGSGQLMVHFLSL/SVMPK IGSVAGINYLVPAPPTATTGETLDVOM/K GEADENH
2529	16430	A	2546	2	365	FVVNDEVGGEALGRLLVYVFWTQRFYE SFCDLSTPDVANGNHVKAKGKVLQAF SDGLALLDNLKGSPATLSLHLCCKLHVD PENFRLGNVLVCLVAH/FDKEFAPP
2530	16431	A	2547	375	1	GFACERMOKRVREVSIAERESAASKVR ANGSGKQNEGMNVTWATATLALQSAVSS ATYTOMOPHSLIQOQQHILQOQVVIQ QQIAIHQQOQFOHRQSQLHTATHLQGA \OKOKOQOHEWR
2531	16432	A	2548	3	376	ELGSDVA/GAEALVDRRQERKEIDAHE DSFKSADESGQALLAAGQYASDEVREKL AVLSEERAAELLEWELRQQYEQCMDLQ LFFRDTEQVDNWSKQEAFLINEDLGDA VDS/IKELKKEH
2532	16433	A	2549	360	1	RGEMLWTV\NNRFLKNFVPGKIEPFKSH SLYFP CYVHDVSFWIDQKGFDELEFHT VGRVSDTIISIQFLSRFOHPKTOQVS LCYRLTCQCDKALTOQOVASMRSGIRK EIQHQY
2533	16434	A	2550	2	403	VVAEEDTELDRLLVQTLENSGVNLRIKA ELRAGVFALAEQEKVENKPTPLVNESLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						KFINTKD\LOGLEGRENLRDLGIIEAE GTVGGLLLEVIRRCQKEKGPPTTGEA LDLSDVHSPPKSPGKTSAQTT
2534	16435	A	2551	1	409	VPRNPTPLGGPGGPTLRSREGGPPGLPR EPSPVLKREPPTRGGGRPPGFPPLPRRV RPEKWNVPNGQTFPEPKLRPRG/HHPGG QTKNPPFKKK
2535	16436	A	2552	256	1	HEMDGT/LGGFPFPPGSSKGPSTLGPPI LQSGGP/APHTPSSSSPANLKT/CTPVCP SHLPW/CCPLCLPMLPWSVPVPPVSKSS DPLLY
2536	16437	A	2553	398	3	ARQQQLLQOQHKI/NWLOOQLQVGGOL PPLMIPVFPDQRLPLAAAQGGFLPLPG FSYKAGCSDPYVQMIPTTWAGAAAATP GLGLQLQQLYAAQLAAMQVSPGKLP IPQGNLGAASVPTSITHDKRCI
2537	16438	A	2554	20	517	DRPFSPTKRRTDPLRGAPDLSRPGFAPV PECPFH/SPRKKTSACRFPPLRPSHSS PLP/SPQPSHSTPQASCFLPEALSPAP FRSPQSYLRAPSWPVVPEEHSFAPDS SAFPPTPRTEFPEAWGTDTPATHRSS WMPRPSPFD
2538	16439	A	2555	361	3	KSSQEALEALRQRLEELKKLCRREGEL PGKLPVEYRLDPGDDPPIVRRIRGP/AF KLDEQKILPKGEEAELELEREPATIQSQ ITEADRLASDPNVSKKLRQKRTKYIN AVKKLQVY
2539	16440	A	2556	470	2	LKAAVTAGLEVPSVSDRAFE\WLSAFP L\DSFYSIHHPRRIQVSSEKEAAPDAGA ERITADSDLAYSSKVLSSPGLEELYR CCMLFVDDTAEPRETPEHPVKQIKFLLG RKEEPEVLVGGWSPSLDGLGPQADPQV KVSNAIRCACAGTGTV
2540	16441	A	2557	2	315	VVAEDTETRDLLVQTLNLSGVNLRIKA ELRAAVFLAEEQEKVENTPLVNESLK KFLNTKDGKMFSLPLFTYL\EFNLDTI WEKSGISGLFFVFNCRYSF
2541	16442	A	2558	372	3	CNITSSHFANKCQDVIARVNMTSQTH HAV\KIIPGFNINVPGLPPDPDETLEV QKVSNPQYHEVMNILELNTLDQHSYSLP TCRISYVKKLMELAYHSLLEAASSDDQ CADQLFYSVRCI
2542	16443	A	2559	64	435	WGDASCTGRAQLGIANKSVLPTLTOKFN TIPAKTTPMSFFKEDKLTPEFT/WKNRT PRTVK
2543	16444	A	2560	113	375	VPGFARDSTQRRVKNKKELMSIPGIP GPVQVPGGGSLT\GMRGFPSSSLGFLTI PGGALIPFSPAFFSRVGGDLSRNTGPG QKPG
2544	16445	A	2561	431	51	RKIYRVYERENFRVEIMFRFSHTSKKVC KGNV/DVAKFIKLHRDGHVNLNVQACCH OKGGIYVFRSHVLELIGYPPRSSSHIK IGDKVRVKASVTP KYKNGSVTHQSGV VKGNI IWIKFLMLTFH
2545	16446	A	2562	1	455	PEGIALEVTVTESTGKREHTFPQGDNV VCEGELINLQGGKILSDGNKI TIMHKEH DLKMDLEFPAQELRKYFMGDHVKVIAG RFGDGTGLIVRVEENFVLPSGLAHGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2546	16447	A	2563	407	1	KVLFPPLQLCSETAS/SIN/VGGQHEW KWDHPLSKCEVPCGGSTISSNGPVSYPG FFSPY\TSSQDCVMMITVPSGHGVRNLNL SLQTEPSGDFIAWDGPQQTAPRLGVF LRSMVKKSQVSSSIQVLLKFHRDAATGG IFAIALSAYPNTKCPPTIHPCI
2547	16448	A	2564	382	1	TQBEVAVSLDRAPAQSGCQCSSETLSQN SNSNKTWLDHFGSLDSDLDRFSACTV FTPREQVSSHTRMFIAALFTIAKTSWQP /KYPFVIGWIKK\MMHITYMEYYAIAKK DEMSFAGTWKLEAMY
2548	16449	A	2565	429	0	PLQSCOTSCCHQNCRSKRTSLHFPDGLA TFEQVGGSPAOVPYPIPLDDIPLLEVEQ EPVSLQLQDVSLVSVSREGLOPASITGS RGHLIVQLQELLHWHVLRSAVKSRWVTV GLEVSLTILSLVFAIRLR\SASRAPVLL RP
2549	16450	A	2566	464	1	VIHGVI\NPFVHQDQYKKKFLK\FYQE IYESPFVTETGTYKKQASNLQESNCS QYMEKVLGRKDEIRQCKYLHPSSYTK VIHECHORMVADHLQFLHAECHNI IQRE KKNDMANMPVLLRAVSKGLLHMIOEHVL RALGRIPTSYVVMQS
2550	16451	A	2567	3	178	YNPGGGVCSDLISSHCTPWWVT\SETLS QKKKKKKKKKNFLPETRERALPGKKKG GGG
2551	16452	A	2568	215	411	IHLIFIHLVFDIYLSVRHSSKILGYISE QIRKRN/SWLYVVAHTCNPSTLGGGGQ ITRSGVDQPG
2552	16453	A	2569	170	430	TSSQLAPQCLAV/VSGFLAACPELTSA SPWLQVRTNAMASPLLKFAEDLLFKAA LSQFCVIMNAKLSVQKYEK\LI SAFSD SR
2553	16454	A	2570	3	463	CRFFGYSTAAAFMPTSSGGSTLSGITAP AVPNI PSPIGVNGFTGLFPQANGQPAAE AVFANGMHYPYPAQSPITVADPLQQAAGV QYAGGPAAYPAAYGQISQAFFQPFAMIP QQQREWEQGNLSIYHLQEFQFDS\ELM QWVLPFGNVISVK
2554	16455	A	2571	3	424	LKTMKGGTNGLEIMLDIQODEYLPVMG ETGTSPTSGAPLHGRSPQP/PARGFLGF TVRPG
2555	16456	A	2572	1667	2046	YIFFFTAFPLAALTFQVTTIAPLALLV RSAKMNRASHDKPTANIITLN\GKTRAS KQRREERNRQEVKLSLFTDDMFLYLES P IVLAPKLLLLINFSKVLAYKINVOXLLA VLYIKSSRESNEHN
2556	16457	A	2573	1	399	FATSQDHPALPSRPPSLHHPKPGTITPH PDLPHQATCSRPIRHQRTWPEDAPLAKA DTVSPAHEHPAAATKAP/TR/PAPDKFG GTSDPQTGPAP/PASPPCSGP/APQVPF RKPSRAAPS KSVSTVVRVRVPTFP
2557	16458	A	2574	2	452	AKVNMKSPMRKGTLLNKEERLNQLE SSLWEASDEGSLGSSPTKCAVTFDLSD MDLSLSESSSEFSPPHLDSTPSLTSRKI HGLSHSLRQISSQMSVLSILDSLNPQS PTFLASMPAQLPP/RDPKSTPTP/SYC GRCRGFSLTS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
2558	16459	A	2575	2	369	TLVYFATTFILLSICICYNIVTAVFLTT SGVPYKVIAPGGHCHENQTCOPEYI TPEIAKACPGALCNFAFYGEKSLYHGYI PTTHVYNLFFVFLWLNINFLVIALGQCCLA\ GAFATYYWA
2559	16460	A	2576	406	1	RQEGTGPSYLLLVGITFRSPWGFSPPLG PSGKNPIKTFGGPLQCGFFFRVQMGVLLP LPGPSGN/CSIKVALNSSPSPGTVNPG EASLPWF/CFEMESRSVAQAGVQWQPP PPGFKRFSCLGLLGSWGYYRPPLV
2560	16461	A	2577	3	410	YISPFYITHMRAHNLEGGFF/KLNQRAD ALVSAAFADAQTFHSILHLNAGLRKRY GLSWQVKEIVKHFSAQVGLHLPHQAG VNPRLGSPNSIWQMDITHIPTFGKLSFV HVSVDIYSHFIWATYOTGEATAHVK
2561	16462	A	2578	386	1	TERIKRQRYORETEKDKRYTEROKTER IRESDRDRERQNIERDRKAT\ERDRE KQRESRETYRERENQIETERDKRQSD RDRETQRETGRIRYRERERQHOTESDRD RERESDRETQRHRECI
2562	16463	A	2579	2	432	LLYPAKRYGAAPGECQCAADKACCLPK LDELADBGKASSARQRLKASLOKQFER AFKAWAARLSQRFPKA*FAEVSKLVTD LT*VHTECCHGDLELCADDRSDLAMYIC ENQDSNFSKNECCCEKPLEKFHCIAEVC END
2563	16464	A	2580	3	426	NLLNDALAIREKTLGKDXHPAGAATLNNL AVLYQKRGYKEAKPMSKRALEIRKKVL GKDHDPDVKOLANLALLCONQKITEGE YYYPRALHIYHTKLGPDDPHNANTKNDL VACYLKHGTVKQA*SLNKENLTSAHWD V
2564	16465	A	2581	10	389	KLAG*GLWGHFLITNPLTEPLTYFPLGL YL*SIITSSICLLQTDL*ALIAYSII HIALVITAILIQT*SFYGAVALIIAHG LTSSLLFCLTNSNYERTHSRIILFQGL QTLRPLIAL*LLA
2565	16466	A	2582	1	192	LIPTLAIITR*GGQPERLNAGTYFLFVT LVGSLPPLLIALIYTHNTLGLSLNILLTL TAQELSNS*ANNLI*LAYTIAFIVKIP YGLHL*LPKHAHVAIPAGSVLAVALLK LGGYGIIRLTLILNPLTKHIAYPFLGLS L*GGQPERLNAGTYFLFVTLVGSILPLLI ALIYTHNTLGLSLNILLTLTAQELSNS
2566	16467	A	2583	2	438	QAHGFLAGCRLRFRSPSPVLWRRRRRW RQRKWKTKTATAAGMYASWTKACRGL EBELNLTRLNVSYNHIDLSGLILPHGI KHKLRYIDLHSNRIDSIIHLL*CMVGLH FLTNLILEKGGDDNPVCRLEFGYRASI FQ TFAQL
2567	16468	A	2584	3	415	GRAILLLEAIQYLSGIEIDLIDTDRGE WDSLTQARR*KEAGLQMFVQLARFHN VKEAFQTLIAFLSEIKSLGHPFLAER IYSMLNYFLQHLIPKMGAEVNDPSEF DP*POQHVSDSGAIYLDLGDENFC
2568	16469	A	2585	2	453	DAKMYLSGYKATVINRLREGTCPEASD ECKPEKRCALSHHQRKCDWSDISGVK IKCVSAETTEYCIA*IMNG*ADAMSLOG

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						GFVYISGKCGMLPVLAEYNKSNCEBDT PEAGYFAVAVVKKASDLTWDNLKGKKS CHTAVGRNAC
2569	16470	A	2586	3	413	MAVESRVTQETIGKEP*KPIDR*KTCPL MLRVFTTNNGRHHRMDEYSR*NVPSSEL QIYTMDATLKELTSLVREVYP*ARKKG THFNFAIDFTDKRPGYRVKEIGSTMSG RKGTDDSMTLQSQKFQIGDYLDIAI
2570	16471	A	2587	1	798	LEVMLMLVKAGADQRAKNQDGMNHLFA TQSNHVRIVEYLIDHLKDLNQDPEKG RKPFLAAERGHVEMIEKLTPLNLHTSE KDKGGNTALHLAAKHGHSFAVQVLLAQW QDINEMNELNISSLIATRNHGASLVNF LISENVLDHQKAEKESPLHLVDINNHI TVVNSLLSAQHDIDILNQKQTPHLVAA DRGNVELVETLKKAGCDLKAVDKQ*TA LAVASRSMHSLVVDMLIKAERYAWREE HHESIRDPSTGFTT
2571	16472	A	2588	2	285	AWSTAPSHHSKVPFGPRRGKAGRPGA AAQAAEQAEVHPSSGSPPLPARQPPVW QIPPTPSLKTTRRGAQPPQHSRRLA*S RSVSVLFKRM
2572	16473	A	2589	11	438	AYYGLNWHLGATLSQKKKKKKKKKNFP RGGGPPRPHFWIGGRPGTPPRGEKN GLKNQKKEKFLAPR*KKSTGKPLKPPQG KGWGGGPKFPKKRPPRAGGSKLPKPK NREPFALAKSLPGVFLGGFGGNPGMGLK NQ
2573	16474	A	2590	313	391	VHLVRVKLGL*SRIVKELLQNLNTT*DN PI*KWATDLDRHFTKYTMVDRLMKCK STS
2574	16475	A	2591	62	616	EVHQGTQEVDRSEVRRRPPQARGPLMFAER AGRQRNLVPALQPPRRGGLR*RGAVRQH GAHPHGLLLQDQKIPALPGRKQAGSLHA PGTEGEPDHGGDPVLDAQIQHRRQQRHP TADHLNPGEHRRGEAHVRAAV*PARGAE GAACKERRAHQANTALQVHRR*LSSFAEL RLLRKRGORTSVWPSPM
2575	16476	A	2592	345	438	HKRNLVLPVILYQHLF*VFGRPEVYILIL PGF
2576	16477	A	2593	479	313	QOGLDLLTS*STRESLPKCDWYRRPEPL KLINLQSSGVGLHVLFPSPPCDQLL LTLHSLNLPPEENSGLT*PEATNAYWTF LPSAIRLFPPELFFIAVLVLSVLPDETET LSDAHSWRLTFKYERDANYHLMASQER LERLFG LHGGTIPIVPTADFHDSISGAS DTDIAHSGLAYTMERSARQIMRTAMKY
2578	16479	A	2595	1	419	HKCEGRYRGKTYGGYVSLCATVNKALDE RTPTTSASYATVTLVDHVRNILGSDTDV SMPLL*ERHRILNETGKFLVDKFGGSP NCVR*RDNIAMHMLHVLVESFYSYRDT LFEGN*VAFYTRAQILVTDGTGVLEKG
2579	16480	A	2596	199	397	SPTALNTDDVNPFGSSSRGHRHQFTG IVSDHPAEAGPIS*DEQELPYAVLHPHK VQPLEPKVTD
2580	16481	A	2597	154	3	MLSRLRGFFCLFVCFETGS*YAAQAGLKL LGSGSPPISSFQSARITGVSHL
2581	16482	A	2598	425	223	QITGHGGKCL*SQLLKGFGGQENFLNLGS

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						RSFN*FKLLPGTSGWVTMLNSLGKKKKV TAYLNKWMPTP
2582	16483	A	2599	3	441	QGPSRDVSELYQINAFDTPESLLMIGK DHSDDPIHHTFDHMMWRTKEHNEAGWLLR SVDKVMKENDELGDSISQLQKQILSLKY AKIALTERLISCPV*TEIVLNYT*SLIM LLTDLL*KVHAQSHHAHQASNCNVMT LIGLOH
2583	16484	A	2600	131	423	GPAPHVILFHLTGFLLAFLPLSHLLTSY LVPMILSGTDGHTFRSACLPRNLEAEWI FGGVKYQYQGNQESK*CFETG*SYVYNG SSGKVPWETFSRT
2584	16485	A	2601	222	447	SGTIFSGFL*VVEGNKPRGLNAQILKDLG VSPGSDYGLKNGISSGLDNGVTTSDHD VLKMAIVGRKIWILGDSG
2585	16486	A	2602	2	457	FICDPLIKAIKTEGTDIVLSEPMNSFAK STEVMGDGLNDEHLBELGGLKAKLEG HFKNQELRQVKRQEDNVDQVEMSLQDE DECDVYILTKVSDILHSLFSTYKEQILP WFEQLLPLIVNLICSSRPWPY*QWGLCI FDDIVKHCSFSL
2586	16487	A	2603	1	297	DHKQKLYAHTCEGKALKWSSVICVHOKI LEEKPCBGTKYDNI*PSNRGCPVPVPRM HAVEIPCK*TECEKATGVHGRGASEFL PERPTGMNMAKCESR
2587	16488	A	2604	1	405	RFDVSDGLELRPKYNGIAHRLTTIWIYLD GLRGLYKGVTP*IIYSAGLSWGLYFVFYN AIKSYITEGSSERLKASEYLASTAEFGP MTLCITNPLWVTKTGLMLQYDAVNSPH *QYKGMSDITLVKIIYKHGGVQGLY
2588	16489	A	2605	165	3	PEELLVFFPFVLKNTGIRPGAVAHTCNP STLGGIRITRGD*DHPGQHGETLSL
2589	16490	A	2606	3	455	KRYGCFSKRMNKRSA*NVFFCARKEVL GLLGHNGAGKSSSKVITGDT*PTAGQV LLKGGSGWDALEFLGYCPHENALWPNLT VRQHL*VYAAVKGRLKGDABVAITRLVD ALKHDLQMSPVKTLSQLKIKLGLFCL ILGKPSGGLA
2590	16491	A	2607	1	429	VDYTVRKFCIQQEGDMTNKRPQRLITQF HFTSWPDLGVPTTPIGMLKILOKKACN PQYAGAVDHCCKA*VGTGTGPDIEAML DMMHT*RKVDVNGFESRNRAQSCQKVQT DMQVYFIIQALLEHYLYGDTLEVTCTLE TPW
2591	16492	A	2608	166	435	KFLSNVYVHFQNFKKVLKFLKHLVLNY FKNIVLGVQ*RATEGIPALWEAETGESL EPRSSRPTWAMWRNSISTKNAQKNIVL RILDPG
2592	16493	A	2609	228	431	IFSICIFNGFNYPFIVGHIGRIYLFIE TGSCHVCTAGVQWCDVGLQP*TPGLK* SSHLRLPSSWDH
2593	16494	A	2610	439	175	RNGGLHLWSQLLRRLRWDFHFSFGSGGC SKS*SYHCTPAWVTQDSSLSKQKKRIS TYTSLSVLNETVYIIVVYTKLDTSPK RKKL
2594	16495	A	2611	1	439	LLGSILSSMQPRGLVDQETLRKAR*QA ARLNKLQEHKQKQVFRIRMEKESHV V*DSGHITT*VQSMNSIERSILHEVVEV

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						DGLTSYFYGGEDDCRYGMIFTKDAAPSD EELDSYRRAEWDHPMADDKRKLTELAR RPDDDA
2595	16496	A	2612	1	439	VIRKVTGTEGSSSTVLDYITIPSSGGM VRKSEDQTDTRKTVIKTMEDYNNNTAP AEDVIMIQVPQSIWDQDDFESEDQDDK STQPISSVGKPKATVIKNVTKPSAIVKY PEKESEPFKILKFTMDVSHVIPHEVK SS*YSA
2596	16497	A	2613	2	453	EKPEKEECNLWTEMWQENVPSSGGGIRL YLQELMTITQKALHSPQWKKMKAQGAIA ASMAQTNSLVPYLGMLTALVEGLAG RTWALKEELLKAIACVETARSAL* KSV PNQPSSTHEI IQADLKCKSKENGYPKI * P VICAADILHA
2597	16498	A	2614	2	441	LEPALPGRWGGGSAESPSSGGSVRKTRQN KQRTPGNGGGST*APQPPRRKRRARAD PTVESEAFKNINVKVIRPEELKPWLD EDWDLVTRQKQLPQPAKKVDAIL* EY ANCKKSHGNVNTTEYAVNEDVAGIKEYF NEMLGT
2598	16499	A	2615	1	430	RGRDRDLCHTESQSSASTEEGHDSLVGVI FEEDSQLEFILDPPKSKPPAWLIMGIMTC *DFELLNPRVRVFLLEVDKDALTRQIIL LHKGLSDYEKSTTLQBLVLKSSRSRSGPP LSIEDLGLNFQL* PSSRVYGFTEELKP SGE
2599	16500	A	2616	373	552	ICKIKYKLFNSALLFRQGLALLPRMEC SGAIKVHCSLDPLGSSNPL* RKIKESTL NLEKSLCTRIGIFLCKYEEVPPQFLKICF QIFLETGSRVSQAQVQWHDQNSLQPR PGLKSFSCNLNPKCWDYRCEPPRRALCS
2600	16501	A	2617	498	157	QLIGSSTHQAALRSRLFPFAGPGTFHFF HYQGAWVVKGGTSPDPSLLGRGVSV QLHPRGKEQSGASDT*HKCPVKLTIIGG KYRVSETSRIFSLPPTTLQAGLDGSGS SL
2601	16502	A	2618	255	389	LSEFYTTYEGSIRPPIGS*GTNLPLPLS YIPRSPSAVDENLDE
2602	16503	A	2619	3	207	QHSSLIITIRATAIKLGIAPFHF*VP*VA QGTFLTSGLLLLT*HKLAPISITTYQISP SLNWSLLSGT
2603	16504	A	2620	3	207	QYSSLIITMGVGIKLGIAFHF*VPEVA QGTFLTSGLLLYT*QLTLPSIMYQISA SLNWSLLSGT
2604	16505	A	2621	45	447	WRRIDCRILNLCVTTASLKHFFSIHKKFH LHNGSHLQSQHSCBAQLRTARTFICCL PYGSGSQWPTLTLEKANLWLTIVFNN WKDWEYDSQVMSNFRSSESMNIIW* RSIDNLPHIICTSLINTNSFL
2605	16506	A	2622	3	142	GNOATPKTAPATMSTPTILVATVAHAYR **VAEKEHPLKFGGRACS
2606	16507	A	2623	2	453	HGPGGLLDYIDKERTDRFLNGECMCVEP DGGLVPKSLYRTA*DIENEDLKLWTDIT YQASVFKGAPHEILILQIVASTVITWD YHVCKGDIVFNIYHSKRSPLPNKDYL AHSITFPDGNVHLNKNVWMLGPDYIMW ITTLITNNEN

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2607	16508	A	2624	1	315	EEKQAPGFTTIGRKLTLPLCAHAVRFII STSLTYKGAYP*ALKGKEKY*LAWEVWY NKKGLWNNNLFDDGVHLCPVEVRKYLA GKGLDPSIGLYHLLILLFFFF
2608	16509	A	2625	232	478	LOGGNYFTV*WTKTSHCTFP*LYILLNF HLNFRYVLCDPYGEIIVSEVMAQRCPMK PTYAIPITITSSQFGHQEADWKE
2609	16510	A	2626	3	430	TSTPHVHMGSTSLPGDSTTIEDATQSHS ESASPALSHPNLSPTGWSQPKTPVP AQRERAPVSGTPDRDKLRCGQRD*GY WEIEASEVMLTRIVSGSGTGYQGWKH GDVALAILQVVDSTPEQFGGRNDVAGL RI
2610	16511	A	2627	2	341	ALCKHEDTDCFCVVVSCPHKCSVOTLLR SE*SAHLSERVIASTCSFKRYGCVFKG TYQQIKAHEASFVQHVNLKKEWSNLK KKGSSFDKECDVKKNSIHCWHIQCSSV I
2611	16512	A	2628	2	179	RHTGLWVTSPLPAVFFGQVRRTLFITGLP RDARKETVESHFRAHWLVGDFSPCCIS RTGEADPVHHRTPQRQEGDCGEPLVVS RWVGSFLIHYIQEHCL
2612	16513	A	2629	1	418	GFSPCHFPVVKRRHRDSDPQ*TPGLK*S CLGLPKCWDRYHEPLRPANISY
2613	16514	A	2630	3	442	FTCGTIIAIPNGVKFT*LATLHGSNM K*SAAVL*ALGYIFLFTVGLGTIVLSN SSLDIVLHDTYVNAHFYALSIKAVFA IIIEGPIH*FPLFSGYTLQOAYA*IHFTI IFIGVNLTLFFQHFVGLFGMPRQYSDYP DAYTTR
2614	16515	A	2631	2	454	AAPMELCWSGGWGLPSVDLDSLAVLTY ARFTGAPLKVHKLINFW*SPSGTLFALR TSHGEIVSYPHKIITHLKEKYNADL SARQCADTLAAMSLEEKLLPLGVHTFW IDTKNYLVEITRWKAEAMPFSLNFFLPG RMQRQYM*RLP
2615	16516	A	2632	131	410	WMMSSKAPHCFLPSIGDADTVHQCKMS FQKCHSALEGLVHLVFKPDLVYQTLQ PPRKCCNLPGAVTHACNSMTLGRSR*F TRSGVQDOP
2616	16517	A	2633	2	230	FFSETSSLLIEQGLARHGGTWRRLRQENN LNPGGGCSSELRS CSCAPAWTVRLDLR KKRRNRF*KILKNYLKIEVI
2617	16518	A	2634	2	370	GTSSSDPAQPGDDKEFIDASRLVYDGIR DIRKAVLMIRTPPEELDDSDFETEDFVR SRTSVQTEDDQLIAGQSARAIMAQLPQE QKAKIAEQVASFOEE*SKLDAEVSKWDD SGNDIIVLAKO
2618	16519	A	2635	2	376	MTDTDALY*RELFDPADKDKMDHSRRGI ALVFNHRRPFWHLSLPERRCTCSDRDNL TRRFSDLGFEKGCFNDLKAEEILLKIHE VSTVIHSDADCFVCVFLSHGERNHIIAY DAKIEIQTLLTALF
2619	16520	A	2636	1	461	DMAFLLTERKILGYGQGRIGPNVACPY GLLOPPGDIAI*LFTKEPLKPVSTTITLY ITAPTALATIALLL*TPLPINPLGNLN LGLLFILATSSLAIVSYL*SR*ASNSNY ALIGALRAVAQTISYEVTLLIILLSTLL

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2620	16521	A	2637	2	384	TKGSFNLRLTIT ENFALAMIAFGQYRQKRFEDHVKLAN D*LNFAKTCVADESAENCDSKSLHTLFGD KLFPATLRETYLELADCCAKQ*PDIE CFGLQKYDNPYLPRLVKPNVDVMCTAFH DTEETFLK*YLVEIA
2621	16522	A	2638	1	373	TFIYLLFLFSSAYSRGVFGDRDAHKSEVA HRFKDLGDENFALVIAFAQYQQCP EDHVKLANEVTEFAKTCVADESPEN*DK SLYTLFGDKLCTVATLRETYGEMADCCA KQEPDRNECFLO
2622	16523	A	2639	2	375	KGFCYRLVSTGTQRRHGAVALNKLHC* CNVGA*GPHCEKCTLPCTFNEEPLKAL TFFREHGP*VSDPEVATAPTEKEIPSLD QETTLEPGQPQLSPGISTIHLPQFPV VIEKTSPPVFVEI
2623	16524	A	2640	215	478	KYPLASHTSLFICTYARLTCTTAEPKQ IESHFGRDLADLVF*KSDDSTVVDVIP SKPV*TSGLFSGKCL*HIVEGIIRAVDP RKLY
2624	16525	A	2641	208	376	ILRNLIKNHFWGVAHACDPNILEAM* GQTRSDWDHPRKRSAPSVLRHIA KGEPLPGLGKWT*GPRAPGAGTPHAG FKTRGCPFLPQGRNKAQVNPDCPRER FLPGKSGSRVAPLKNAGLGGPPYPHP FGGSPRVPPLGFGVQTHLGNKPKPPFP KKKKGGTGCVSNGNPKSSQTLSPQAS
2626	16527	A	2643	190	3	ELSTRGFOGPHRRIRAGLKQCLVMPFELE RSGGLSEH*HLHLPGSSDSRAS* IAG ITSVCH
2627	16528	A	2644	2	339	CCEKFLLEKSHCTAEVENDEMPADLPSL AADFVESKDVRRNVAEAKDVFLGMFLYE YARRHPDYSVLLRLAKTY*TTLEKCC AAADPHECYAKEFHEFKPLVEEPQNLIK
2628	16529	A	2645	81	369	VEVTGQPNASFVKRNRRWLLPLIAALA SGSFWFVFTPDG*TSVVR*IHNNMTQLI NNHLRA*YSVYRDIYFLINIAI**SS*PA SVLLFTADYCEP
2629	16530	A	2646	1	348	DMDMNLPRQNYRFG*ELKADIDYHFKE DNDEDDHQLSLRTVSLWAGAKDD*HIVE SEAMNYEGCPIKVTLATLKMSVQATVTL GGFEITPPGDLRNKCGSGPVHIMGLHLV AGEE
2630	16531	A	2647	1	178	GYTDTLIDVRSQRVSLGLGNSNPFNGS VETKNL*QILNGGESPKQKGQIKRYDL YLT
2631	16532	A	2648	181	244	TKIRYKNVNIFFYFNFF*GLNSLAQA AAQWNGSLQWQPPGLKSGSSCLSPCS *GYTIFYLSIHQLIDITWVSTFSLFLH VSAYSSIKMS
2632	16533	A	2649	2	369	KWITFISLLFLFRSVYGVKFEFLLDAPKN DVARRPIDFGEQHFALAEIAFDHYFLH CPFEDLVTLVNE*TEFA*TCCLADESA*N CDKSLHTLFGDKLCTVATLR*TYGEMAD CCAKLEPERI
2633	16534	A	2650	1	349	VTFISLLFLFSSGYSRGVFFRLDAHKSEV AHRFKDLGDENFALVIAFAHYLQQCP FEDHVKLVNEVTEFA*TCVADESAENC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RSLSLTLFGETLCTVATLRETYGETADCC AKQD
2634	16535	A	2651	21	403	CVCCVCVRESRSTESLPGDNEDFNKNAS VKDVRVCFHDCDSQNDPPMEATGFTAQV TIYSLINLHRLKRYFETLDLH*IAIFFS KVSILNHPGQIIADYAPALDCHCTCIAC KYAELKEMIDRRSVK
2635	16536	A	2652	1	355	ARMSITDITYGQHLIAGGLMTQEDVSEIK SSIYAKSNDHLNMAHYRPTALNLQAHW HGLAQAEAIITWSSGVFPDILLMVGMM TVGVPA*ELQMHSLLKTHDQSRMMNMMY GIKLDW
2636	16537	A	2653	2	360	LFEBHL*YKFNALLLRYTKVQVQLTP TIVKVSRL*KVGIKCKHPKAKRWPCCA ODYLSVLNQLCVLHEKTPVSDRVAKCC TESLVNRRPCFSALEVDETYVPKEFNAE TFTFHAD
2637	16538	A	2654	360	314	YTCATVPCKLFWNCCRDVSLCCLYWSQ TPELK*SSCLSPFKC*NYGHEHTNPARI IFNLNLYKSG*ATARKCPPTKVTPSSHQ Q*HCTNPFYFYFK
2638	16539	A	2655	1	353	NWTL*TLKKIFSLDKAIKRIKIQSVRWK KIFAKHTSDKGVESKYI*RTLING*ENN SIKNWSKNLNRRTKDIQKANKHLSAT SLVH*ESKLK*Q*YHYTSIRVAKMKKTD YVTSW
2639	16540	A	2656	340	10	GREDEKSEKCYLKPGRSQPDGRGAKSSPG VP*PPAPPALPGGGRSSPFPQGSAGKD LRPRQPSQPGGPGELIFPVTKKKKKIKE RKTLLAWTRSNERPEIAQREGGCLRO
2640	16541	A	2657	509	261	IPYFKIHCLHSALGVAETEKETAHLDL AGASSRPKDSQRNSPFGIIPPPSPDSKKK SRGIMKLFGK*VKQ*TSQMGVPLHVA
2641	16542	A	2658	345	3	SAHLSHPKCDYRREPLHILARISFLFKA SPSLYGRATFYLSPTPLMDGRWVASIFW LL*IVLP*AWVYKYLSETPLSIF*KTGS LSAQAQAVQNHNGSLQPQTPLGRSSH L
2642	16543	A	2659	271	56	VILYIVMPTIPRCFPHPIVHTHTHTHT HTHTHTLGRKF*LYSW*LPGYSTNGN KIPLETYLLPILLKM
2643	16544	A	2660	366	68	PQOQSKIWPGTERKKGRKEEREEREKE EREGKREGKNEGTEVIEGSSKTQEQ TRIKAS*LNLSYTTVPKQRRKKGKHP KDSNFKD*RNISPHR
2644	16545	A	2661	351	199	LLRLRQENLLNPEGRGFSERPSHYSP DWATE*DFWSNKK*QKVQYSKY
2645	16546	A	2662	1	160	ERAWLHLSPGDGVCSSEPSHCHTPTWVT E*DSVANQPGWDRVRLCLKPTWTE
2646	16547	A	2663	233	3	GRDNWLKTVAKPELSGKRGPSLLRKVF NPFVYVILFLPQAPKGMKLSFPFPFFFF FFFLRGLAM*PGCSAVAQS
2647	16548	A	2664	96	349	QMFSSVLTRVANAYYSGFFFWFLKQKFC FVTAQVQGRSIS*PGPLVPGFRFLGL TLSTWNCRRAPGLVIACGFKMSLLTL
2648	16549	A	2665	322	74	DTYTLPRLNQVESLNRPITGSETEAII RPTTKSPGDRFKAKFYQRYKEELVSF LLKLFQ*IEKGIGWARNLMPVIVPL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
2649	16550	A	2666	2	228	NLALSPLRLECKSQGFTMLIRLVSVS*PC DLPASASQSGAGIMGVSHQAQPLHSLYLR PLILIKGDQFKYAPNLFSC
2650	16551	A	2667	129	301	VRPLAGLGSPLIFFFFFEKSLAFVAQAG GQRHNLG*LLPLPGLKGFSCNLNPSTW D
2651	16552	A	2668	318	21	FSLLVKDFQNDLAVNSSSTFPSTFLFLV RS*LDVFNLFNFYFLRDEFSLCCPGW TRIPRLKQSSRLRLSSWGKCVPLHPA INRPL*CDFISISY
2652	16553	A	2669	2	322	QDGLDLTTS*STRGLPKCWDRREFFR PAPINKLLSIYHGGPGSLGTBEGKGQD YIPAEQLTDQWRRLTWTCYCAVAED SMGVVWPLLPGYEAKEAGRPH
2653	16554	A	2670	29	261	EPNTLSKCVWIY*LFSLSLSLSCVVCVC VCVCVCVCLCSVCLFYGSPICLHFMHP DTLSESFHFQLITISKELLKC
2654	16555	A	2671	5	224	GSAWLITPVPALWNECKAGRSPEVGSRL PA*PRDPALASASAGITGVKNLIALEL NEWKSCILLIFSLDKV
2655	16556	A	2672	126	321	WGRGCAARLDSHRLRVSPELALLELR PSTMAHICNPSALGGRGWIT*QDEFET NLNLNLEKPC
2656	16557	A	2673	360	74	SRLLKRLKREVGVLNLGGRCSSGPRLHHC TLAWATERDPSDKNKNQKNQRR**TL PETNSLLAWEPDVCVCKTNKLATRLTMA QKSCSORPOYH
2657	16558	A	2674	192	357	RIRKWLYYYYYLLRNSLALSPLECRG TILAQCNFHL*SSRSPPASAPVAGIT ACNPSTLGGRGWITRSG
2658	16559	A	2675	236	375	EEVLYSRKDRHVASYSRK**RSGAEAH ACNPSTLGGRGWITRSG
2659	16560	A	2676	236	2	ATKVSINSIGTLVKVGVGLLEGRRRLRPL PKQSSCLGLQSSWDHR*VQPHGNFTL FVETRSMLARLVNSNPQAIQ
2660	16561	A	2677	164	389	LTVQHGRLRLRLKLTVMVSEGGQASHLLH KAAGRSECCQGNQMLIKSSYQPCAE HACNPSTVGG*GERITRSG
2661	16562	A	2678	208	1	CSVYEGSCFCILVRVRVCVVCVCVCVC VCARSCILYVRSENH*QLPSSSILT*RF *IQSTFRSNKRLR
2662	16563	A	2679	159	382	RWLKHNHTQARIQVRGLLDRDCQTQW LWESGVQPLATTPRRHSEMGWPGAVAH ACNPSTLGGRG*ITPPRESKLEDCLT GTARHRLGCGSQGCSLWLPPIGGIKNG VGRQWLTPVLPALWVAEAGRSLEVR
2663	16564	A	2680	29	367	DCQSEQLRLRWEHHSQGV*GCSQP* SHHTPAWVTEQDPVQNKOTKNYNTHQRA GEVWRSEINCLSTEQLTELYSEITQILAL SVRN*KL*YVKS SVISAETQISGGKTF
2664	16565	A	2681	256	1	ENIVRVEFLCYHRLFAILIMV*LERKR DHIVHNLTLTEVYLKKWQTRPNVAH ACNPSTLGGQRRITRSRARDYPGGHGE T
2665	16566	A	2682	1	395	LLIEHILIAMALLTERKILGGCTQRRK GNVVVPGYGLRFPDTAKIFAREPLOG VTSITLYMTAPTILATMAVLL*TPLR PNPLVNHDLGLLCILATSSLDY*IL*S R*ASHSNYALIGALRACPH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2666	16567	A	2683	3	349	VRIDNAACVLLY*AWAEFIWALANLIIR PDLDPGNLLGNDHIYNVIVTAHAFVII FFIGITPIIYGGFGN*LVPLIIGAPDMAP ARITNIRF*LLPPSLLLLLASAIVEAGA AGT
2667	16568	A	2684	99	2	LTVAHACNPSTLGGQSG*ITRSVGREQP GQHG
2668	16569	A	2685	325	4	SSFFMSFIINSPIIIFLYTTIFLIFYDV VYSPFEPK*VCFCITECWDYRREPQCSF LPCKRV*VLAPFIKNFFFFFLRKNFI FVAQAGQVQRHLGSLQPPPPNFK
2669	16570	A	2686	382	269	MGFHHVQAQDLLELLGTNDPPALASQSG ITGVSHHAQPKLT*TFSY*ACVQSSP QFILVVOHGLAGNSPCCF
2670	16571	A	2687	3	381	GHLVLTFFNSQICLPRITYKTKCKSF WLPFLNLVSLCAIEGYKTKKVPNSV*KG IFIHHQTFILRMQGWLNIT*TSINGIYH ISRIEDKNHKTMFIDAEKNFHNH*HPFI IENIRPGVVAHICN
2671	16572	A	2688	289	91	IKYKELGVACSKTSRNSVSYCYHHHHH RCHYHHHS*RLAALCEESGWRKALGST SMGRVAFHRH
2672	16573	A	2689	3	211	LHHVQDGLDLLT*SAPLGLPKCWDR TEPPFPAPNEFLLHLSLKHVALGRPH TPERRKKASSILR
2673	16574	A	2690	2	197	DLTTS*SAHFLPECWDRREPPRPASY AFIKYFCPALSCFWCIBTGPYLIFAYLR EESFVRSRT
2674	16575	A	2691	253	356	AVPVKMAIVKKTRNNRCW*GCGEIGTFL HCWEC
2675	16576	A	2692	211	339	PGHPLSIIQLQIWGEDTRRGPMEALH* PCCSELRSCHCTPAWPTEN*SI*KKKK KWLGLKEKQKMACAND*PGHPLSII LQIWGEDTRRGPMEALHGSQGDGVYA VRLITAY
2676	16577	A	2693	1	175	RHEGLNLGGRCGCEPSSCICTPAWPT* DSVSKKKRKGKKKALILFNSGNVLPCH LG
2677	16578	A	2694	234	13	KTSREPFSEFLSIKGEQCCSGLLYVFC FQMESHYAAQAGV*WCNLG*LQPPPTGF KQFSCLSPLSPSSPASAS
2678	16579	A	2695	149	2	SOQEDFTKTRALQWRSRSSVVAHACNPS TLGGRGWIT*GOEFKTSIAN
2679	16580	A	2696	2	194	CIGLGVAGACSSRLRQENDNMLGGGAC SETRSHHCTPAWPT*DSISKKRKRNR WGTRFSN
2680	16581	A	2697	338	357	YLIRKKISINSKS*FSWPGVVAACNFS TLGGRGRRTTSASVRNPGQHGDPKFFL VSS
2681	16582	A	2698	53	293	TISIKSKKWKNGQGEYKWCNENWLAIC RRLLKCPYVLVHSCIAIKNYLRGLNL* RKEV*LAHSSCTCTGNMAEKPHRR
2682	16583	A	2699	2	335	LYAAKVPQLQACIRTSYISFFIFFFFF FFGQSSFGPGLKARGGTPLIGTPPLG VKRNFLLPQFSGKPGITGCPPLPQKFWFP KKRGLIF*PGGVNSDPPKGGPPNP
2683	16584	A	2700	166	3	DYRRVPPRLVKR*GFTVV*AGV*WRNHG SLQTQITGLKQSSHLATCDYRYE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
2684	16585	A	2701	209	340	YRNTVPFARHGSHSTCNPSLTGGRGGMW T*CHEIETTLGNMVKP
2685	16586	A	2702	78	341	EVACNCLLPATGCFASVTVV*SSVLL*F EL*VLNENSS*FNFH*FF*NRVLICCP DWSVMA*S*FTEALTSQTIRSSHVSLS SWDY
2686	16587	A	2703	258	185	TMIAPVHSSSLGDRAPYLFQKQK*GLAL SPLEWTGAIIVHNLEFLCSSNPPTSA SGVTGITMEVERHGWIQETFWK
2687	16588	A	2704	361	41	NFGPVYKTNPGSRPGWGLPKGPPGPK FFPFVGPSPFPFKGSGVSPSPGGQKGP FKGVWGFDP*PRGKKTPTQQGPSPKVP NWDFFKGGFFKKKKKKRKLIN
2688	16589	A	2705	12	329	SCTQLQITPRLK*SSRPSLPNN*DYRHV PPHPASFP*FSEMF*DSQTIFLNSLKFS S*YVLVIFFFKMEPCSIQDGVQWCDLS LSQLP*PRFKRFSCLSLPSTRP
2689	16590	A	2706	232	1	KKRKRSKTYKFFFLNSFKNQCFYAI GHLPFSIIFFFLKQSPQLVA*AGVQWQ DLQSPQPPPPGPKPSHLRLR
2690	16591	A	2707	135	1	CFPLIFFFESSDTCAGV*WQPPGPKRS SQLSPSRSDYRRTISPR
2691	16592	A	2708	1	157	LDLLTS*SARLHHKFCWYRRFPFPAD YKVFLEKVASLVKLVLCCKLNEF
2692	16593	A	2709	88	344	MQEHYYPFKRGKNMIRKYVQLHANKLD SLDKIDKFQVKNHQN*L*KK*KSMPGAV AHACNPSTLGGRGGMWTKS*DRDHPWLT C
2693	16594	A	2710	1	383	LHKVTVLRFLSKPHILVLYFYTYTCVHV SVSDMWCWFLY*IFTDMYNAVQ*LDEF KLSIKFLRCIC*CV*IFIPVIYCFEL YLICLFLSYFLNIYVMLFYILCIYF YVIFSSSSIF
2694	16595	A	2711	227	1	IFFPSNSFLKISLGFNLFAFF*PKKPF PFLSFKINQNFPGFPNFKLIPKFPF NKFFK*IVLTFPKKTKDK
2695	16596	A	2712	1	136	KNTKISQGWPTPVIPATQEPAGSSLE RGRQRLQ*RNLSLQPLPPTFKRSSCLR LLSSWDYRRRPPPLANFCIF
2696	16597	A	2713	3	349	LIPRGQSTVVLPPYNPATISFGNDLNI KMYGHAKTCIWMFMTSSFIIDTRKRQ* CSSVREWINKQ*CIQTMELVGRNFFPF FFFFFFFVFVFPGGPPPKIQIPKEI NFO
2697	16598	A	2714	181	342	TSOLLNLPLPIKA*AIRKEKEIKGIQL GKEVKLFLFAHDTIVYF
2698	16599	A	2715	3	205	FRHVAQGLLELASSSPTLASRSAGIT GVSHQCP*TVSSLRLGFDYTSFKIADI QCSFNVLYCYLQSLNEL
2699	16600	A	2716	388	23	ASNOSKNSFEKGEKQGVSMVKTSQCAL NKRAFFDMIRSVYQKTYK*RNA*EROS PSLKVENKKEVPSLLLENIVLKVLVNT GHKEK*KAHRFDNIIQFANDMIYVEN PKDSTKRLS
2700	16601	A	2717	4	194	FSCLSLSSSSWDYKSMPPHANFLYF** RGPTMLARLVLSNWSHAGITGVSHHAQ PFNYFFI
2701	16602	A	2718	1	212	LCCPGWETARLKRSSRLSLPKCWDRH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ESLHLAFGFFLL*YFGPYLMVYVSPNL YDFSLVLSYLGTSI
2702	16603	A	2719	53	299	KAVRVNIFFTKRVHLMTQIVLSLSLFP FSLFHSLSLSSEL*RDVRLLCYFG*S AVQC*PTWQIPQLR*ASCLSLVGS
2703	16604	A	2720	139	320	QPTWHSFSF*KQETISIFLKVSSSLHMT LRFLFFFFLLDRVSLCHPWSTVALS*L TVAK
2704	16605	A	2721	1	99	ILAYSSITHIG*I IAVLPYNNPITILN LTIYM
2705	16606	A	2722	215	361	LTFFFFFRESNFVTOAEMOGNLUV*L KPRPPGLKHFFYLSLQSTGNY
2706	16607	A	2723	335	24	AIPLRPEF*THPGNGKTRFPLKPNLT GVGNARYSQFPKRLRLKIPLEVEVGS INPNFHPGIPFWACKENFFPKKKKKEI IMLNFSLICYNLFFLYICY
2707	16608	A	2724	27	314	WKQLKYPFSDIEWIKMKWCHAMEYLAIK RNKVLQCVT*RWRLMDTKK
2708	16609	A	2726	1	112	GFHHVSDGLNL*TL*STHLSLPKCDWY RHEPLQCAR
2709	16610	A	2727	271	3	RSPMLKNQAIKSVIMVYIGTIWRSAGPF AIFFLAEYTNII IITLTITFIPTTYD ALSHELTYTFVTKAVLLTSLFL*IRTA YPRFR
2710	16611	A	2728	121	1	ENKRYFGAVAQAYIPNTLGG*GGWIT*G REFETSLTNVEK
2711	16612	A	2729	2	290	NRHFTKENIQMPTRHKKRDPOSSLVIRE MQTKTKRVYFILTIRMAKVKKIDNTTC* *GYEKLNSPKLQTTKCPIFEWVNKLWHS QIVEYFSGIQHA
2712	16613	A	2730	98	264	LVSSE***TYQILFFPFEMECHSVSQVV VRGSNLC*LHPLPPDFKRFSCFSYWEG
2713	16614	A	2731	2	286	PFFKATVIRTVVWY*KN*QIDQWNRKES PEIDLHK*SLLI FAKGAKAIQWRKDSLF NKWC*NRWISTCKNESMLGVVAHTCNPS TSQGGQGR IA
2714	16615	A	2732	323	181	RDVLLVEITMLARLVNS*PCDLPASA AQSGITGVSHRAPFLD
2715	16616	A	2733	272	131	GRVDRLNPGGGGCS*LGSCQCTPAWKE TPSQKKNKILICPYAPFLI
2716	16617	A	2734	227	87	AASITLTLSLIPFLITLTVNPNKMSYP HVKSVIVASTFIISLFPPTIFNCLDQEV IISN*H*ATMDF
2717	16618	A	2736	25	415	FSKYLIDHQLSAGLLVQHGRGLCSLSL LHSDDSLSPAVSGKVS LAASIRNKLLEP ET*RALM*NHGHPLFEGM*PWT*EP GS*RC*ELGQPGQARRLACNPSTLQGRG GWIMRSGVRDQPGQDVET
2718	16619	A	2737	390	1	KGFFLETKRKKFFFTNGFFPLLGKGVF PGKRLGPPILGFYPQORVFFPKPPFP PGPFKRGQKPPGGGKNF*RGPPGPPKKG GAPTGGKKKKEERKEKEKTPRNISKP LSHPPFPNFPFCATVRGFS
2719	16620	A	2738	96	331	QFTYTHGLFPFNPNRLCVFFFS*KLVG V*LCPCGWL*TPGLKQSSCLSLSLSTWY KGVPCLAEHFFFEKKSPLSL
2720	16621	A	2739	379	14	LREVVFFFSPPKIKCFSKNSFKYFPFP VVFKTPPTPPFFFPPLGKNFFPSPLEN

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						FCPPRGFF*RPPLFFFFFFFFFFF FFFFFKVYSLLLYLFLPK*MLTF KTSISTQCY
2721	16622	A	2740	198	38	ANPLFFFFFLRDGLGVLYRPGWSAVVQS *LTADSTPWAQVILQQRNP IEHDF
2722	16623	A	2741	290	39	MSKVGPLGLVLTSTFRVLLKGPEIKGDP LLANPLFLFLFFLDRGVLYRPGWSAVV QS*LTADSTPWAQVILQQRNP IEHDF
2723	16624	A	2742	1	399	ILIRKHSIDIGTLVLLFDA*TGITGTDLS VLNRTELEPDQATLLGNDPVHEVIDTAH ALGIIFIVIP I I I I GFGGN*LVPLIIGA PDMAFARINNISF*LLFTSLLLLLASAI EEAVPGTG*TVYPSLA*NYCR
2724	16625	A	2743	398	2	SPPLIFFLWGFYIFPPPKKFFFLINP PKKSPPPFFFKPPPPPPPPPP*EBKK NFCSPPPPSPPPPFLPPPLFFPPPS LKKKKKKKKKKKKKKKKKKKKKK KKKKKKKRRSRSTSPTRP
2725	16626	A	2744	295	185	FFFFFFFFFFFPPPPPPPPPPFLP FLFLFXPKP
2726	16627	A	2745	374	4	LKKHKSTRVF*NVKSGK*NYSPPFKTRP WAQKRAKKKGAREKKAD*EGKEGKLLK KKSFRDGGK*G*PKGQRNPEKKPVKS QGPNMGMVIPAFKEKKRIPPVAKIPTI*G AQKKGRPLAI
2727	16628	A	2746	2	382	QDATAPIIDELISFHDHALIILICLCPL ILDALFLTLTAKLTNTNISDAQIEITV* TILPAIILDLIALPSRLIYITDEVNDY SLTIKSIHQWY*TYEYTDYGLVFNYSY ILPLFLPRDLGLL
2728	16629	A	2747	2	374	DWPFPTVKRKTNPRAQSTADRIFILLFTV RGLTGIGLANSLLDIVLHDTYVVAHPH YVLSLGAVFAGIGGFIH*FPLFSGYTLD QTYAKIHFTI IFIGVHLTFPQHFGLLS GMPPRYSDYFDA
2729	16630	A	2748	55	230	QTPAK*INKYLQN*KKKKKKKKKKKK KKKGACLPKPGGAKESWGRQLFSPK GG
2730	16631	A	2749	161	3	NGNYTLVKKCFNTKEIKRWKN*IFFFP MRWSFTLVQAQGVONCKGLSLQPL
2731	16632	A	2750	362	1	PEKKSFAIKGVKAGKQCKFCDAAPKGN PCKKANPTQTEKRVLKK*PREKEKNSP QRKKNTAKNKEKEAPQEEI*KGPRYI FFISIFPPPPPPPPPPSIVINLFGT FIATITL EA
2732	16633	A	2751	311	110	ITLPRHGGPHVQSOLFRLRWKDHNSLG DRGCSLSCHCTFVWRQSKTFSKIKYG RNGTDKAATCNPRFSWGRKVA*QES ETSLSNSRTRL*KNKINWKRDRGGYL
2733	16634	A	2752	223	16	KKTPOKKNTEGKGPVKKSFPQKFLKST PP*IFFYVCFPPFFFLYIYLLFRISF FFILEVYVYLFILP
2734	16635	A	2753	367	10	PAPRGGVYGRQASLSCGLHLPLRASNP LCSPTQA*AMAGAPPPASLPDGLISDC CASNERGSGVGLS*SGAGDNLVCRLL SGKCRNHPSSASLTLAANDNSCSYAIL APPLKNS
2735	16636	A	2754	14	341	PGPNF*FGQNSPGKNQLSLPT*KGNG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
						PGNPKNGGGTVPGETPPTRGSLRLTLQG PLRPSGTPPTIRAPGTPVGNPGF*PRDF FAQKGFNVREGLKQGNPKGLNPPP
2736	16637	A	2755	15	172	HSWWECKLVQPL*KTVRRFLKKLKIDPP YYPAIFLLGIYSEERKSVKQSRG
2737	16638	A	2756	263	2	QKPLPFRNDPVFPKGPETPRPTWGFIP GGVPLGKGFITLLVSFFFFFSPSNLFF F*NRVSLCRGWSAVV*SWLTAASTSQA QAI
2738	16639	A	2757	311	106	FVCFRLQRALLPLECSCVILAHNLRLL LCSSDSFG*QSETVSKKKKKKKKEKET GNL*RSLLMKGR
2739	16640	A	2758	23	328	NITYYT*LFVLNFFVDPGHTVVEFFEXF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF
2740	16641	A	2759	1	338	DR*LFSTNHGYIGTLYLLPGA*AGALGT ALSLLMRAELGQPNLLGLDHTYNGIDT AHAFAILFMSLAIIRSFNG*LVTLII GAPVLAAPRITDISW*L*PHSVLLLLA
2741	16642	A	2760	120	2	INKYAWLGTVAHACNPSTLGRGWTA*GQ EFKTSIANMVK
2742	16643	A	2761	251	3	CRGQIGTPTLHYSSSSSSKWKIDLVNRV KTIKLSENTGVNLELELGDCLDDTKS KNSTRKIRK*SLKETFFLLGGTR
2743	16644	A	2762	11	303	ALVLRSSSCLDLLKCDWYRHEPHLALS EILMYRFCL*IFDIFWYSREIDLIFV Y*FFFFFFFFFVFFVFFVFFVFFVFF PGYKSSSCLGLPR
2744	16645	A	2763	236	356	DWLIFVFSVERGFCHVAQGL*LLGSGD PPASASQGAGIT
2745	16646	A	2764	2	332	LTQTGLK*SACCLLPECWNYRCEPHFP AGFLF*RHFDKGVS*LLIYPGTGWS
2746	16647	A	2765	297	19	KKKSWFFFKKKKNGGATKFN*RGFFL KFVYFFFFIG*GVFFFFFLISIIIFPF FFFFFFFFFVFFVFFVFFVFFVFFVFF FAMKINVFY
2747	16648	A	2766	1	147	QILRLRWENCNVLGGGGCSEPLRHHT PAWVTV*NSVSKKKKNPLLF
2748	16649	A	2767	357	183	NWDYRPLSPRFGFLDF*VNRGFPLLTK LVSNF*PCNLFPSTSPKAGISGFNPRAQ P
2749	16650	A	2768	2	193	RWESCLNPGGGYSEPRSCHCTPSNVTE *DSVSTTTTKEKERKQRTWSENSLQK YKDTNH
2750	16651	A	2769	333	173	VSQDGLDLTS*STHLGLPKWNYRREP PRPAQKLMLVIWLGFMSSPKSPLLE
2751	16652	A	2770	3	331	CMENCMVIPFKKVKHGNVHMIIQFYFK AVQQLSTELNIL*FYDPAITLLGIYPKE LKTSFRKTCT*MLTASLFVIAKTWKQP RCPSVGE*LSNL*YVQTMCEYSVLK
2752	16653	A	2771	209	55	RFGRFQVLRVRFPQNRNPGGGGFSEPK *GPCPPANGAQRDFISKKKTTIT
2753	16654	A	2772	213	57	RFGRPQLRLRLQKLNPNPGGGCSEPR *GPCPPAWVTQRDFISKKKTTIT
2754	16655	A	2773	148	1	KATGRKTWVSRCWGVTVAHTCNPTLG GRGR*TARQEFKNSLRTLAK
2755	16656	A	2774	2	364	WSAVRRDWITALQPERQETPSQKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						KKKKKKKKKKGGVRHGVSKRKP*TSGR PGRKNHWQIQGQKTPRERAEALKNRV GLKLLFKTPGHVNGAGNPKFRNGKSGKP PEVHLNGAW
2756	16657	A	2775	121	2	HLRSGVSDQPGRHGKAPSLKIEKLAGE GGTCL*SQLLG
2757	16658	A	2776	195	3	GRVDINTLLALLLIITF*LPOLIGYIE KSTPYECGDFDISPARVPFSKFFLAAI PFLFLDL
2758	16659	A	2777	3	285	FLNTRNKVSLCCPS*A*TPGLKQSCCLG LPKC*DYR
2759	16660	A	2778	135	379	HWSATVKLYAILLGLLKWESGTLKCSKD VLFFL*G*SSAYSIESVIMQKAT*VKG KARVOLGAKKLKAYWORKSPGIPAG
2760	16661	A	2779	364	1	GSPTGAVILLIAHGLTSSLLFLCANSNY ERTHSRIILSQGLPTLLPLIAF*LLA SLANLPLPTINILGLSGLVLTTPS*SN ITLLLTGLNLVLTALYSYLIFTTQWGS LTHHIANIK
2761	16662	A	2780	356	1	CCLRHAHVPOKGNHESGVHLFDKVCRO PTQEDCINEITTVQAQIFLVHFLQSL TLSEKRRKKRKKKKRNRRESPEINTHI YCOLIFNGKAKKIK*G*NSLFNKTYLDP WISTCK
2762	16663	A	2781	1	204	AQVQLQDASSPRIELTTFHDAHLITF LICFLVLVYALFLTLTT*LTNTNISDAQD SETDCYSQSYIL
2763	16664	A	2782	1	522	YKCNCEGKVFNQQAHLAQHQRVHTGEKP YKCNCEGKTFQSQMSNLVYHRLHSGEKP *KCNCEGKTFQSQMSKLVIYHRLHSGEKP *KCNCEGNTFHNSTLVSHKAIHTGEKL YKCNCEGKVFNQKTTLARHRIHTAEKL YK*EECDKVFQCKSNLETHKKMQFSKTD SAFSLQ
2764	16665	A	2783	1	327	ENRLNSGGGCGSEPRSHCTPAWATERD SVSEKEKEQKQNFHLNAQSNQCLKSP* KYLKHPKTDILSKASQYNQLTADQSI LKFKTKTFDQKQKRGKMGWTSYNS
2765	16666	A	2784	335	128	FSLIFCRAGILFCCPCGWS*TPVLKQSSC SSLPKCSDYKQEPYILACATLKCYQIPN FYCWPHIFKRMFY
2766	16667	A	2785	208	3	RFICPLSLNGVSLFFFFFLDRDRVLICH TGSANVAQVCNTHACYSPLK*SSCLSL PSKNNHLLPR
2767	16668	A	2786	49	332	VBMGNSPINKRYVYPKSYNRCLKCNTEE QVLNDLGAENTCSKSLLLIFPKGI LLCCPGWIEVVSQLTASSTLGLK*TFH LSLFGSWDHR
2768	16669	A	2787	331	187	GCSEPRSPPCNAAWATKGDVSKEKKKN KKREEKKH*HNTSGEKNIL
2769	16670	A	2788	325	34	RSQLRGLPSMSIS*TSNRLK*RRRLRP FIFCRDRVSLCCSGWSQTPGFKQTHRS LPKCWDYRREPSPLAQIRYLGFLFSQGL SSAFCYVAMVSGF
2770	16671	A	2789	3	150	AASTRQLIFHTSKHGFGEAAA*YHIF VDVV*LFYVSIYWL
2771	16672	A	2790	86	311	NIHPLNDIFTRLKNGPKKKEISLVKNEP NKGT*SLISIKVLTK*F*PIRPGVAHA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2772	16673	A	2791	2	123	T*NPSTLGGGGGWT*SQE GGGACSEPRSHLCTPAWETE*DSISEKK EEKK*LQIYTI
2773	16674	A	2792	302	162	PLLRLRPENCNLLGGGFN*PRSRNCP PAMATKRDSLKLNKLNKFN
2774	16675	A	2793	1	238	GGCSGLRLCHCTPAWETD*DPVSKKKKK KNFTRAKLILFGTLVLGKVKRGGPFKPR ILKLPWETWQNLVETKKKKIFFLNRRGG GE
2775	16676	A	2794	199	3	VGPTRHDKPPHSLQCLTSPATQLFS SGKILKNTHLWPGTVAHACNPSTLGG*A RNITRSGDR
2776	16677	A	2795	1	302	GGCSEPRSCHICPANATEPDSI*KINK* INK*K*K*KINRNKKGKNHFLSSST*PQ VASSPLTGQHRVTKL*SSQKVLDSATL QSKSNAEVRVNRNTTD
2777	16678	A	2796	228	326	NDNGQSGGVVAHACNPSLGGGGGWT*G REFKT
2778	16679	A	2797	270	1	KFGISAPFAPSPKV*KRGFFNFLNGNP PVKIPPF*TPL*NSKPGKNPPFF*KT RFSKIFPNPGFFFFFVFEGLVCCPGWS ALTRSW
2779	16680	A	2798	307	36	FKNFCCG*EVSLLCCPGWSQAPGVK*PSC LGFPKCDWYRCELCPLASCSL*CDRNQT RISAVLVNIEFHLSPILPVLPLFLKPKQ AGLLCF
2780	16681	A	2799	132	5	IFEVTV*CTK*HKRNMQGVVGHACNPS TLGGGGGWTMRSGV
2781	16682	A	2800	32	314	KQHFNGPNPSGKGPGRASRFLKKNFF F*KTPPKKPHTPCKPSPKGGKPERLFWH FFNQKFGPLPMGPNPDQAGFCLRDP*G GGKNRSPPTL
2782	16683	A	2801	139	3	AASTPYIFPETTLIPTLAIITR*GNQPE RLNAGTYFLFYTLVGGC
2783	16684	A	2802	238	3	AASTSHVYSSMNYIYIIQFKTPFVFFF RDKVSLCHTGWSAVAQS*LTASAALTS CVQGLPTQPEVITRPLRLFL
2784	16685	A	2803	110	291	KKLVSGFGFGFKTSNFIMCAKQGLPN LG*LKLPLRGGFPQSPGSLSLSGTWDYKHT PATR
2785	16686	A	2804	97	2	SYNNODSVVLEKEKTNRSVKQN*APIPE KKKKKNVGGTLDPCKTYYKATI IKTIV WWRKKRQIGQ*NRIESPEIDPHKY
2786	16687	A	2805	268	1	ATFLLFYVYFRPQIPYLL*IFILSLF*Y RHSGGPPYVGGPQQVYPQPGGPGFYVPG GPGDFPCRLPTRKNWLVWLPQNLPTVW PTIT
2787	16688	A	2806	153	3	IFPLKGLLVPLGVFLKVFVFFVFF* RVSPCRPDNSAVASRLTASS
2788	16689	A	2807	3	216	NAARDHIVKPS*PLTGALSALVMSGL AM*CHSHSISLLILSLTSTLTITQ*RR NVTR*TSYQGHHTPTDQGLRYGIIIFI TSEAFPLS*FF*AFYHSSLSPTPQLRGH NPPTGLSPLNPLEVPLNLTSELLAS*VM PLSLHIASNTKPTNQHTNHIPKAQCNT INLIPRPHTN
2789	16690	A	2808	168	354	FLERESGVAQAGGQQQLS*WKPFPPFI LGHFSCSLRLRSWNVYGPSPVPAKVGGF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2790	16691	A	2809	61	360	WRNKTY YVSNKSCSNHRK*SLFFFFFPERESSFV PQVELHGRDLG*LQWLPGFGKFPGLTF LRNGDDGPRPQPPANLGLLVKTGFSPVA HLGVNLGTGDCCPALP
2791	16692	A	2810	236	3	KMFFQMRYTMLKK*QATPGFYLALKNVL KTFLAPIFFFLRRNSALVAQGVQWRDL GLPLPLPSGLKRFCSLSLPS
2792	16693	A	2811	140	210	NAKITKC*KGYGKRGTLMHCCNQFQKMGQ LLWKTGYQFLKKLKELLSNVPVPLY*I WKKGNPYALLAI
2793	16694	A	2812	230	1	VKLCFVSLRTGVRPLTSSSEVIFILNCK FNIGV*LLPGSLLLLASAVIAGAGSG *TVYPLAGNYSHAEPYALV
2794	16695	A	2813	3	345	HEVRIDVHTRCTCFPTGIIIAIPTGVKV FS*LATLHGSNMK*SAVL*ALRFILF TVUGLTGIVLSNSLDTVLHDTYVVAH FHVLSIGTVFAIIGGFH*FPLFSGYT LD
2795	16696	A	2814	2	184	ARVGPHHIDQAGLKLTL*SAYFGFFKC WDYRHEPPRLALKFNKIKKKKKKKT GEKI
2796	16697	A	2815	276	3	ARVHRIDHGLM*HQDPLGLK*SLCLSLPS SWD*SMQPCPDVGYTRSDQKPTFKSP YVSQTGLEHLGSSDLTPASASQRAKITGM SHHALV
2797	16698	A	2816	3	94	HENQYSSLIITIAIAIKGIAPHF*VF EV
2798	16699	A	2817	93	1	GGGCGCEPRLHCTPWWVIE*NPVSRKK TRA
2799	16700	A	2818	1	197	GTRAQSSLLGLRLQKNQLNLGGRGCSEP KSGHLTPAWAT*PDLVSTKSCITLYLV TQALHITLLP
2800	16701	A	2819	109	2	GVF*GVFLAQGLTLVAQAEVQWHDGLSL QPCPPRLKRLV
2801	16702	A	2820	2	347	ARAPGFAENEVVFSSCFVMMVGGKGE NABLMQPPSY*ESQHFFPAPPRSCSV* LCSLGPILLGLTIFCQFTLSELPRFRKG *FSSSLKKVFCGDRVLLCHPGMSAVQ TQL
2802	16703	A	2821	1	353	CTRRDVTRESTYGGHRRFPVQKGLPYGI ILFITSQVFFFT*FF*TFYHSTLTPTPQ L*GHWPTGITPLNPLKVPLLNTSVLP SRVSI*AHHLI*NNRNQIISLLIT LLGLV
2803	16704	A	2822	261	400	VEHSNSNKENFLOGGTGCHACNLNVLGG RGGRTWESGV*DLQDQ
2804	16705	A	2823	273	97	LNTPRMORLTQATVILVLFPHKDGQFAML PROVSNS*AQAICHGLPKC*DYRREPP GOK
2805	16706	A	2824	159	355	KKFFSIFFFFFFF*DRISLCHLGSVA VQSMLTAAST
2806	16707	A	2825	67	338	LSPEL*LV*IF*KPFS*QLSLTSHSPSL FSALLLLSISPTWLHISQSDKNHLHFSF LFRDSVLLCCLGYSAVT*SWFTVASN AQVVL
2807	16708	A	2826	3	359	HEQKYSFLHDSQTLFCF*DSIPTPSNMD ETQQKSRLVLVRLSLLLIEPWLEPERLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RSWANNLVYDTSDDDYHLKKDLQEGITLMGRLEYGSRRTQGMKQTYSKFDINSHHDL
2808	16709	A	2827	3	338	LERNLDTFFLDPAAGGDDPILVQHFL*FFGHPEAYILILPRPGIVSHIVSVYFGRLEPSGYLRMG*PIISUGLLGFIV*SHHIFSVGVDIHARAYSYPGSLVMAIPCTLEVPT
2809	16710	A	2828	1	406	RHEGEKLRKPFFGPHRRGAGTAKMSASLVRATVRVSKRKLQPTRAALTITPSAVNKKIQLLKKDKPEHVGVKGVTRTGCNGLSYTLEYTKTKGSDSEEVQDGVRFIEKKAQTLTLTGTEMDVYED*LSSEFFVF
2810	16711	A	2829	332	3	GITVMQATATATALIGYVPLPGGISL*GATVIAYILAAIPFIFIGDLVQ*I*VGCSDVSPTVTGFLAFFFVLAFLIAAVALLLRFLOGTGSNPLGGASQDKIAFQFSC
2811	16712	A	2830	186	349	YSEREVAFFFFGNGFCF*QAQWNGNGLG*LNLLPPR*KEFSCKIFPRTWNYSP
2812	16713	A	2831	303	590	NILTTLLNKQSKSNGLQNKIIHTTYIKIKIFFFFLRQSLSVTQADVQWHCLSLQPPPGFK*FSCCLLSSWDYKHAPLHPANFCIFSRDGISPS
2813	16714	A	2832	1	370	BELITFRHVAIYSFLICFLVLVYALFLTITTKLTNTNILDADQIGTV*TLPAIILVLIGLPLRLIYITDEVDPSLTIK*NGHQWD*TY*YTDYGLIFNSYILRPLLEPGELRLRDVN
2814	16715	A	2833	207	1	QFFIFLHRSTFLFAQAGMQWRDLGSLQFSPPGFK*FSYLTSLRGLARKITLAQEFQTSLGNMGGPHRA
2815	16716	A	2834	223	1	DLNAHKGKTRVYLKSRNKLGGGGAGNLSLDSIGSRDHRAPFCPANFVFLV*MGFPHVGQDGDELLTSCS
2816	16717	A	2835	1	321	GTRKPS*PUTGALSALLMTSLTW*LHFHSITLLGLLNTNLTITVQ*WRDVARESTYQGHHTPPVQKGLRVGILFITSEGGLFAGFF*AFVHSSLDRTPQLGGO
2817	16718	A	2836	57	370	INWGRVLWKNRLYGVFCRAFRNVAITSRVWAEQDPRVPKTLSDVDPKLPFFS*ISVRGOIYTF*FFFFFETESHTVAQAGVQWNGDLG*LQSPSPGFKRFLCLSLP
2818	16719	A	2837	2	345	ARAHROLED*LRPGERHPSW*SEETVERQRTKT*SESSQTGTSITSSRNARRERESEKSLHLETLNKEEDCHSPFTKPTPDHPLKVPAPSPKENAWKRSSNPPARSQSS
2819	16720	A	2838	15	376	AKIEPLYSSILGNKSETPSGKGGKKKKKKKGKGGGKKKKKKTEGGTRGLTQETQFFGNPKGPKHLGARN*KHRAQAKRGNQPRYRFTTEKKGEKLFNPGGGRSQKPKTGWNSAGGKK
2820	16721	A	2839	3	336	HELLASTILLIY*CRDVTREIRIPLAHHTPPVQKGLRYGIILFITS*VCLAGLFL*YLHSSLPSTAQLRGHWPPTGITPLNLEVPPLITSVLLASLCSFI*AHSLIEH
2821	16722	A	2840	338	3	KIIFYLFFLRSLAFLAQIBGHWAVFSSFKLWPPGFKHFSASTFLVNRVFKGGRPRVNFPGFFIKSGFFPI*VGF*LLLLFFFFE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
2822	16723	A	2841	2	149	TESRSVAQAGVQWHDLCSLQAPFSSC
2823	16724	A	2842	348	175	ARGCSEPTLHPCTPAWVTE*DSISKKKK KKVECSNGNVCRIMCICCCFW
2824	16725	A	2843	338	118	SACKVVSITGMCHA*VIVSVLLV*TGS LHVQVGLERLTSDDMHTLASVSGGITG MS
2825	16726	A	2844	189	47	DPGGGACSEPRLKHCTPAWVKRDFVSK KKKK*NICK*HAKSOTVLYSLFLYFS* YFLMRVSVVHIPOGSTK
2826	16727	A	2845	335	139	KCVALLSLFLSCSVM*RNACFRFAFCH DCKFLEASPAMLFIQSVEL
2827	16728	A	2846	3	352	EVSPSWFG*SQTFDLKRSACLSLSKCDW YRPGVSHRRLNGSELTOLYSEMTYFPI IWVTLQVFR
2828	16729	A	2847	2	269	HEORITPEWKKAAATALGDVVVKAVGADAD KIHSLGGQGVQGFPTTKIPGSNNRP* DYGGGITGEATVDAALSALRQLVKDRLG GRSGGYRSLGQTSYRSSKKDVIELTND SFON
2829	16730	A	2848	317	28	ARGLFSTNHKIDIGTLYGLFG*ACVLGT ALSLLRNRLGQPHLLGRDDISRIHVK RTIPGCGTLDGISVGRECACLWTFACSR KCARG
2830	16731	A	2849	326	107	SFLFN*KLGHGGRFL*FQVLRRVRLG CFSLEG*GCSEPWSCPCPLTATETDPP SREKKKRRRREEKAERKNNRRVPSLSV FLEEYVELTIL
2831	16732	A	2850	224	3	FHHVQGDGLDLLFS*SAHLGFPCWD*R CKPPCPASRNFKTLKLVHIFSNLIE*N *KSITRGTLTQLPQGN
2832	16733	A	2851	27	329	SILQAWLKVPSPFGNPLGLQSQVDEFF *RQGLALSPGLDCSGMINAHCSLKLLGS TDPPTLAS*VAGTPSSC
2833	16734	A	2852	351	60	VRTAAINRPGFLLPCFIGNFFFY*RFE TYRLGV*MILTPH*YLLSSLSGLDCVIF FSFILLFFYWFIVYCHVMVYLFVFLVI LFVLVCVVVCFYLLFV
2834	16735	A	2853	186	365	NLLSSLGGRFLPRPPGLSPHOIFTPHG GVPL*LPQPKSRPEASLNPRS*PPPGQ PRGNPPPPKKNFFFTVLLCRPGWSAV AQFQKKNLLIC
2835	16736	A	2854	17	239	LTQLNLIT*YQNGIEYPQPYAQCGPRSG NAQIGHSFPNG*QVPASGMHGLPWTHQ GLKK
2836	16737	A	2855	325	140	HFPTLQISMLLTETLARHDSLHLSQL L*RLRRNDLLKSGAGGCSLGLHHCTPT WTEQDPVSRPQAVASEH
2837	16738	A	2856	1	157	GFRVYSQDGLDLITS*SACLAFFKWCY RHKPCLAAIFYIQSRVFLAVISITHS SPOLL
2838	16739	A	2857	157	361	GTRGFHHVQAGLEVLTSNDLPVSASQS AGITGESH*AHERSDOYANTNSPC
2839	16740	A	2858	3	346	LLLRIVSLFWKSSFLGVQAEWYRPDLF VTKPPPPD*DKDCSLSLITWYRLAPP LPANLEF*I*TG
						HEGNHFKFIVNHLR*LNQNL*SGLEGD KVIWRNI*TSVTLFLC*MNGKQNPDLFR QFTYEVGRIFFFSLKD*VNLCCLGSGSTV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DLGSLQPPPLGFKQFSCSLSPSSWEPPCPA
2840	16741	A	2859	18	233	KNPTLLCCKGGGAQA*KPRLLGLRLRQEKGLTPGGEGCRDLKSLGIPWPATRPKLLLKAKKKKGGKKTLF
2841	16742	A	2860	356	3	RVRFKFGKKGFCCPGGPFVLTGPDGLGPLFFQGGDSPSKLPKPFECFVAKSTTLNVQFAFCVLRPTPN*SVTQAGM*HDHSSLQPPQPSLK*SSQLGFPSSNVYRHAPPSC
2842	16743	A	2861	115	374	IVCGKILNV*YTG*HNKLNKNKVD*PTIKMLISQSLGILIFIQKRDFFVNVGMILKRGWPGPVAYVYCNKSTLGGGGQGIT
2843	16744	A	2862	163	360	LKRIWLLILHSHPHSTPHDRGVTOLAEAGPRW*TYEYTDYGLIFNSYILPPLFLPEGDLRLDLA
2844	16745	A	2863	1	236	GTSPPFFSFFFLSFFSFLPFLSPFNPTTLLSLHNSIS*KVLFSEFEMESHVNRLKSGTISAHCSPAWATGTSIS
2845	16746	A	2864	67	364	VVCVCVCVSVSVVCVCVYIITYICMYVCA*YRIRRYIMPLTVYNVSCPEIHDSKSCALHTGATRATR*PCLCIHIPVCLTVCLTVLWHLCLSVCM
2846	16747	A	2865	2	155	ARGLTQENRLNLGGGGCSELRSHHCIPAWATE*DALSQRKKKKGTGYGII
2847	16748	A	2866	344	81	IQPNSFIFLKFIFISDGLLCCPGWSPNSWAQQSSRLNLPKCDVYRHEPHLVVQFL*KHMYKWKHVHCVFVSHYKIFGTQTKTEN
2848	16749	A	2867	217	340	RVSDFYMNKLKSLKRRRTWGPLVAHACNPSTLAG*RGQIT
2849	16750	A	2868	3	349	HEATSPITQELITPHDHALIIILICYLLIYALYILTLTKLITITMSDAHEHTA*TLIPALILDLPLCLRLIYVDEVNDPLYLITISIGHQWY*TYEDTDYGLIFNSYILT
2850	16751	A	2869	1	352	GTRIDVYTRAYPTSATIGIAIPTGVKVF*S*LATLHGSNMK*SAAAL*ALGFLFTVSGLTGIVLANSSLDIVLHDTYVVAHFHYVLSIGAVFAIIRGFH*PPLFSGYTLDDTYA
2851	16752	A	2870	2	342	ARARFRTSLLLAFALL*LPWLQEAQAQAQTVPLTLTLDHMTLQDHRHAQLADTQVEFETYIPKQKQDSFLHDSQTSFCYSDSIPTPSNMMEATQOKSNLELLRIFLLIESRL
2852	16753	A	2871	254	2	YPGYQAISSQSDWQSYAYRHL*LOPPGVK*SSIVSLSS*DHPPVPPCLANEKNFF*RGQLAMLQSRVLVNSWLLLYSHAEFRA
2853	16754	A	2872	282	3	HTHILHYIYHHGHIST*HLSPPTNIYSLCNIKILYIPTYDH*IRIPLHQEHAHVRRLIHIHITSVCVCVCVSVCVACVCVCVCWVLV
2854	16755	A	2873	278	3	LWPLKNSGPPQPMQMDLKGQVQVTPVYVYKKG*KKFFRK*KNPGFFFFFLRQSHIAEAGVQWRDLGSLQPLPPGFKRFSLNQISSC
2855	16756	A	2874	2	348	ARA*SLTLVSLIIPNATSNLGLLPSYF

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						TPTTQLSINLAMDIP*AGTMVIGYSSK IRHALAHFLPRGTPHTLIPILAMIESMS LLIQPIAMAVRVTDNITAGHLTMTLTGS PTV
2856	16757	A	2875	1	260	GTRENHLDPAGRGCSKSRSHHCIPAWVT D*DSLKKKKKKKQIILGNGGTGKNQK* RGNPFRGPWGPGRQKIKELGPGGKHGKS KF
2857	16758	A	2876	176	1	EHLFCKLLGSEKGSLSKEFGKWCWNPR *KWNRRPGVVAHTCNPSLTGGRGGQITR VG
2858	16759	A	2877	168	1	QVRVRFSSVPEFSDTCAGAQNRNLGS LOPLPPGPK*FSCLSLLSSWDYKRTFRA
2859	16760	A	2878	67	333	WQGLGRAVARVPSRYETWAGNLKGA* FQQLFFFFFFHLLFFFFFFF* FFFFFFF* FFFFL
2860	16761	A	2879	335	1	GRKEGREREKERKKKKERKKERKKTIF KKHPIPSPLAPPRKAWKLKEIQIKLVAH* KINQOARIGCPPNKRPHFPQNMKPGRE EGGGLETSRDGERNLWIFGPGSVGLR
2861	16762	A	2880	3	345	HERHETASTILLIATLFFNNILSSQ* TNTNQYSSLLIIMAIKLGAPFFH*V PEVAQGTPLTSGLLLT*QKLAIPISIIY QISPSLNVSLLLTSLISIIAGS*GGLN QT
2862	16763	A	2881	347	156	WLFVLLVEMGFHHSQOAVLKLASSDP ASMTSQSSGITGLRHCAPR*AFLIALC LPSSAKI
2863	16764	A	2882	338	2	IKKAL*HE*LREKKKSPRTSQSSKAP* NLPRS KKKKESSNNYQL*AHKLQKVKE MGKILETPNLPLLSQKVAEPLNQPIISS KIETLIKPPYHPEKS YGHDEVTAKFSRA
2864	16765	A	2883	206	1	IRTRPFTPMFIFYMFIYLATRS CPFTLA GVQWNNHNSLQL*PGLKESSCLSLSS WDYVACLHAELV
2865	16766	A	2884	341	140	DGGCREPRSRHCS PAWVTE*DSKQNKTK QKQNKRYNTISSPQTSPLCYFSAYTPLH NMFGNIMFSSL
2866	16767	A	2885	360	247	FHRVSQGLDGLTS*SAHLSLPCWDYR REPPRPKAL
2867	16768	A	2886	229	351	KLNNRPGVVAHANFPSTL*KLNNREGVV AHANFPSTLGG*GGWIMRSGVRDQPNQH GETP
2868	16769	A	2887	359	2	FYSSSSSSSELVPCRDQVQVPHYLEGLF LRSCFMEIKYDT*KRKIKYTHVHTHTHT HTHTHTQREKERDPPPTAKWKANLEAG SGYATASSIRAVLWTTITLV
2869	16770	A	2888	4	305	ADSHNWKYKAPGPTIKLLKSKSI*GYHQ DWISSRYODLFHKDMIFKIMSYWKRO VDHWDRIESPETSSQMYEHLIYNKONIA EW*EKDSFLSKCWDN
2870	16771	A	2889	1	436	IAILT*YDVITLL*RVGPRGQEGFTRATV ITNLLSAIPYIGADVV*G*GGYSLOSP TLTRFFTFHFILPFIILASLATHLLFLH *TLSNIPLRITSHSHQITFPHYPTDQYS LRLLPFLLSFTLLLLILNLFYFP*TT LTFFP

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2871	16772	A	2890	1	218	RKISPLIKLINHSFIDLETPSNISA**N FGSLLGACILQITITGLFLAMHYSPPAS TAFSSIAHITRDVNYG* IIRYLHANGAS IFFICLFLHIGRGLYGSFLYSET* NIG IILLATIATAPIGYVLP*GSLLGACLI LQITITGLFLAMHYSPPASTAFSSIAHIT RDVNYG
2872	16773	A	2891	3	368	LSNS*ANNLI*LAYTIAFIVKPIPLYGLH L*LPKAHVEAPIAGSIVLAVALLLKGGY GIIRLTILINPLTKHIAFPFLVLSL*GI ITSSICLRQTDKSLIAYSSISHIALV VTAILIQTP
2873	16774	A	2892	3	342	HENLI*LAYTIAFIVKPIPLYGLHL*LPK AHVEAPIAGSIVLAVALLLRLRGYCIIRL TLINPLTKHIAFPFLELSL*GIITSS ICLRQTDKSLIAYSSISHIALVVTAIL I
2874	16775	A	2893	2	361	ARVCLRQTDKSLIAYSSISHIALVUTA ILIQTP*SFTGAVILI IAHGLTSSLLFC LANSYERTHSRII IISQGLQTLPLLIA F*LASLANLALPPTINLLGELSVLVT TFS*SNIT
2875	16776	A	2894	229	3	YTFVGSFISFVWLFTICKVCLL*PAHSMV CACBCVCVCICVCLSSKLIIPLECL VLQILIVLSSAIYNSRFE
2876	16777	A	2895	3	391	GLFITNNISPAFPOTTIPLYLKLTALA DTFLGLTALDNLWNLTKLKKISPLCTF YFSNITLGFYPSITHTTIPYLGLLTSQNL PLLLDLT*LEKLLPKTISQHQISTSII TSTQKGIIKLYFLSFFF
2877	16778	A	2896	381	2	GRCRVSGSITIDHRMAPQKWRYYTKGGPHQ WHNFCFF*KKGVFPYGPVFLFRAPVFS PPGPPKRWKIKV*TPPPALFFFFFV EMGSHCVAQAGLKLGSSTPTPTASQGA EIAVSHRAQPHAS
2878	16779	A	2897	324	1	LYTNNTKHINPQONNTK*YQRNTKNRRK KEQQTKNKIKRHITESARKNS*HRNIQ KANKSQSNKHYRARSRRNNNNNNNN KKKIKENSHAASD*ITSSGGRSRA
2879	16780	A	2898	120	345	PPAPSS*YTSLIQDRFLMMAVLSSAS LMRGNVGSNIMNALSHFLPGQTATLFI VLDIMEAISLLIOPIALAV
2880	16781	A	2899	381	219	CVSQDGLDLLTS*STRLSLPKSNWDYRCE PPRPAGSGHLYSSFFKQTDGTHNF
2881	16782	A	2900	1	224	LSWCLTLYPAYLLALFYFFYLKILDLAI LPRLVPYSWP*ASSPASASQSSGITGMS HYTWLPQTLNPLFLFVP
2882	16783	A	2901	1	228	KYLINNRLITTOQ*LIKLTSKQMITHN T*GY*YNRSGSSFNGVYDHLRSESEH PMWIDNTEYDEIYTRGGIE
2883	16784	A	2902	2	332	LPSPFSLLLAPSPSSSLPSPSSSLPFS PSSSLPSPSSSLHTSHSSLTTPSASCT LTITESFTQRLAQSYITILP*ASRTTGM LKXYITLQITRNTHSMRPAKTKI
2884	16785	A	2903	3	243	DIGFOTDSBNTFKAKTKCVQGLDFIKI *NFWFCVTAHTCNPSLTGGRGW*ITKLG V*DPQGRGETTQKLACHGCVDAV
2885	16786	A	2904	179	2	CGYFNATYCYSLLCFLYLLSLCNPFWKK

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						1FLPLFGLVFFVFFVF*NRV*FCCPGWSA VSQ
2886	16787	A	2905	108	2	GRVDIKLTSKQMITIHTKGR*SLILV SLIIIFIA
2887	16788	A	2906	318	2	YKESNSKNEKKKITRQRKROKKNRPS MVHTCNPSPMAGRDGQIPSLFNQPHSP RIIRLTLINLNPITKHIAYPFLVSL*GI ITSSIGLRQTLQSLIAYSS
2888	16789	A	2907	17	308	KLAGVGMCLMSKLLERFPNNHLSPRS EGLMP*SHNCIPDWT*QNPVSQVQTG FCLTFLNPLNPRNLNSGPICCOLSLRL LGRPLFAASVSGV
2889	16790	A	2908	378	1	RSLSHSTETAKTHGHOTHFGLSTFSK*TPPTIASIPINPNHCLDAFNSTTSASYP SECVLTSFFKEIIADPR*KYSSIN*HPY HLFLLKFVFFCSRDGSLTMLDIRPGLNS RSQAILLPPWPPKVL
2890	16791	A	2909	1	129	HLFGTNRHDIGTLCCLLFGA*AGVLGTAL SLLIRAEGLQPSRTP
2891	16792	A	2910	1	323	CVCWGYRIFRCNIGHHLKFFFFSLPFFF FGKVKWFCSEG*RCGQQLIMEPLASGF KGIFFLNLQPNWE*RVSPKLPKGKFI* LKTGFLVAQVVFELRTSGDQMA
2892	16793	A	2911	367	136	ETPGNHLSPGV*GCSEL*SCLCFPAWAT EQDPIKQKRTKSKLTKNTKADLTRW KHIKSAVCVICLCLMVMCLRE
2893	16794	A	2912	258	140	FLIFFCLDCFLNIVKLVGVPGFPSLKKK QT*RGQLALSRLSCSLIIAHTCTLEPL GSRNPLTLAPQIAGATGMSH*VOGYNEL
2894	16795	A	2913	48	242	YSMIFCVLILPVSFTSSDGIFFLLINLFL FY*STYPLAFFKTESHVSQTQAGVRWHHL GSLQPPPPR
2895	16796	A	2914	309	76	GFICVCVCVCVCVCVCVVFIFTEYSFH SLPC*IRCCVFYPLALLIGFVFWNR YLEVYNISFEVWASLNFNRLLL
2896	16797	A	2915	1	122	FSVETGFHHVQPG*PFTSGDPPSLAS QSAGITGMSHHA
2897	16798	A	2916	167	1	GNMCKSESVSHTNINRKP**YNPRLGT VAHAYNDPSLGGCRWITGQKWSL
2898	16799	A	2917	2	356	ARGILLRLMLTLTRYE*RDUTREST YQHHTPPVQKGLRYGIIIFITSEAPFL PRFLPPLFLSSFPPTPSLLKPPPPSSFP SLPSFFPPFLPSSLFL
2899	16800	A	2918	2	351	AREYTSQLILQMTFIMAFCTDRTLVE LAPEC*LMRTLDIITR*GNQP*RNAGS YWLPYTLGLTLPILLIYIHTLGLSLN TLLTLTAQELSNS*ANNLI*LAYTIAF IVKI
2900	16801	A	2919	32	321	ALMGITFFFFFLGKGVLAFRGGGRGNPG LWGPPPPGLGPFSG*SLQGGGA*GPPQ AGANFGFLILRKTSGSPGCGGFWTGPG GDRPAGAPQGGG
2901	16802	A	2920	1	361	GTSTRGLVLLLSLHAGSINPLGITLHS DKVTLHPYTIKDALGLLFLLSLMTLT LFSDDLGDOPNYTLANPLNTPPHIKPE *YFLFAYTILRSVPNKGVLALLSLIL ILAIIPIIL
2902	16803	A	2921	3	152	HERLYSVPLRILRLRPLDPLSIPOGWRHV

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						<p>IRSAVYKSHLTLPARRGLQDGIILFITS EVVFFAGFF*AFYHSSLCPTPQL*GHWP PTGITPLNPPESPLNTSVLLASGVVIT *AHTKAISHVLEAFKGTG</p>
2903	16804	A	2922	410	1	<p>RAGYRQKQWSLATVIGQLGPFVERGWYG PSGEGGTPQRHCSLVLDLHVITQNRRA NHRPCRCGSLSELKAPALAPGPRQSK TISOKKNQTTTKNNTKQPGSAHACN PSTLGG*GRQITLPSGVRRQDQPGH</p>
2904	16805	A	2923	2	145	<p>ARAAKGVIT*SHVFAQRDLNLLSSRD PALASQSTGIGTGMHOCPC</p>
2905	16806	A	2924	29	340	<p>EMNEVERRRGRK*LFHDSITGR*EYRCAP OCFAMS CVLM*RWGFMPLKLVSSDLPA LASQSAGITGVSHCANLVFLPLSTSF SORHLYLPPRA</p>
2906	16807	A	2925	2	337	<p>ARVLILPGFGTISHIVTVYSKKEPFGY IGMD*AMISIGFLGFI*AHKIPTVIGID VDTRAYFTCATIIAIPFGVKFN*LAR LHGNCMI*SAAVL*SLGFI FVFIVSGOA</p>
2907	16808	A	2926	76	388	<p>RYCTPAWATETPSQKKEKKKKCTFEPE SSFPVCLENGSGGNFI SLFFFLILSL FFYFY*FFFIIFVSYYYFYFCLFSYFF FYFFINLIIFLLNYYYYFFFI</p>
2908	16809	A	2927	48	374	<p>KDQEPDTMGSAHFQVFKGRQVSGANED RINSHGGPVMFSGQYGGOLVRFLVY*II IFFMLLFFSLFYSYFLFISIFFVLVFC LFILPLFYFSFFFI FVFVFFFYFIVIF</p>
2909	16810	A	2928	3	294	<p>HGFPHYSIQDGLLLTS*SAELGLPKCW DYRREPPRPAPFTLRILWYLKALYTV LGCYREYAYRPNWCWTHRMDGGQVEGR RBTGGGHIIGF</p>
2910	16811	A	2929	7	420	<p>IRRRDVLTLTSLSPAARICYNGRR GNRLNSLAYLSKELLAWSLRKPSHGLL TPIRCVLVIRGHHF*LLPPSHLLLASA IMGAAGGTG*TV*PTLARNYSQPGVCVN LAMSLSHLGSVSSILGAIITITAINME APAITQYQTPLFV*YGLITADLLVLSLP DLTAGITILLTRKLSLTTFFDPAGGGDP ILY</p>
2911	16812	A	2930	11	253	<p>GLLHKAPSP*KEFFSPDKPNNFFKPSFI FSPPKKFLSKNPHIVFKPPFKGKIPT FPPLPKFGPPRVFFKAPPPFFFFFF FFFFF</p>
2912	16813	A	2931	70	341	<p>DSSFFS*LATLHGSNNK*SAAVL*ALGF IFLFTVCGLTDIAPNSSLDIALLOTYY VVAHFHYVLSGAVFAIIRGLIH*PPLF SGYTLDS*AKIHCAIIFIGVYITFFPH HSLGL</p>
2913	16814	A	2932	3	340	<p>NYSHPGASVNIIFTVHLGAVSCILRAI NFIITIIINIKPAITQYOTPLFV*SVLI TGVLLVLSIPVLSAGITILLTDRLNLT FFDPAGGGDHILYQLLF*LFHPEAYIL</p>
2914	16815	A	2933	2	364	<p>RVQKGLRYWILSTSEVLLFAGYF*AL YHSSLAFTPOLGGHWPSSGITPLNPLEV PLLYTVLLASRVFT*AHRLIQNNRN HIIQALLITILLGLYCTLLQAS*NFEPF FTISDGIYG</p>
2915	16816	A	2934	2	367	<p>PRVRPRVRYLLFGA*AGVLGTALSLIR</p>

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						AELGQPGNLLGNDHIYNVIGTARAFVII FFIIVIPIIIGGFGN*LSPLIIGAPDMAF PRINNISF*LLPPSLLLLLASAIVEAGA RTG*TVYPPPL
2916	16817	A	2935	3	365	YHIV*PNP*ELTWALSALLMTSGLTM*F HFHSITLVILGLLTNTLTIYQ*WRDVSR *STYQGHHTPPVQGLRKYGIMLFI*DR FFFAGVF*ALYHSSLAFTPHLGGHWPTT GITPLNPLE
2917	16818	A	2936	3	144	DSHGRHVING*TCVTICTFRQLIGHFTS KHFGFEAAA*YWHKKKKK
2918	16819	A	2937	3	422	QRLLATNHHIDIGTLYLSFGA*PGALGTD LSLLIRAEGLQPRDILLGNDHIYNEI*TG HALGLFFIGLPIIEGFGN*LHALIIG APDMALPRINNISF*LLPYLLLLLASA IVEAGAGT*TVYBPPLAGNYSHQASVE
2919	16820	A	2938	3	382	RTGLFSTNNHIDITLTYLLFKA*RGVLE AALSLLIRAEGLQPCNLLCNDHIYNVIV TAHAFVIIFFIVIP*II*CPGN*LLPLI IGAPDMAFPRINNISL*LPSTLLLLLA SAILEA*SGTG*TV
2920	16821	A	2939	225	3	NISWERNQIVPFGEPYNGVPVFSVLWFH KMFIFETGSHSVYQAGV*RHLSLHPH PPGIKQFVLSLPSWDY
2921	16822	A	2940	1	247	PTRPPIVYSTIFAGTILITALLSSH*FFT* VGLBNMLAFIPVLTKKINPRSTEAAX YFLTQATASILLALLFNKKKKK
2922	16823	A	2941	3	369	TRDSTYLGHHPTPVHTGLRYRILFITS DAFFFGAGFF*AFYHSSLAFTPRLGHW PTGITPLNPLEVPLLYTSVLLASGVSVT *AHHSVLVEDDRYQIQALLITILGLYF TLQASEDFE
2923	16824	A	2942	3	401	LTVCCVIVLRLLKTLFFFNKFLITOKGY FNTPEEGFFKPKNRRVGPSPMTDPTML TNLIKGVKPKAPPRILMGGGINMTF*GF VTPRAPFPLTLRLNPLMQQIGDILLTLKA SGGSPASGNFLKELGURSINF
2924	16825	A	2943	189	348	RNARGWVTDKERRLRIGMVAHACNSSTL GGDGR*IA*GQEFETSLANMVKCL
2925	16826	A	2944	2	349	ANSNYKTHSRITLLSQGLQTLPLFIAP *LVASLANLALPPTINLLGELSVLVTT FS*SNITLLTGLIILVATYLSLYIFTT SQWGLTHHINNPKPSFTRENTLMFILL SPIL
2926	16827	A	2945	621	929	GCSSGTGCCPTLCLEPRPWSRGVGGSE SSTAHLCPRGWRSGRCFLPLAS*VDS AMSLIQAANKLMAVQTVKASVASTK YOKSQGMASLNLPAVSWKM
2927	16828	A	2946	379	395	SOHPGRLLRREDHEVRSS*PRDPALTSQ SAGITGMSHCARPLVATSIHKIDNRYID DRS*NNIGITFINLLIYLSIYLSIYL SIYLSIMYSTVAGAGVQWRDYGSLQPE SPGPK*SSCISLSSSRNHSHTPPHGWVD PKIP
2928	16829	A	2947	2	357	HTYDIRKPRR*TLACALSALLTTSGLAM TDCPHYITLLILCLLTNTLTIYQ*NRDE TRESTYQGHHTPPVQGLRYGIIIFITS EAYFFAGFF*AFYHSSLAFTPQLGGHW

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						PTGTF
2929	16830	A	2948	2	357	PRVRYSTDHSDIGTLYLLFGA*AGVLGT AISLLLRRAELGHPGNLLGNHDHYNVIGT AHAFVLIIEFVITPIIGCCCA*LGPLII GAPDMAFPRINNTSF*LLPASVLLLLAS AIVEAG
2930	16831	A	2949	2	217	KNLKIYQVGDNCILNSQLRLRLRWEDRLS SGG*GCSELCSCHCTPAWTQQDCLKKK KNFWPVGVEVKGRHML
2931	16832	A	2950	2	354	AIPTNTARELTTHAEVLIILERTTTTTKD VKNPRIIAAATASCLGGLEDAISCOY GIATKDRPTGLGTPEVLLGALPGAGGTQ RLPKMVVVPAALEMLRTGRSIRAHRAKL M*LVD
2932	16833	A	2951	3	150	LFSCSPTFSSDPLTTPLLILIT*LLPLT IMASQRHLSSEPLSRKKKKKK
2933	16834	A	2952	283	344	EKKKKKKKKKKKKKKKKKKKK*KLRRKKK KKKKKKKKKKKKKKKK
2934	16835	A	2953	3	378	DAWADAWNQTPLN*SVLITAVLLLSL RVLAAGITILLTDRNLNTLFDPAAGGGH PILYQHLF*CFGHPEVYILILPLGLIYY RIVTDYGTKEPFYIGMV*AMRSIGFL RFIVRAHHIVTVG
2935	16836	A	2954	3	387	ILYQHLV*FFGHLEGYIILPLPGFIITSH MVTYYSGKEEPPFYIGMV*AMISIGPLG FIGRAHHIFTVGIDVTRAYFTYATII AIPGTGVKFS*LATLHGSNMK*SAAVL* ALGFIFLEPTVCGLTGI
2936	16837	A	2955	2	432	PRVRPRVRKHIAYPEPLVLVL*GIITSS ICLRQTDLKSLIAYSSISHIALVVTAIL IQTF*STCAVILIIIAKGLTSSLLFCLLA NSMYERTHSRIILLSQLQTLPLPKKKK KKKKKKKKKKKGGLKESLGGFNLTG EGK
2937	16838	A	2956	12	391	SYFISSSKPHLSPPWLSPPDEATSKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKK KGGGPK*KRIGGSFKGGGGEKIFFPKK GKKKKTGGFFEKKFPGLGGEK*DNLPKK NKTVGEKNFLGGG
2938	16839	A	2957	1	352	PTRPYFPVDAGEAQHFRFCRRPLRALW SSHHERMKNVLTCTHCSLGVFFLYCTYY IFVLFI*SSCGLTLFIPITCIIILFGSIS FFLPFTIVFSIIIIVTFKFRLLYSIIFL SYLLC
2939	16840	A	2958	1	243	NLPRLNPKIEIILNRSIICNKIKAITKS LLSKSSGHNVDVTAEFY*TPKEELITIL LKFLYLPKKKKKKKKKKKKGGPF
2940	16841	A	2959	373	3	FSSLKKRVTPPPPPKTFGSLGHLHLKK NFPQKPPPPKSFQKNPPPPKKPPF* KKKKPPPPPI*HPPPKILQPPPPPPFF FFFFFFFFFFFPPPPPPPPPPFTDMR GFIVRKFRTRG
2941	16842	A	2960	2	136	PRVRSITLPSYKWNRRALMKAHLIMK*F TEYPKTTDELYLHDNT
2942	16843	A	2962	1	358	HTPPVRKGL*YGIITLITSKVFFVFRFI *AVYHSSLCPTLQGLGLWPAFGMTWLN L*VPLCTTFVLLA**VSIT*AHNHLIDL NRCHYIALVITILLRLRLFTLLPASEYF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2943	16844	A	2963	2	373	EAPLTIS RAYDIVRPRF*PLLGSALLMITYGLAM *VHWDCTLLILGLLINTLAIYQ*WRDV SRESTYQGHHTPPVQGLRYGIILFITS EDVFFAGIV*AFYHYSLAPTQLGGHWP PTGITPLNPLEV
2944	16845	A	2964	403	61	LLFFLEKKNFLPPGFSAFFSPSP*KFFF SPKALIFWGNFSPFFPPPKIRFLPKIPP WVFFSPFFWEKLFSSPPLNFGPFRVLF KGPPLFFFFFFFFFFFFFFFFFEGECW RL
2945	16846	A	2965	2	360	LTENLAWVTR*GNHPQRLNAGTYLLFDT LDGSLALLIGLTYTNTGLSNVILLTI TAQELSNS*ANNLV*LAYTLAFIEKIP YGLHL*LPKAHREAPIAGSIVLAAVLSK LGGSGKN
2946	16847	A	2966	321	2	STGMHFFHINMATAINPPPPRPPPLFP NPKTKPNPTQ*KGGFPPLGPF*KKLSPF LTLFFFFFFFFFGHHPGPWQKKKKKVF FFCVCFSPQRVNIYKNTHQQ
2947	16848	A	2967	200	1	RRTYTSHLLACLRQGLAFSPRLCEGKI RAHCSLQLYGSSDPT*APQTAGTKQHN ORIAQCNDN
2948	16849	A	2968	2	354	LLTASSSSIAPLQSSLSGRARLCLIK*K EGVLNLSI*SGNQGSYANVYRLLDPI PKIYAEATP*NVNNTNLETSKPTIQK FPEDREFKNDFFETKNGDRETGAHPF LLFLV
2949	16850	A	2969	99	400	ALGIHFITVSYGLYIGLANSLHIVLH DTYYVVAHFHYVLSLGAFAIIGGFTH* IPLYSCYTLDTQYAKIHFTIIFIGVNL FFPQHFLGLSGMPRRY
2950	16851	A	2970	2	377	NILLTLTAQELSNS*ANNLI*LAYTIA FIVKIPLYGLHL*LPKAHVEAPIAGSIV LAVALLLKSGYGLIRLTLILNPLTKHIA YPLVLSL*GIITSSISLCKKKKKKKK KKKKKKKKGGP
2951	16852	A	2971	1	407	GTRSYTHLYRVFLELTKMSVVDLHPIV MVISGHVRLAFYGVIVHLTLILNLLTHI LYPFLVLSLGVIISSIFLRRTDLESL IAYSSIHHIALVVTAILIQTP*SFTGAD ILIIHVGLTSSLLCCLANSNYER
2952	16853	A	2972	10	259	SRSVATYFKGMASA*RMFSSKKKKKK KKKKKKKKKKKKTKAITKKTAKWKN *RTEKIRHRTLPLISSRDAKCVDFLYT
2953	16854	A	2973	12	400	LNCRTPSLYLQAGELLVENPHIWCQ CVRKNFFLFFFTFDLYCPHICAL SITCFALASISGLFAFFLLSNFYHFII VP*NFSLSIYLCLHSLFYVGFSSPDM IFSILT*TLFFCLFHL
2954	16855	A	2974	125	3	RPRRPAAGVGVQ*KNLSSLPVPPGFKL FFPLSLLSSWAS
2955	16856	A	2975	2	332	RECTNYPAQPPPPLEAEEGFPPLPFTD TG*LECLPLGGGGHRLGLGATWHLEN ACALVLADLTGPKPSGPGSQACGASG RLPLLSGPIPLPLGGGHTLSAWGHA
2956	16857	A	2976	7	329	SRDILVMTDEGEFF*GHV*PDRSRAD TPRLGGHWPETITPLNL*PVLNTSV

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						LLASGGSI*THRLLEYIRHQYIHALL ITILLGLYFTLLQSEVFESSFT
2957	16858	A	2977	2	339	AHHITARIDVDTRAYFTSATIIIAIPT GDKAFS*LATLHGSNMK*SAAVL*ALGF IELFTVRGLTIGIVLADSSLDIVLDTYV VGAHFGYGLSIGAVFAITGGFIH*CPDLF
2958	16859	A	2978	394	0	QCSEL*SCHCTPANVT*FPVSKKKQ RK
2959	16860	A	2979	149	383	PLCFPSQHWGKSSNCLSLKYFPSSGLP LRCKAELDDVQKQAKDELVDVAHACNPS TLVGQGGRTTLRSVG*DOGQOH
2960	16861	A	2980	2	378	ARVSIIGLGLIVGAHDMFTGRMDLYRT YCTFATILIAHTGVVPFI*LATLHGSN MK*SAAVL*ALRFFITSTVGLTGVLP N*SLDIVLHYMYAVAHLYVLSIGAVF AILGRFIHRLPVF
2961	16862	A	2982	2	409	PAVAEAYLFPVDDSDSGSFLWGKPDLDG IRECCQRNFGWNRRTDESLEFPVLKQLD AQQTQLRIDSPFTLAQGEKDDAKRIKSQ RLNRAVTCMLRIETEAASSEIAVSV* QKELELDIKAVACHLEYMYETDP
2962	16863	A	2983	3	453	HASAHASAHASGQRKAAPAEKKCGAE QHEGLELRVENLQAVQTDFFSDPLQKVV CFNHDNTLLATGGTGDYVRVWKVPNLEK VLESKAHDGEIEDLVLPPEGL*IVCPD HYSFVGINDPFWLL*LNWGNRLYFPHIS VYLMHFHRTF
2963	16864	A	2984	3	417	LILPGFGIISHIVTYSYSGKEGFGYICM V*AMISIGFLGLIVRAHHIFTVGIDVYS RAYFTSATIIIAIPTGVKVF*S*LSLHGS NMK*SAAVL*ALRFFIFLFTVSGLTGIV LANSLLDALHDTYV*THFIHYVLSI
2964	16865	A	2985	273	408	MKIFVF*VSPPLFFFFFFFFFFF FFFFFFF*VSPPLFFFFFFFFFFF LAVETFI
2965	16866	A	2986	176	335	TSFQSELWRNTALLPRLECSGLTIAHCSL ELLGSSSPASAS*IAGTGSIIRY
2966	16867	A	2987	65	398	KKEFKIGRKAEEKTRNNINAFQGTAN ECTVQWFFKKFCGNKSLDEDECSGRPL EDDNDQWRAIIEADPLTTREVAEELSV NHSMAVQHLK*VGKVKKLNKWPHELS
2967	16868	A	2988	2	158	PGWMLTDPDLR*STCLSLPKCWDYRHKRP SPTSRSQTFDHA PNKNSSSPPIYM
2968	16869	A	2989	435	23	GVVFPNFQKSFYFQRLKIWGGGGRKRF PPKKKGFSQKTPESF*KPPKRRKKIFH DPGKKGPPIKGIKKGPPPLFFYYYYY FFFFFIITIECLHSRFPHRHNNKCF PNPSPRFPQHLNTSLPNKKNKEP
2969	16870	A	2990	410	3	GGRGHFFSGAFFIKFPWNKKGISQPLCF PRGGGSPPLGPFVKGGGGPPCWGLCHKG PVKGTGAPRGKNGISPPFCFPLGSGFNR SGFFWALLGSPPLFFFFF*DRVSLHHE GWNVAQS*LTKTSTSNWQVILL
2970	16871	A	2991	371	132	KQSLFFKVGFFFFFPEVENATYPDSHTA FYSW*KRSTFSKKKKKKKKERKRKKEE RKEGRKEGRKERKKEGKKEIENA
2971	16872	A	2992	336	1	CPRWSRTAGLK*STCFGLPKCDNRHES PCPASSVLND*QLSTVQRAT*WQTKSLV LKAPPARGALPVSRVSPFFSSHHFAYF

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2972	16873	A	2993	317	440	LHMI*QVSCFLFLR*SLALVPOAGVQ*RD HLGRLRQEHHLSPG*LRKFFFFFORDGV LMLSMLVNSWTQVMLLPQPPQVLGLR
2973	16874	A	2994	2	181	FHHVGLDLLTL*SACIGLEKCDYRREP LCPALVILLTAKFTNFRYRVKNVCTEHV ESN
2974	16875	A	2995	1	165	GFHCISRDLGLLLTS*YARLGLSNCDWY RHEPPSPAPLFLISYSICLFLSKLIQFL
2975	16876	A	2996	405	2	KKGFPIFSRMFLYKHKIEKPLASQKFG DPKWSPHPRPIFFLLKKGVLYVWREGF KFHP*FPPPGPKRWE*RVKPPHPPPF FFFFFLYVEMGSHCAVQAQGLKLLGSSTP PTSASQGAETAGVSHRAQPHAS
2976	16877	A	2997	2	415	CLFTGGGLTGIGSAGSSLDIVLHDTYV VAHFHYDLSIGAGFAIGGLIH*FPLFS GYALDQTYARIHFTIIFIGVNLTFLPQH FLGLSGMPRRCS*PDAYT*SMSSVG SVITLTAIVLILIMIREAFDSKRTVL
2977	16878	A	2998	349	370	HHFY*STAFRFQHMELRNFFFLFLFF FFFFFLVFLFI*FLFLFYFLFLYEIYL ILFFL*HHFYSAV
2978	16879	A	2999	36	139	LCHCT*FANETFSKEKKKKKKKKKKKK KKKKKKKPGGS*KTALSHDCATVLPQ RLFQKKKKKKKKKKKKKKKKKKKK
2979	16880	A	3000	104	373	SADREXISKTDNLH*TNVNVCKVRVP IOSVFSHSGGLKLEINNRKMKESLNT* KINNISVWQCSSLINLNKSNYSKSDNT TTQYMY
2980	16881	A	3001	1	396	LDCSKISSYLOKSSSHVLFFSFSFFFFF GGGGGFALENPYPAGLGPKKKTLSPP WLVGPPFPPEKAPP*GGHFLGKKPKQNP GGQNPKRPSGEGNFFQPPGGEKKQIGP PTGGGKPPFSF*PRZPPGP
2981	16882	A	3002	412	104	FFFFFLVROTFYPQPFVFFFLPFKFF FFFF*AFNFFWGFPIFSPPKGFFFSKI SRLVFFSLPFWEKFFFLPPFFFAFLRF PFKGPXKFFFFFFFFFXKY
2982	16883	A	3003	400	46	LLLLFFFKLPPPAFGGFFPPFPL*NEF FPDGPFFFLGGFPFPPPPPK*VFPPKPI PGFFFFPPF*KKFFFSPPFFFLPPPGPF FNPPPPFFFFFFFFFFFFFLPCLVU VQVEAY
2983	16884	A	3004	411	69	YSLPPLFFSSPPSKFPWPPSFLFLTR VYKQFFFFFPFELFGPGPLSLGSKPP PVFLGGDAFASIPHRVGLSPPPNP FTGSPFW*ALFPAPLFFFFFLSSFFFF F
2984	16885	A	3005	3	200	DAWG*LFSTNNKIDITLVLLFGA*AGVL GTALSLILIAELGQGNLLGNHDIYVI VTAHAFVII
2985	16886	A	3006	259	146	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFGLLDNILL
2986	16887	A	3007	118	414	QNQPPONKATHTVKIEKKKEPETTKVAK EHNKAKTAEKSEE*TKKEVGGKQEKVN HTAAKVEQKTPSPKPEKEDNKKAAVS KHEQKDQYAFRLYMI
2987	16888	A	3008	427	111	FFFFSPVGNFSPPQGFPPFFPPFPKIF FPPPL*FFWGGFPFPPPPKPVFPKFS

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						PPGFFFFPP*GKKFIFPPPP*FCPPPGF FLSPPPPPPPPPPPPPPPPPPP
2988	16889	A	3009	3	302	SLASCLSYLVLCVIFLGQPKPTI*LNST PHKK*NPTERYVKTCTQIFIALFRKEK QPRCSFAGWINKMLYACTIEYWLAIKR YELLYATV*WYLEKI
2989	16890	A	3010	1	409	KLHDAITFFIIEELTIFHDHALVITFLIW LVYLCALFLITLTKLTWNISHAGEIET V*TLAAITLALWLPSSLRLIYITDEDN DPSLTKSIGHQWY*TYEYTDYGGLMFN SVILAPLPLEPGDLRLLDVNDNRVV
2990	16891	A	3011	157	2	GRVDLKTQKLRCGGACLOSQHTQONHL NPGEKCSSES*LPPCCPD*VTQ
2991	16892	A	3012	2	423	ARAARAHIVTYYSKKKEFPYIGMW*AM ISIGFLPGIGRAHIFT*IDGHTRAYF TSATIIIAIPTGVKVF*LATLHGSNMK *SAAVL*ALGFIFLFTCEGLTGIVLANS SLYIVLHDTYVVVAHFHYVLSIGAVPAI
2992	16893	A	3013	2	140	ARANILLTLTAQELWDPANNLI*LAY TLAFIVKKPLYGLHL*LPKARVETPMDG FILLAAKLLKGGSGIIRLTILNPMTK HIAYPLGLSL*GIITRSICLRQTEK WLIAYS*ISHIALVVTDILIQTP*SKHF TTNSHCPRTMGPSQQLNMTSLHFSYS KETSRLTFLMTP
2993	16894	A	3014	2	420	PVLAAGISILLDRDLTLTLPDGGGGD PILYQHLF*FFGHPPDDYILLPFGIIS HIVTDYGRKEPSGYIGMW*AMTPVGFL GFIE*AHHIFTVGDIAHTRAYLTSVSL IIVIPTWRQVFS*LATLHGSNMT*YAALF
2994	16895	A	3015	6	292	AHHIFTV*IDVYTRAYTSATIVIAIPT GVKVS*LATLHGSNMK*SAAVL*ALGF T*LPFVGLNGIV*SY*LLDIELHDY* FVWGCPKRVYF
2995	16896	A	3016	3	422	TPITIGGPGN*LFPLIISAPDMEPRIS NISL*LLPSSLILLASAIVEAGT*TD* TVVPLAGNYSHPGASVLTIFSLHITG VSSILGAINFITPIINIRPPA*TOYQTP LCA*CDLMTAVALLLSLPDLAAGITILL
2996	16897	A	3017	21	490	TPFPGRHITMFSILHAGCSLTGAINYI TTLINI RPPAITOYQTPLE*SVLITAV LHLLSLPGLTAGVTILLADQNLTTFD PAGGGDPILYQHLF*FFGHPEVYIILP GFGIISHIVTYCGEKEFPYIGMC*AM ISIGFLGIV*AHHIF
2997	16898	A	3018	98	402	LRSHSKSFQISGLKPSQEWPOISPST DYIINT*HFNAQMLKNY*HQPGLHDF FPKPKKKKKKKKKKKKKKKKKKKKK KKASSSSKKDPPGGGPT
2998	16899	A	3019	399	229	PPFPGGGGPGQFPFPFGSLPKSPGGVF YPPFRGGKIFSPPPGFFGPPRGFF*GAP P
2999	16900	A	3020	2	401	SDAVL*ALGFYLVLEGGTGLIVLADSF LDLELHDTYVGAHFHYVLSIGAVFAII GGFVD*FPLPSGYTLDDTYAENHFTIIL IGANTFLQHFGLGSGMPRRYSDDYDA YTT*NLSSVGSFTLLAALL
3000	16901	A	3021	413	67	PPFPKIFFKTKPKKKIFFFFPQ*IFFP

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						PLPPKFFFSPPNP*FLLGGFSPFFPPQK KIFPPKIPPNFFSPPLKKKIFFFPDP* IFPPPRFFLKPDPFFPPPPPPPPPPPPPP FFF
3001	16902	A	3022	2	332	LTLSTLSITAGS*GGLNQTLRKILAYS SITHIG*IIAVLPYNNPNTILNLTYYI LTTTAFLLNLSSTTTLLLSRT*NKLT *LTPILPSTLLSLGGPLPPLTGFLPKW
3002	16903	A	3023	1	412	RGPPIPPFFFCVFFPPPPPPPPPPKGC HSKRPPPPPPPPPPPPPPPPPPPPPP GWRSLPLFFSPGGRGFFPLSHQVGFN EVLVFFKKNLELFRGSPARKKKKKKHL E
3003	16904	A	3024	279	1	LGRNTEWLKSGKGMIDILKTNCGKLANEP FRQPRVLIGGEAPRAGSPPSRAPPA* TPGSSAGSWP*PPGTGRAPRGAPAP GARSPPRG
3004	16905	A	3025	151	401	KKPLGGPNLTGEGKKKFFSLKGGKKPK GKFLKKTFFLGGEGKMGKTPPKKLP*GK KKIFKRGKRGKKNPTLAVKKFSKKKK
3005	16906	A	3026	416	140	YLSPLKKFFTPPPPLRMFLPPNPLKNFF PPQLKIFWGGWAQNSPPPKGFFSKNPK RVFLPPDIRKRYNPPPHGKILAPPKNL* SAPPPIFF
3006	16907	A	3027	379	31	PPPRAGVFFFFKNFKPKPPPPPRGGRF* PPFPPLKF*FFPKPQNLFGGGGAIPTPPP KRGLOQIPTERFNLSPPPTQKINFPFPG KGGPPPLPKPPPPPPPPPPPPPPPSL NSFI
3007	16908	A	3028	28	420	MQTTMAHIFLCKNFANCAHVPR*SET KPMSTPLQFD*TYGKESCKYAEHRTW KQ*CVFSLYQIIPT*EKTWKNQCQGTN* NQFFKQTTTL*NHTRDNQICFSRIGLEY YYRITTRQHLCLKRTVCIL
3008	16909	A	3029	1	401	LGNNGEAVSEKKKEKSKESKSHNVVGF FFFWGKPPFPVQAEQGGGRNFC*PKPMP PGWGFPGPADPAGGGGGRQKQGRGNFG V*REKGSWGGGGA*PFGPNPHWPWP QGPETGGTTRHPSPGLEKT
3009	16910	A	3030	285	397	MFIKGGGLNKLKPSAAYACNPSTLGG* AGRITRSGD
3010	16911	A	3031	265	2	KKESSCKATNSNSLFFLF*SVFFFFVF FFPPPPPPPPPPPPPPPPPPPPPPPP FFPPPPPPPP*HFKSALLAVTDLOFLNSD PRV
3011	16912	A	3032	410	49	GFSPPPP*KFFFSKPLNFWGGGGGNFP PPKKRFFPKNPPGVFYSPPKKKKKFFSP PP*NLAPPKIFLKSPPPPPPPPPPPP FFLSNVNSGLTNMILPCKDPSCPTTFP ILGSLISL
3012	16913	A	3033	177	2	VTPPPPPPPFETRSHSVARTGV*SDRCS LOPHPPSIK*SSHFLPSGWDYRSMPPH AS
3013	16914	A	3034	75	395	MSYRHXKXKKKKKKKKKKGGAP*KKPWGG PKLTRDGGKKKFFSLKGAKKKPTWFKWK TLILGGRKMGTTTPPKLKLPLRKKKIFRG *RGKKHPKSLPVEKFSRGRKK
3014	16915	A	3035	400	83	KKEGPARVVSVPVTPPLEGPGVRSQTR

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						NF*PTFPTRKSLPS*KSXIDWRGIPLY PPPPRVKPKKSPNPNRRFC*TKIFPCP SPWAPKTHPPFPQKKKKRVYK
3015	16916	A	3036	3	196	DSMPQT*NKSFARAKKKKKKKKKKKKK KKKKKKKRGGPPLKLTGGPKLPGGKKK NFFFRGG
3016	16917	A	3037	1	411	FCYDVCVSGCADYSIVTIMKKKEK*K KKKKKKGGGPKLKNPGGAQNYPGVEKKI FSLKGLKKTTPRGNFKEKPYFGGGKGA PPQKNKPLGKKKFKREKGGKLLQFPW GKKISLPGFYLLKKIYPGRGFFNFS
3017	16918	A	3038	3	429	NFFFKKPRGNGFFPPPKKFFSPSPSLK FFFFPPPPFFGGGGPHFFPPPKRFFQ KPPRGFFFPPL*EKNFFPPVPVFADPP VFLTPPPP
3018	16919	A	3040	1	111	IGLSGMPRRFSYDPDAYAT*NILSSVGS FMYLQDDNK
3019	16920	A	3041	76	967	QLLKGGVSGVCPLLMFRCSRFFLLVGS WSSLASGVKPTFAVSUTVLKAARLELF IPPRGLVVSLSAGVKLQTFVSVTAHKS SVDPKNSGAQLASPSGSRTRAAGGAACQ SRRCRVPALLSPWVDGTGRRGAGGGARR GGSGRTGAHGVGGRRLRHGSLHVPSPAPW KGS*GLARNRAGRWRAGTAGGSPSTPSAA ADPGAKSLTALCEGHPAPAGPTPTPT PTRNSWPAASVARSPPSRCLSLHTSLQ AEGVSSSLGQPSKGLPOCSGGAGSLKLC RQSGSPGRGGTESERGL*GLPQCSGGAE GLLKCRQSGSPGRGGTESERGL
3020	16921	A	3042	39	141	LSIRGLNIIKKRQL*DNKQODSTLCC P*EIH
3021	16922	A	3043	2	405	LFSTNHIYIGTLYLLFSTRAGVLGTALS LLIPAEGLGQPNLGNLDHINYALVTAHA FVIFPFIERPIIIIGGYGN*LGPLIIGAP DMAVPRINNITF*LLPPSLLLLLASAIE EAGAGTG*TVYPPLAGNYSHEG
3022	16923	A	3044	3	134	HLNPGGRGCSERPLRHCTFSWATE*DSV SKKKSKRGWTLGFI
3023	16924	A	3045	44	187	DPRVRQYQTFLEV*SGLIFAGLLLLSLP TLGAGITILLTRMLHTAVFDPDGGDDP ILYQHLF*FFGHPEVYIILPGPGIICH IVTYYSKKKEPFGYIGMV*AMISIGFLG FIAGAHHIFTGGIDVDTRAYPTSATIII AIPTVGVKVS*LRLIRPNLCRLTSPISP NPRGRHHYITNRPQPHRRV
3024	16925	A	3046	434	40	GAPPPPPGRRFFFLNPRDFTFFPPPKQK GFSPPPPPKFFSPALFFPGGGWPNSP PPQKNFFF*KPPEFFFPFLKKIIFFP PELFFPPQIIF*TPPPLFFFFFFFFFFF FFPPFFRGCKINFIVRGF
3025	16926	A	3047	1	399	LETGGGLTIVLTNSSLIDVLHDTY*VV PHFYGLSIGAGFAIIGGSIH*PPLFSG YTLDOQYAKIHFTIPIGVKLTFFPDHF LGLSGMPRRYSYDPDAYTT*NILSSVGS LISLTAAILIIFMS*EAFASK
3026	16927	A	3048	116	367	GASMLISSITFLECTVGGFVFSVYLFK QLILRQSSIMCVLFCFPERSCSVTQA GV*RRHGSL*PQPGGLHSPSSRDGHV

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3027	16928	A	3049	6	345	SQLLRRRKENCNLNGLGGGYSHQR*HQC PLAWATE*DYLKKKKKNFSLFKTGGFY PFLKKAPLGTTLSPKNNLPPLPLYKKRT GPNWNRKNFGKXKGGVIGLGGGKTIPK
3028	16929	A	3050	261	2	NKKSPFVNLMWKMGGFFFAKRVLSWK GGGGFFFSWRRSFTFVAQAGMQWRNLS SLQPRLPDLR*SACLGPPDC*DYRREPQ YP
3029	16930	A	3051	160	2	ICVDEQASQVMRYGLSQAPFPGLATLS CLSLMSSWECROPPPLG*FVFCPR
3030	16931	A	3052	89	3	PLTSGLLLT*QKLAPISITITQSPSLN
3031	16932	A	3053	344	2	HVEAPIAGSITVLAIVLLKGGVIGTIRLT LILNPLTKHIAPPLVLSL*GIITSSSI CLROTDLKSLIAYSSISHIALVVTAILI QTP*STFGAVILITAGHLLTSSLLFLCLAN SN
3032	16933	A	3054	266	2	FQPPISAYTKISPSLVNLSLLTSLTSLI IAGS*GGLNQTLRKLKILAYSSITHVG*I IAVLPMNMITILNLTITITTTAPLL LNIN
3033	16934	A	3055	3	32	KYNLSINPMIATITLLNLYFYLSPLLY **SSCPP
3034	16935	A	3056	3	33	KNNLSITPTIATITLLNLYFYLSPLLY **SSSPPS
3035	16936	A	3057	57	445	ANVWAPHGPAKLTKNDNVHWTSSKRLKI ANMTIKKLNEVIGLTLPDKTYVELVG* RQNAID*RKHQKPVKQSPKA*PHYSOL IFHWGAKANHGKDSLFLYK*CW*NWTIS SQKLNLTDLTNTFTKIN
3036	16937	A	3058	311	1	RVGLLLKINKISWPPFFFYGPS*EKEPL CFSGIQLFLTRTMVNLNLSPPVKTREY NKIAPFRELFPPFFKDRVSLCPGMSAVV *SOLTATSTSQASSDPGRV
3037	16938	A	3059	138	411	WERPWAQAEAVFNI*VSFAWAPPPLMEK QIPPDLEQHYRNVPGVNRNPPVSPFLR WSLTVQAQGVNWRDLGSL*PLLPGFKRF LCLSLLS
3038	16939	A	3060	1	189	FCRVGAQGLKLLTSSDDPASAS*SAETT GVSORAWSKITILKSSSFYFPNSCKMC FWLICLN
3039	16940	A	3061	3	406	DAWADANVLILPRFGRGTSHTVITYSGKK EPFAYIGMV*AMISMGFLGIV*AHHIF TVGIDVNTRAYFTSATIIIAIPTGVKGF S*LATLHGSNMK*SAAVL*ALRFFLLK KJKKRGAVLKPWGLPGCG
3040	16941	A	3062	451	82	PPPTNYFSPPPALKGGGGPPRPPPPPK WSPTPPPVIMPBPKKKKKFFPPRGM GPPEKIF*KPPPPFFK*KNPPFSPGPE NRGVFFSTKPPPPWPKKNFAAPGAPPPP PPPPPPPRGGG
3041	16942	A	3063	430	1	FFPPKOLIFWGGGGKSPFPKKKKFFPKK PDGVFFSPKKKKKKFFFPPLNLAAPKI FFKSDPPLSFLFFPPPPPPPPPPPPPP FFFFPLSVOTLLKRTAPPDOPPLD*EK APAPRPV*TEGMPAVNVAFAPPPFYKE RPS
3042	16943	A	3064	1	409	PTREPRESTYQGHHTFPVQKGLRYGITLF ITSEVFFFAGFF*AFYHISLAPTPOLGG

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3043	16944	A	3065	1	137	HWPFPTGITPLNPLEVPLLT
3044	16945	A	3066	4	426	HTFNFSIYQKATVIRTKVWYNNRHTVE SPEINFYIYS*LIFLFF KLEN*KNVLKEIKEDLNKQTDILFS*LQ RLITVRMSILPKLIYKFSAPIDQIPA*F L*IKIILKCMRKG*TRIAETLFFFFFL SQSFLSKLDHRGGITAMCTPPWAIRG KLKLLKKKKPPKTKPEKFFIQKATGAEG GVH
3045	16946	A	3067	411	187	RNLNVVPRPRTFVLLVKTGVSVQVGGG CKLLASKIPSPAPKSGWDYRGEPPRPA PRKFF*LNKEKIVGGPKN
3046	16947	A	3068	193	471	CCTCTKVHSGQKGTSTPLVIGELQIKIT LGCYYTPTLMAQIKKTDRTKCK*GYGAI CMLILCWRECKIVQSL*KRWQFII*LN ITYLAIKLN
3047	16948	A	3069	323	478	FFXFXFLFFLILXYFYF*KLFLYLFLX YIFKIVFYIYNFYIILFYIIFIF
3048	16949	A	3070	1	378	GTRRFFHSTITLLILGLSNTLTITYO*W RDVTRETYQGHHTPPCQGLLNGILF ITSEVFFVAGFF*AFYHSSLAPTQLGG HWPFPTGITPLNPLETPLLNTCVLLASGV SIT*AHSLIENNR
3049	16950	A	3071	201	2	TTPIDQLKRYHT*NFNFNFIFEIGSCS IAQAKVQWCDLCLQPTQLGLKSSSHLS LQSSWDYRHA
3050	16951	A	3072	261	1	EKAMGGGPFVKKSPGEGPTTKGWPLKG PLEGGQRGLTGPFKSNGRLFFPFGSNE VSLCCPG*SRTPDFK*SACLSLPKWDY RHG
3051	16952	A	3073	333	52	EIPKKKKGGGRFFNKRVPFRPRVSNR PRAQFFLETFFFFPGRGFFFFFETES YSVTQAEV*NYLGSQQPRFKRSHLS LPSSWNRYCK
3052	16953	A	3074	7	214	SQLOENRLNPGGGCGEPRSCHTCTPVWA TE*DSVSKKKKKKRGWVPPSLGGG KKKNPFENOGGL
3053	16954	A	3075	180	419	QKHLSTLHYLFKRDVFFFLKGSFVVSQ VGGQGHNLG*LKAPPRLTHFSCLTIRE TWKNRPYFECFFIKTGPHHVITRE
3054	16955	A	3076	371	208	QKLSGHGSRK*SF*EAKAG*QLVSG GRCSQWL*SHOCTPAWVTE*RLVCKR
3055	16956	A	3077	349	3	TFQWQKTYMCRSLCHPHFRTWTKKKR PPFQKGGDAPPYKXVQRGNPPPLKGR PSRGPPEKCKVFKAPVFLPRFSPPPFF PPPLFFFFFF*DRVLFCGWSAVAQLT ATS
3056	16957	A	3078	124	1	ISSETPAVKSSFWPGVVHACNPSTLGR *GKEITRSRDRDH
3057	16958	A	3079	205	1	CLVQNTWACVSHWRYIMSKGCK*RLGLM CVCVCVCVCVCVCVFCSCCCCCYC*DE LSLCHSDCSAVA
3058	16959	A	3080	3	413	GHTPTQVQKGLLYGTLIT*EGFFFS FF*AFYHSSLAPTQLGGHWPTGITPL NPL*VPLNTSVLLASGVSI*AHHRLL *NNRNQIIQALLITILLGLYFTLLQASE YFETPFTISDGIYGSTFFVATGPHR
3059	16960	A	3081	1	321	NSLNPDDGGCS*PRLHYCTPAWGTEDLS

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						ISKEKKYPYHVHPSMKMTIYNRQQNV NHIYIMLVEHSQTOENTCFMISGNFFFN LPVLGEKEKNQHSISFKLFFNF
3060	16961	A	3082	117	484	VLKYFIDSEVNAVLFSTISCSFVDFVL FFFPKGVSFCPPAGIKGGGFGFLEPLA SGFKRIFFPNPLEKWE*RARPPRGKFW NFFFFFLKRELFFAPRWEGRKILVYL KGPPWGYPHF
3061	16962	A	3083	381	227	CISRGGFYHLGAGLELLTSDPPALDS *SVGITGVSHRTRPLLLRLNQF
3062	16963	A	3084	2	391	SHAYHIG*PSR*PVTGALSDLLMTSGLA M*IDFHSITLLILCLLNTLSIYQ*WRD VTRETYHGHHTPPVPKGLRYGILFIT SEVFFFFARFF*AFYHSSLAPTQLRGHW PPTCITRNLLDVLLNT
3063	16964	A	3085	2	248	IMASGDRDHFC*HGETSLLKYRLLAGH QGMRLWSQLLKGCTADSHHHVLLILET FYSLRRRHILTSVPTLGMWYQADIR
3064	16965	A	3086	276	243	EKKPD*SRACPVLCRGNGQYSKGRCLC FSWGKTECDVPTTQCIDPQCGRGIC MGSACNSGYKESCEEAPRYIPEKE
3065	16966	A	3087	3	130	GFVHVGAGLELLT*SACLSLPKCWY RREPPRPAHTPPHS
3066	16967	A	3088	277	2	SSSVFCLLVMTSSSSSSAARLPPLTG FLPKWAIIEFTKNLSLIPTIATITL LNLFYFLRLIYSTSITLLPISNNVKIK* QFHTKP
3067	16968	A	3089	404	60	PSHGKMRFFSPSPKKIFFSPQSFYFLG GGGAKMPKKRFFFKTPRGFYPPP*K KKNFFPPPVKFGPPRGFLKSPPPFFFF FFFFFFFFFFFSPPTFTVHLMLKSD ND
3068	16969	A	3090	405	186	INKKPEAFINTVDQMLINSRHTFYFTA TACLSGAHRTFSRMDHV*DHKTSLNKF KTEITLSTLSNKHLEP
3069	16970	A	3091	371	1	SPPLVQKGLRYGILFITSEVFFAGFF *AFYHSSLAPTQLQGHWPPTGITPINP LEVPLNLTSVLLASGVSIT*AHHS LIEN
3070	16971	A	3092	263	3	NKRSPFVNLWKMGSFFKFAKRVKISWK GGGQFFFFSWRRSPTFVAQAGMQWRNLS SLQPLPDLR*SACLGPPDC*DYRREPQ YP
3071	16972	A	3093	1	392	FFFDKFKMFLINHSKMETTTYFELKR NEATASENC*DAVKAVLGKFIYLSSTII RKEERPRINNISFOIKHTKKI*+GEO KKKKKKKKVTGPELPKPLIVKSGKPPKV ILTGAWGPIKFLSPITRL
3072	16973	A	3094	3	367	EM*IEITMRYHYNTAARLKF*KTDNICK **GHGTSGLTYHQE*KNVQPLWKIV* QLL
3073	16974	A	3095	3	257	HEVSQDGLNLLTS*SAKLGPKCWYDR EPPCLAIILPDDCVIFQKLLHNNLL NLSCIDVLMGIYSLNSFSQSNFFFFFF
3074	16975	A	3096	189	414	KGLVMTS*CKMFFSLISFFFFFQRF FFAQAGVQGHNLSSLELPPLQKQFFCL TLPRS*KYRPAPPCANFY
3075	16976	A	3097	1	299	ENYRPTSPMNTDAKILNKILANQIQCS KRITHRDQVGLFGMQGGFYI*KSIIKSI

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						NAIHHSRLKKRNHMTPSIEAKKAFNTHS*FWKKKKLAPOET
3076	16977	A	3098	362	126	PIHTHTHTHTHTHTHTIYIYIYIYIASFQW NAIRGRMKCINKP*KDMEELKCIPLSER SQSAKATVLLYDSNVITLEKAKL
3077	16978	A	3099	3	423	RHEHAYHIVKPTF*PLTGALSALLMTSG LAM*FPHFSITLLILGLLNTLTITQ*W RDVTRESTYQGRHTPPVOKGLRYGIIILF ITSKVFFVAGFF*DFYHSLIAPTQLRG HWAPTGITPLNPLEVPLLYTCVLLASGV
3078	16979	A	3100	392	83	LRLNTNCGHGAPFINSPPFFQPLVKNSPA YFONKEKDVGKPPPPFRAPDGAFFPKKK KK*GLALSSRLRYGGMISLELLGSSDTF ASASRVARTTGQCHHAGPT
3079	16980	A	3101	81	247	GGWGGFPLKPLPF*KRTGKNFNPFFFKG KEKPPPNPRGGGKGGPKPPVIFPFF
3080	16981	A	3102	3	388	HEKKEFF*YIGMG*AMISIGPLGPIV*A HHIFTVGIYVDTRAYFTSASIIIAIPTG GKVFS*LATLHGNNMK*SAVL*ALGFI FIFTESGLTGIVLNSSLDIVLHDTCYL VAHLHYVLSIGAVFAI
3081	16982	A	3103	3	387	HERHEELSNS*ANMLI*LAYTIAFIVKI PLYGLHL*LPKAHVEAPIAGSIVLAAVL LKLGGYGIIRLTLLNLNPLTKHIAVPLV LSL*GIIITSSICLRQTDLKLAIYSSI SHIALVVTAIIQPT
3082	16983	A	3104	3	381	HEGSHAYHIVKPSF*PLTGALLALLMTS GLAWGFYFHTLLILGLLNTLTITQ* WRDVSRESTYQGRHTPPVOKGLRYGIIIL FIT*EAFFFAFYF*AFYDFRLGPTPQLR GHWPTGITPLNSL
3083	16984	A	3105	412	111	FLGHPLFRKKMGKKRGLPKMGV*HEPA PKGKPPPLKKKKKKGGGAPLSPSG GEGKKNPLTEGGGPKNPNSPPPPPGG KKKNPPLSPKKKKKK
3084	16985	A	3106	298	98	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF F*L*IIY*AICAINNIRGAGAEVLYSRD FVCY
3085	16986	A	3107	2	417	ATHVGLQDVTSPMIEQLITFDHALMNI LIICFLDLGALFLATKLTCTNM*YAO EI*TD*TILPAIILNMLALPSRLMYIT DEGDDPSLTIKSIHQWY*TYEYTDYGG LIFNSYIRPFLFEPGELRLLDVDR
3086	16987	A	3108	8	430	VGLVLFLSELPLNGGILTFHHGIYSFF PGGRTWALMVGWGLVMASTDLLGPLCH AFTPATQLLLNLAVASPL*PAALRIGCH SKTTNALTHFLPRGTPTTPRPIVTTIET MSLLIPPIAPDQRLAAGTFAHLLHL V
3087	16988	A	3109	3	453	PRAIKFYRDWEGHERKRIAWGDPCHMV LIKDEGLMCQKKKKKTPFFWAPKIPLV FPPAQKQGS*PNPPGGGNGPPLRGP RKPKPALMGPPSSPGGINPKSFFYLN GPAH*PGCN*LGVPFENLFLPLKKKIF LWGLRCSOT
3088	16989	A	3110	398	2	SLFQKNENPLVG*KKKGKALPGQFPPLF PPLGAGPGGSGRGNGPFRPPWGNFF

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3089	16990	A	3111	3	371	F*NTKIWPAGKGAFPSFPSEKG*AGGFF LPRGGGFLITQIPPPPHLGGKSKPPFQ KKKKIKRQGTSSWMQGWGPO SSDPPTSAPQGSSTTDMCHHHHAQLIFN FFVETGSCYVAQGVQWHDHGSLLSQTP GLR*SSGATYLVNAPALGPRRPDPTRME SLVLMKPRGLIRACPDCLVFWFSFF HEAEGCASEC
3090	16991	A	3112	233	449	FALFS*LATLHGSNMK*SAAGL*ALGFI FLFTAGGLTGIVLANSLLDIGLHDITYV EAFHYGLSIGAEFALIGGFH*FALFS GTYLLDQYTPKIHFTIIFGGNITFLPHQ FLQLGMPRRSDYPAATT*NILSSGG SFNAINAGSTT
3091	16992	A	3113	458	2	RGFFPPFPKPPFF*TPGKNFPFPFPG VFPPPSPPNFFFSPPPLEFFPGVPPIS PPPPKFSFSPQTPRRFFPPPPPLKNFFS PPPLFLPPPPFFFPFPFFFPFFFPFF FFFPFFFPFFFCDDLESELPGTGMACVI LLRANRKARTRG
3092	16993	A	3114	1	418	LNTTFYFDGGDPNLYQHLY*GHDP PDIHILPRGIRSHIDTDSYSGKKEPYAY VGMGWAMTSIGFLWLMVRARPLETVGVG VDAQAYSSFASITIAITPGAEVFS*LCP LPLSGMK*GGAUVWALGLRIFTCSGR
3093	16994	A	3115	1	425	PRINNTS*LLPFSLLLLLAYAVEAGA GTG*TAYPPLAGNYSHPGASGNLTIFSL HLAGGSSILGAINFITIINIKPPAITQ DQTLPLV*SVLITEDLFLSLPLGLAAGI TILLTDLNLSTTFDFPAGGGDPLVQHL F*FFDPAGGGDPLVQHLF
3094	16995	A	3116	2	383	GLSCTNHKDMGALYLLLAGRAGVLSTAL SLLIARLQGPYLLGNDHIYNDIVTAH AFVIIFFIVITVLGGFN*LOPLIIGA PFTAVRININIS*LPLPCLLRACAI EAGAGT*TVYDPL
3095	16996	A	3117	1	259	PTRALVVTALLQTE*SFYGAUILLIA HGLTSSLLFLCLANSYRTHSRILISQ GLQTLPLLIAP*LLASLANLPATPTTP HO
3096	16997	A	3118	3	174	LIRGGRGCEHRSRHCPTAWATRTALS QKK*KTTNPKKLCILFPFGKKKKLKG PDPFNKSMDDKKTARGMEDSSSFCFFK RDRVLLCCPGWSAVAQS*LTAAAS
3097	16998	A	3119	155	1	PPKFFFPFPFPPLGEGAKTFFPKRTF FLKKPGVFFPPLKKKKFFFSPP*FLA PKIIFKRPFPFPFPFPFPFPFPFPFP FFFPFPFPFVLVFLVQVKVHLKCFN IQFPLASDNS*PSMHEKFYCESNIEF
3099	17000	A	3121	48	387	RDPVLQKKEKKKKKFPNQKKKKKGSP F*KIP*GAKIKPGKEKNFSPKRGAKK NPGNFEEKTNFGGKKWGPFPKN*RFK GKKKFLKGGKKKTQIPWGLKIFPFGFD
3100	17001	A	3122	237	2	FPPVVLPPFLKASSSP*SL*FLLGWGF NLPSNPKGSFPKPSWFLFRPP*GKNF YLALPR*PWPQGLF*LAPP
3101	17002	A	3123	448	130	PPRFFPEFFYSGPPKPPFFKTPVFLGK PGVFFFSYQKPTNFGPKMGAL*RIPL

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						FETPIWVFPKGGHKKKPPVLN*PPTRK PPPDKILKKKKDDCISRLARN SSAREGGGVPPPPKIIFFPPPIFSWG GGCTKSPPPREVFPRNHGCCFFSP* K RGKYVSPPPRMGPDPGVFFKPPDPNFF FFFVFFVFFVFFVFFVFFVFFVFFVFF FFKAFRMSPKPVPPFFFCNRYVVRPR VRPRVRPRV
3102	17003	A	3124	453	3	
3103	17004	A	3125	443	2	YFPFFGRVINGDSLGAQVLPNPPRHKGT PFPKKIIRSIPGWSGGPPLPPQORQMW GGPPPLFLGLFRPQGIKIPFPKKIKFP GGVCVGVGVCV*KKKKNPFPFLWAGLK EPCFFFFFMEFECSCCPGWSAMARSO LNCNLHL
3104	17005	A	3126	3	186	PVIYSTIFAGTILITALSSH*FFT*VGLE INMLKKKKKKKKKKKKKKKKKKKKKKR GGG
3105	17006	A	3127	171	38	KKKKLFFPPREKGGPPNFKRAPPPFF FFFVFFVFFVFFVFFVFFVFFVFFVFF
3106	17007	A	3128	16	189	ILGEVIVW*FF*FKKKKKKKKKKKKK KKKKKRGAFFKTPGGQITPGEKKKIF SL
3107	17008	A	3129	401	85	LVNFFSPQEKRGFFPPPPKNFFFSPRG FFFLGGGGIIFPPPKKFFSKNPGVFF SPP*KKKIFFPPPLFWAPPRFFFKGPP PFFVFFVFFVFFVFFVFFVFFVFFVFF
3108	17009	A	3130	2	312	ANNLT*LAYTIAPIVKIPLYGLHL*LPK AHVEAPIAGSIVLAAVLLKLGYGIIRL TLILNPLTKHIAVPLFLVLSL*GGGVF
3109	17010	A	3131	449	3	FFFVFFVFFVFFVFFVFFVFFVFFVFF LGGKKKKPPFF*NEQKPLVGLGAPPP LCFIHKKKGGGKFFSPPL*KGDFK KFFVPPPPKGPPLPLKNLGRVFFKPP PKKKALSFFKKKKKKKKKKKKRAAR DLELADAW
3110	17011	A	3132	95	448	VINRE*KCVC*MKKKKKKKKKKKKKKK KKKERAGKGGG
3111	17012	A	3133	60	442	LGGFFVFGGKGFCLWCPRWGAKAGI PV NGTTPRGV*RNFLAQPP*EGGITGPPPL FQ*FGFLRENGVPLRGGFEPPLILGEP PPLPPQKGGKGRNPPPLKGFVLVFKK EFSSLVPSWKARGDP
3112	17013	A	3134	236	45	FFFVFFVFFVFFVFFVFFVFFVFFVFF FFFVFFVFFVFFVFFVFFVFFVFFVFF FFFVFFVFFVFFVFFVFFVFFVFFVFF FEATIMGV
3113	17014	A	3135	441	88	KQQTTPGLIFF*KAPRREIFLPPPIVVF FSPSPSPKFFFLSPDPIFGVLPFFPP PKKGFFKKNRRVFFCPLKKKNFFFLP PFFFGPRVFFYPPIPIFFVFFVFFVFF FFFVFF
3114	17015	A	3136	2	328	TMLSPKPOOLNQONCSPEHYEPQLKTOR TW*KKKKKKKKKKKKKKKKKKKKKKK KKKKKRGGGOKKKMVGGEKKKPG*KIFF FFIKKVKKKTALGDKKTOFWGGS
3115	17016	A	3137	281	2	KATKSGTPIFSGGQSLAWSWAGISGAQ PALLHS*PIGKIFKNCMEVGRKSPQLP RNTSWQLGAHVPSNSTLGGRGGRITR

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3116	17017	A	3138	448	3	SGVRDRTRG FFFLPPSPFFPY*KRGSFLGRVVFNP PPVFPFPWFSQIFGFQALILPFPPLP FSFPVGFQTALFFPFGFFPFGFHLFP LLRFPCPRK*VFVGGFPPFFFLRDKVS LCHPGWNAVQSEFTTALTSKAQATRP PTRPTPTP
3117	17018	A	3139	2	436	DR*LFTNHKEIGTLYLLFGA*AGVLST ALSLLILAEGLQPGNLLGNDHIYVIVT AHALGKIFFIATPIIIGGFGN*LAPLII GAPEMATPRINNIS*GLLPPSILLLLAS AIEEAGAGTG*TDYPLAGNYCHPGASG DLIIF
3118	17019	A	3140	362	2	KPRGKFFPPREGGGGFPFPPPKNFFFF KGGKFLGGGGKNSPPCKGFPFGNPGS VFFPPPKKKKNIFFPPGKMGAPGFF*R GPPPPFFFFFPFPPFGSQGVK LKSPKCKL
3119	17020	A	3141	440	102	PTPPCCCKFSFKRPPKKTLLFFPTNLVE FSDIPP*NFPPSQALIFVGFAPLIFPP OKKFFSKFPLFFITPPLIKFFVPPPP PFILSPLKIFYKPPPIFFFFFSSP
3120	17021	A	3142	1	79	EKLDYFSIIFPVALFVWSTIEFSL*Y INSDPNINQF*KLDYFSIIFPVALFVT WSIIEFSL
3121	17022	A	3143	3	441	FFFFPPLKKKKFFPPPPNIPGPKSL*K PPPPPPFFFF
3122	17023	A	3144	223	3	LPYKLYPLK* **LQTNQESRG*HFL RPRPFKNQMSGTVAHACNPSTLGGRG RITRSGV*DHPGQHGEI
3123	17024	A	3145	63	414	KKKKKKKKKKKKKKKKKKKKKKRGGP PKKKTTRGGQPNPPPKKKKFPQGGKKK PPLGF*KKTPLGGEKIPPPPKKNTPP KKKKK*GGGGTTPPPPPGKKFSPPRN KKKK
3124	17025	A	3146	410	31	RANQAFRKGKPLCDLAVGNKLSRTQIA LTI*KWINWTLKLRTS*KTPIKTIK RYPFEGEKISDEELYLYQ*KVL*IGKKK PNNPVEKWNALKRSFMKGNILTVFKGM QR*LGSMHICSL
3125	17026	A	3147	182	241	SHPSHSTNTNTKGLL*TLPLTPNPLV NLNLGLLILATSSSLAVSYL*SGGASN SNYALIGALRAVAQTSYEVTLAILLS TLIRGSFNL
3126	17027	A	3148	254	1	KTKKGLTKDPLTRF*ISVC*ITKSI*F FKLLPFFPLLKEHILPKLYFFFLFET EFRSCCPGWSTMV*SLLTATSTSQIQAI
3127	17028	A	3149	499	2	NTPPAAGGGCGGFFFFFGKKNFPPPHPT RFFPPPLKNFFFSRVFFWGGGAQKA PPPKVFF*KIPRGFFFPKPKKIFFF SPGFGAPPGFFLGGPPSFFFFF FFFFFFFFFFFLLINFLLSLQGGF LVSKELFLGLTVKTRFRGCGQ
3128	17029	A	3150	256	146	KNKAVTQVCPEFNKGPG*HTHTHTHSHT HTHTHTLQ
3129	17030	A	3151	333	1	TISCLTRGHEPLSPRRAGPYTGSPLHC CVDVVDKVFSSWKDLTDWPLGDLIDIEYF TDGSSFILRGVCRAGYAAVLDSAVEVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3130	17031	A	3152	43	379	SVSAETSA*KAEIATLALTRALWLGKEQK NKTSLPFWNDYIIEWGAPEPETPPKRAAG ALHSLAQPFSSVALPPECFFDPCAPSLSPG *HALRPLPLCLASSIQTAPSHVPPKS LSPAPOPCPIPTLVNVSQKTPP
3131	17032	A	3153	398	12	NTTFGGGKFFLKKTREERKFFPKKKRGF FPFPPPKFFPOGONFFGGGGQGISPP QKKGFFQKNRPGVFPTPPKKKIFFSPP GKMGPAGGFF*RGPPPPPPPPPPPPPP FFFFFLLKKSRLAI
3132	17033	A	3154	371	105	SFSPQVNFIKGPKFPFPK*IL*RAPNPP LPKKKFSNPPTWGPQPPPKSKSFAR FPFLPPFPFKKPPKKIIFFTKEGT I*KNPPFSQFSPDSIK
3133	17034	A	3155	3	371	DVGADPILHISTGL*LAMQY*FEA*TAF SSIAHIT*DVYVG*VIRYLHANGA*IFF ICLLHIGRGLYRPFYLSKT*KIGLIL LLATITTAFIGVYVLP*GPI*F*GATVMT NLLSAIPYIGT
3134	17035	A	3156	1	398	IAITPTGVKVFSLATLHGSNMK*SAAVL *ALRYILFTEGGITGTIVLPNSSNLVL HDPYVVAHFHYVLSIGAGFAIGGFIH *PFLPSGYTLDTQYAIHFTIFIGVNL TFPQHFLGLSGMPRRYSVDP
3135	17036	A	3157	401	46	PGGRNFFPKKTGPKKIFSTKKKKGGFP LPKKNFFPSGGFFFGGGGPNFPPPK GFPSGNRPGVFFSP*KKKIFFPPG*I WAPPRVLKGPFPFPFPFPFPFPFPF KKSVIA
3136	17037	A	3158	404	18	FFSFPFPPPGGVFPFNKNKFPFPFP PFELGGGPPPPPPP*FPFPPFPNPF FSPPKKGNFPFPFGPPPPPKDPP PPFPFPFPFPFPFPFPFPFPFPFP MEKGRPRGDIGSNPPS
3137	17038	A	3159	3	192	SLVIAGCPR*NLSSTLNLETPSKSPCK FNC*KKKKKKKKKKKKKKRGALKKN PWGGKK
3138	17039	A	3160	205	80	VORDNFGFLQPSFSGVKLF*FCLSLPNKW DFRCGPFPNG*FFS
3139	17040	A	3161	3	384	LIVPTIILLPL*LSKKHII*INTTTT LIISIIPLLFNQNNLFCSPPTSSD HLSPILKKKKKKKKKKKKKKGGGA FKRTPGGAHGGGGRETF*PKGGEKKN RPGVFWQTFWGGK
3140	17041	A	3162	348	70	GPPPKRVFSKTPKVLNPKPQKKKKFI FPPPNVLGPPKNFLKGPFPFPFPFP FFFFFYFFWGCDS*CSWRHSSPPRLSG TPKCSPSVT
3141	17042	A	3163	2	353	LKTIPLTSTCLTIGSLALAGIPLTGFY SEDHII*IANVLYNNA*LSITLIATSL TSAYSTRIILLTGYGPRFPTLTNIETK KKKGGPFNRYPLGAQVYGGQNEKFFLI GREII
3142	17043	A	3164	1	221	PIRPRDCSELRSCHCTPAWATEGDSISR KKKKLSTRTAF*YTEAINSILYSLNIGT FKTYFPKIKTYDRHDF
3143	17044	A	3165	26	383	IFPY*SLI*YTRKKKKKKKKKKKKKK KKKKRG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
3144	17045	A	3166	251	381	GNLCAGAWRLTFVVPALWEAEAD*SRG QEIGAILANTVKPHL
3145	17046	A	3167	391	115	LFKKISPHAGIWFSPSLTP*NPFFSLE PFIFGRGLAIFPPPK*RFLSKNPVVF IPPLMGKPPPPPPVRLGPPIYSFKGA PPFFFFF
3146	17047	A	3168	94	389	SPGILGQKGQIGPIGNHVGGLAAPVTP *FRFKPRLP*GFGPKASPPALAKPERAQ VGTPPPGPRGPNQPPPFKEQGLGF RFRGKLAEKRGFHL
3147	17048	A	3169	3	363	WATALQGQSQSETSQSKKKKKKKKKRG GPPPPFFFKKKIFSPSPGARNKRGKF* KPKKKKKIFPPPPPLKKKKKKKKKKK KKKKKMGGAFLKKPRGAPPPGKRLI FFFLKGV
3148	17049	A	3170	2	171	KEFLGYRMV*AMISIGFLGIV*AHHI FTVGIDVDTRAYFSATIIIVITGVKV FS*LATLHGSNMK*SAAVL*ALGFIFLF TVGGTGIULTNSLSDIVLHDVYVVAH FHYVLLIGG*FYLYRHNHCYPHRRQS I
3149	17050	A	3171	390	27	QSLTVKSPYPVIVILIKTKGHH*VMNGL TRYQSLCENPHIRSEVCITLNPPLLP VSESPVKHSCVQLDSVYSSGPNL*DHP *TSVDWELVVDGISFANPCVKSLKMTS PAPVTPRS
3150	17051	A	3172	127	310	KNPGGAKILRGGERKNFFLKRGGRKKHL GIFGKKTFFWGGKKWAKPK*WRFFSPF SP*KFFFSLKALIFFGGCPFFSPPKKS FFSKNSQVFFSPFPFKEKIFPPPPP*NF GPRVFLKGGPPPPFLGVFFPPPPF
3151	17052	A	3173	376	3	FFFFFLRRQSLAVTLAGV*RCNLSSLQS PPPGIK
3152	17053	A	3174	365	14	RENFFSPGGAPKKNPPPPPPPGGKKK IFFQKKKKKKIFYPWKNPPPPPKKKKK P*KGGLKSGGPPFFFKGNLPLWGPPI SPFKKKKKKAKTVQERKYNSTQLVSA ETOLL
3153	17054	A	3175	1	377	VPLHSSLGKARLLILKKKKKNDPFLKN FGPLALLGQWGVN1KGLKQKGNPAPS AHTGGCGFSLRGRNTFFPKRAEGICYN SPH*KET*KALEPRGYKGL*QALALPNL KSGKMEHILRGAP
3154	17055	A	3176	352	125	GHEVLDSDDLPAASQSGITGVSHHAL *EILLSMFETTWACDLLFQNSIFKSSI PCFIGHLDFIMPHRYCRFF
3155	17056	A	3177	139	366	TAHTS*GY*VKNYINLSCFPPFFPLERN HSAIQPGGQGHNRSSLQWPFGKQFSC LSLPRSDNGLVPHQLVNFF
3156	17057	A	3178	206	1	KGTLFKKDDFFKNPKVFLGVPKNSLF *KILTLPVLNYPYFFFFFTVSLCH PGWNAVVRLEP
3157	17058	A	3179	330	1	IVSTLETCTYIAYNEEKDTFITLRIYVI GGNGKFLGI*IKQHKIHHQDQVGIPI GMQGFN1CRSINV1HHISIRIGKSRQA WLTPVIPALWEGDAGGSPEVRSRPA
3158	17059	A	3180	3	399	HASAPLQSSLDGYRARPCKRKKKKKKGG GGGGFFFPKGGGPIPLPKGFFSGKGLG KWGLGGAGKTPGKKPLGKPPKRGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3159	17060	A	3181	2	204	KGQKGPHF*KKKKKGGKKLKGFF*KP FKKPLLLGRGVQP*NPHLLGG
3160	17061	A	3182	71	377	CPTACPFW*NKELLPKKKKKKKKKK KKKKKKKKKRGAPFKNSLGSPHFPGAG KKNFFFWGGY
3161	17062	A	3183	151	2	EKKGGQKQKKIINGPPPPGAPQKGMGF FNRGRGKKQITFFPPPPPEKKKPPFF* KKKKKKKKKNCSD
3162	17063	A	3184	152	387	FFFLLEELVPLLLKLFQKIEEGCSPSNF NEAFIILPKPFR*TTKKNF
3163	17064	A	3185	22	336	YFQGFYVACICTSFLFFFFFLKRFEC FVTQVEVQGNFT*LNPLFLGKKFECFL TLQIGWNNRPLPPQVIFCFK
3164	17065	A	3186	344	1	YEKCTALLQMVSSFIWMEREGTHOYSFY RKDFSLASKVNIVSYLSPIVE*FFFL RGSPFAPQAGGQGNLGSWKLPPLGLMP FSCLTLPGGWNCRPPPPGPN
3165	17066	A	3187	296	1	WVLKKIFFYFGRGGGFFIIPPLGGQGG IPWARGF*PPRGPPPKNGF*KKKKKRG GGPPPGFPPPGGPRGGVFFFLGGGGPRK PKKITKKNGEKKKTSKPNQKRTKIK TT
3166	17067	A	3188	2134	1	NPKKILTLPKTKVYKCEGENQVPYII FGIKNIFWKGIF*PKKEREVCV*SMRHI VPVFKKRGSKRSNKSCKYKDTCTRMFIV ALFTIGTKWKQPKY
3167	17068	A	3189	1	159	GVAHAACNASILGGQGGRII*GWFEBS LANMVKPC
3168	17069	A	3190	119	340	LQDHPG*HGEFYSIVKICLARHGSRL *S*LLGRRLQRKQETCLNPGAR
3169	17070	A	3191	75	1	QIKKNRLVSRGKQKNKK*IKP*VDIF FKEDIQAGKQMKRDLISLIEIQIKT TITCYLIHARMGTITRD
3170	17071	A	3192	343	1	LSVNNFPGFTVAHACNPSTLGG*GG IFILGGGFCSPVFFGFGGGGGFFFL QNFFPPRGKIFRDPFF*KKLKRPNMGF F*NFFNPPLGPFNLFFFFFKKKPNKFF LGGFFFFFFFFFFFLAGDLSLSPRL EC
3171	17072	A	3193	105	368	KFKDPFFPPFFFPKQLPPPPGKIGA PHF*TPKGGPPPKKKK*KKKILKGGR KKKKTPPKRPQKIWGPSKKKNPWGGK TPPL
3172	17073	A	3194	1	365	FCRDEVLLFCEDWSPTGLKQFSLCLP KCWSYRC*PPYPAQGVFLK*HLTKSLSC LKLFMASLCLQDKVPAPQCVKGLSKFF LCHLLSTLIPFTHSLFFFLGWFRLQHR SVTAQGVQR
3173	17074	A	3195	1	362	GNQPKRLNAGTYLLFTYLEGSVFLILAL MYTHKTLWSLNLILLTLTGQELSNC*AN NLI*LAYTRALIVMIPLYGLHL*LPKHA VEAPIAGSI*LAARVLKIGYGIIRLTL ILNPLTNT
3174	17075	A	3196	137	3	KGQPRFPFISLKKGSQGGKGGFFFF*Y RIFLCPHGWCPVVQSW
3175	17076	A	3197	1	266	EGRGCSL*SCHCTPA*VTVRYPVSKK KKKKKGGGKSKKGGENTLFGPKRGK LRGPQKRGKKIGPEKKVGNLKKGFFR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/51,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EKTF
3176	17077	A	3198	217	446	YWSERYAMTQVLEGFSYSLQDHFYFCFR SIRRII FYSLIKPS IND*GERELEPITT SQALQIAGRAGRFSSRFKEG
3177	17078	A	3199	345	314	QPGPEGKIRFFFLKIPNLTPSGGKSLKFP LFKRKVPENCLSLRG*GCN*PI
3178	17079	A	3200	2	330	SRHYTPAW*QSKTSLPKKKKKKKKKKKK PPFPKNTQKKPKKKRGLNWGKTPPP LKTQKMGISPGKKLKKNLFLPKKKKPEG NPLF*FRGF*KKKAPFKKKKNPPK
3179	17080	A	3201	2	385	PPFLGGGPQPKFLKFLFRAN*NLGLF FLGGVLKKIPLRKPFSFLWIKPFTPPPK KKIFFKTFFQKPLFF*KKKFFCFPPFP FFLGGGFVFPSPKKFFPPFFFPFL
3180	17081	A	3202	355	2	FFFPSTESCSVAQNGVQWHYLGSG*ALP RPTP
3181	17082	A	3203	156	1	LKSLLEAKVGGCLLEVRSSRPA*ATWRD FISTKN*KISQVWYLLVVTWTE
3182	17083	A	3204	352	175	QPRGRPAFAHPP*CPRLRLFC*CPCPA CCPPWAEASPSGVQASFAAPACPARAL LNE
3183	17084	A	3205	280	373	QRGTRIFSLQI*KKKNKSPFKILLD NALGHSRVLTERTYKDIRPANTISFLRP MVQELIPTFOS
3184	17085	A	3206	1	367	ETESIQIDGHTNKFLGLHLTYLTREVK DLCKKNYTKLKEI IDDEKYDMLMD*N NIVKMAILPKAIYRFDITSTKLLMSFFM ELEKIF*NL*KA*MAETTISKONKAGG ITLLDFKLYY
3185	17086	A	3207	368	12	FAQKKKKKKKKKKKKKKKKRAPPON* RAPQKPLKPPRVFLIPPLGSPPPAF FWRGGGPPPGPFSKKKKMRLTGGGRLF LLA
3186	17087	A	3208	2	356	KYLFSSIPGKREKMGIANLFNETISEN CPSLARDLDIOKTRHANPYNLKSSPOH IIVKLSKVXKERILKTARKECFITYKR TPIRPGMVAYACNPSTLGG*GGWIMRSG DQDHPG
3187	17088	A	3209	359	170	INIKQLPCGGTCLWSQLSRRLRRQDCY SLGGGQCSL*SSQCSPAWATERDSVSK YKINFL
3188	17089	A	3210	295	122	VIKTV*NNWKNRHDQCSRIESPKIHLH IDDQLIFDKDKVKTPE*RNGLFNKWCWE N
3189	17090	A	3211	218	466	ATFDTTLPSQYONAPNNRFDSDL*EGE IDTNTVNIILRLSLNIIVTNPYNI*HH QHDLDYTVDDTGLQVNCAYFINLQ LGLQG*REGNFGSLQTSPPGFKRFSGLS LLSSWDYRV
3191	17092	A	3213	254	40	WPGTMAHACNLSTLGG*GGCITRPGDRD HPG*HNWNN
3192	17093	A	3214	198	25	YNEKEKPVKMLKIANSLGAVAHAYNPS TLGGGGIRIMSGDRDHPG*HADAWVET VL
3193	17094	A	3215	376	3	PPGVF*RGPPGFR*LPKSSSSSSPPFKI LGGPPFLAFGGAPPQKPPSSSSSSASS PPSSSSRAPLKKGGPFNPAGGFPLFGGP PRGGPPFSSSSSSSSSSSSSSSGRRR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
3194	17095	A	3216	393	260	SRTSRTGRTRTG VSQDGLDLTTS*STRILGPKCWDRREP PRPACTLCISSTYNDP
3195	17096	A	3217	3	387	HASASSGSRAPPPFFFNKTKGSKELET TRGTVLTKCLFFKKKKKVLGGPKPLGN PKGVGKPLKGGPGPNWPPPP*KGPGCHF *KNGF*DPGPKKSHIPSWVGKGSSLLP GPLGGPSSVYFSLRA
3196	17097	A	3218	77	406	KMARPELGLGNNLSNDHIYNGIVTAHA FVILFVITPINGGPN*LIPLIIGAP DMAFPRININIS*LLPSELILLSASIV EAGAGTG*TVYPDLAAGNYSPOASV
3197	17098	A	3219	394	2	KRRYFPDGLNFWGGLIKTIVKRVSS LKKKKKKNPPFVLQWGGNKNFKGGGL KFSKNLI*FFFPQKEAR*KVFFFFPRS PQKDPLEFFFFFLRQVSLCHPDWSAVA RSQLTASISRAQAGRV
3198	17099	A	3220	376	157	KFFFSF*KFFFSPLKFGGGVGTIPP PKKRRFFKNPQGVFKPKPQKKKIPFP PVNFGPRDELKGPFPFFFFFFF
3199	17100	A	3221	394	1	VPPQKFKTGPDPPPPREFFFFKKGPF PPLGGFLNPAPKNPPPGPKKVGPGPG PPPPGGFFFSPLSF*NGERVFFGPKI PKRFKLLKWKGGKFPFKKPIPPPPKK KKKKKRAARDLELADAW
3200	17101	A	3222	207	402	SILM*LCCLFPLPGVTFIDGAPHSYRE CYPVLLDGMVGWWDKDLAPGIADSLRH FKVMREKRI
3201	17102	A	3223	309	3	YPPFHLIDLAIHVCVCFTRFYKATVQT AWSWYQIRYIDQ*NGTEISEIPPHIYN VICDKHDKNQWGDLSFNKHCWEN*LA ICRKLKLDPPFTPYAKI
3202	17103	A	3224	3	382	LDREKPPFFWGAHMDIPQLVNLINK GHWANFNFLGYKKKGGEKKKKKKKK RGPP*KKPPGGPK*PPGGR*IPYMG GKKPKPGGLEKPPPLGGAHLGNPPQK YTPPGKKONLKRET
3203	17104	A	3225	133	2	FFETESHVSITRLECSGITISAYCNCLP GSSDSPASAS*AAGT
3204	17105	A	3226	349	2	AGVPFGNPLWGGGGSPRGGGLKPGF PQRGNPPFFKKSQTPPGGGPLLIIPPW GGGAGGSLPQGGQRFQ*TKTGPSPRG KKKKPFPKKKKKKKRKESEMPGFMV LNA
3205	17106	A	3227	3	239	LNKVRGCSSEPRSHCTPAWATE*DSIS EKKKKPESRGILKVKGLTQALFYALW LYLHLPTAQIIGWFIYFSKP
3206	17107	A	3228	205	1	IGLKIQNSCLPKDSLKTKRQATDWRY LQNTSDKASVFIIYKEHLQLSNYKAVDP IK*WAKEMNKLH
3207	17108	A	3229	174	1	VQMLEDKSFETP*FSSETLVLKIPIHVQ PGAVAHTCNPSTLGRGGGRITRSGDRDH PG
3208	17109	A	3230	2	340	KNHSVYLLCVFSIPPTFCFF*FVFNT F*FKLN*IN*FTYIDRVLLCHPGMSAVA *S*LTAALNSWAQAVPCLSLLAHHHAW LIIFKKTAYIIHWWVYVYDTTYPFKVIN S

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
3209	17110	A	3231	1	313	KKSTPYQGFDFIPSPARVFFSIKFFLEA ITFLFDELDALLIP*ALRFIFLFTV GGTLGVVLANSSLDIVLHDTYVVAHPFH YVLSIGAVLAIIGGFH*FP
3210	17111	A	3232	207	355	ELSPFRLKRTLY*LGWVAHACNPSTLGA RGQQA*AOEFKTS LGNMAKP
3211	17112	A	3233	3	355	TTQO*LKLTKQTIATHTKGR*ALT LISLII FIATTNLGLLPYSLTPTTQLC INLAMAIP*ADAEVIGFRSKIKNALAH LLPQGTPTPLIPILVMTINLLIEPIA LARRL
3212	17113	A	3234	2	355	KYLINNRLITNQO*LKLKTSKQMITHN TKGR*SLILISLII FIATTNLGLLPY SFTPTQLSINLAMDIP*SGAMVIGFR SKIKNALAHFLPQGTPTPLIPILAIET ISLII
3213	17114	A	3235	43	370	QGCVKGNVLEEQVRNGLWLDSSSEKTDL KQSGSPGSGWPEHVGGSGVMG*SEAWT QARWLTPITALWEAEGGSLRPGVQWH NLGSIQPLPPRFKFSYPSLPSWD
3214	17115	A	3236	15	356	LIQPSLKLMSIHTKGR*SVILSLI IFIATTNLLGLRPLYFTPTTOLSNLMS VIHL*AGAMVIGFRSNIKNALAHLPQ TPTPLMPILVIEITRPLILPIALAVRL TA
3215	17116	A	3237	1	376	GTRINTLTIYQ*WGDGIRESTYOGHHTP PVQKGLRYGILFTISEVFFAGFF*AF YHSSLAPTQL*GHNWPTGITPLNPLEV PLLNTCVLLASGVIT*AHHS LIENNRD QIIQALLITIVLG
3216	17117	A	3238	1	358	GTRNG*YTNA*ALSITVIGASLTSAQGS RIILLTLTGQPRPTLTININENNTLLN PIKRLAAGSRFAGFLITNNISPGCFPQT TIPLYLKITDLGVTFLLGLTGDLNLYLT NKLIIKA
3217	17118	A	3239	258	390	RQGLLMLAGVLNWSPLQSSHLPFFKCW DYGREPPCLGN*LIL
3218	17119	A	3240	2	372	ARARFHHVSRDGLDLTL*NTHLRLPKC WDYRRFELRPGKTFPFLKKKKNSIFLF RQFKKSLIGIKFRPTGGVLILGNH QNGCKTGLVPSRPGGLAFKICGLWA HDTPHRVNWL
3219	17120	A	3241	3	283	HERLWGWKTGAAGLQRTSSRPASLTQ T*TMTH*SRITGCTGSGRTWRSRHS CAWGMAGLYRVAVASRGPRGM*PTPFH WLCWAMKVP
3220	17121	A	3242	170	3	IKSQAGLVGFLGPFPSQDSNLVVFVGF FCF*DRVSFCSPGWSAVQSEPTAALV
3221	17122	A	3243	2	385	ARADVTPSYLTSIDTMRDITPGGQVFS *LSLTHGSNMK*TAAPLLTLGFI LFTA GGTLGLELTNSWLDIVLHDTYVVGDFH YVLSIGAVFAIIGLLH*YPLFSGYTLTY RTYAQIHFAIIFIGN
3222	17123	A	3244	1	106	GTRYVQAHLKCLTSSDSPASTSQSAGI TGVSHSA*PASTSQSAGITGVSHSA
3223	17124	A	3245	2	360	ARANTLTIYQ*WSDVSLNTYOGHHTFP VQKGLRYRIILFITSEDFYFGFI*AF* HSSLSPPTQL*GHNWPTGITPLNPKMP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
						LLNTSVLLASGVSI**AHSLEIENNRNQ LIQALLT
3224	17125	A	3246	17	160	GG*GCSCSEL*SCHCSPAWVTEQDFDSK KKPAI LASCLKHLNPLSSH
3225	17126	A	3247	236	2	WAHTVMTLSPSPSLKPVQ*KNFYIVST YSLDN*NPSSPKAKRAPKSYTLPYLHL CVCVCECV*CVVCVCVCVCVW
3226	17127	A	3248	2	2220	FFGGGRFSPFGGYLLNNHSSPSPVKL NPGPA*FYPPPTGKNFPFPQR*DSPPKN IKTPPSPFFSS
3227	17128	A	3249	2	372	AYTISFIFGRISFYGLH**LPAKAVEAPI VGSIVLAELLKLGFGFIHLTLIFNPL TKHIAYPFLGSL*GISITSSMWLRQTD LKSLIAYSSISHIALVVTAILQT*SF TGAFLLIDHG
3228	17129	A	3250	293	56	EGSPKVI FNKSPFHHLEFLFFFFFIFF *FFFFFFF*FFFFFFF*FFFFFFF LAMPVLSFFFKQDNQRYQYSIK
3229	17130	A	3251	169	370	LKMTLELRGAPASKPRGQEPFPHYFCHH HHHHHHFL*VTKGGQPHWPSPTRDPGW L*SPS*EDQRR
3230	17131	A	3252	22	156	GERIGLGLGQGCSEP*LCHCTLAWVGD TVRPCLKKKKKKGPPF
3231	17132	A	3253	3	400	QNGTFLD*GGLITAVILLLYLAVLTGG ITILLADRLDSTLFYPAGGGDPILOYH LP*FFGHPEVYILIPGFGIVSHIETNY WGGKEPPFGVGMV*AMIAMFLGFIG* HHIFTVGVDVHTA*FTSAT
3232	17133	A	3254	373	31	REVGPPTP*KIFFPKGLNTWGGGGPKF PPPKKKGFFKSPVGVFPFPPGG*KSGPG PGFKKPPQKGKNI SFAGGKIGPPRGT KRAPPFFFFFFFLLWVVQVER TL
3233	17134	A	3255	1	379	LNLTORQ*R*V*KFL*LPQT*KKKKK KKKKKGAGFKINLKGAKTNGCRKKKIF FLKGGVKKKAGGFKKRGKKKCYLGI FEKKPFFGGKKNWENPKKIKGLREKKK F*GEKGEKKPEKAG
3234	17135	A	3256	42	376	FCVISLVHHCITNDLSFERKKNI FVPGQ INSISSIA*EAHCNKSLHLHAVKKKKK KKKKKKKKKKKKKKKKKKKKKKKK KEGRSSLKKEK
3235	17136	A	3257	353	67	CYPLSPLKFFFSRSLKFWGVGPITSP PKKKVPSONSQEAGFPSPNVLKRRPGFN FKTTP*KEKKNPFPVPVKGPPKESLKR PPLPFFFCGLQ
3236	17137	A	3258	2	129	FHRISQDGLDLLSS*SARLGLPKCDYR CEPPRPAKNKILLS
3237	17138	A	3259	205	415	QOKNRRLHLHFKGARTHNSYNGQPTPS ITAHMYPRLRQSHYIVLRVHH*VPSA IEGVVSV*ALLHSTIVVAGNLLIRFH PLAEKSPLIQTVTLCLGANTTLVAGGWA LTQNSDKRIAAFSTSRGLGLI IVTIGVN QPHALLHICTHAFVKAILFMCSGSIIR NLSREQDIRKIGLLITIP
3238	17139	A	3260	3	393	SFNLSLTITQEH*LLPS*PLAI*F ISTLAETNRTFPDLAEGEAEVLVSGFNIE YAAGFPALFLIAEYTNIIINTLTITL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						LGTTYDALSPELYTTYFTVTKLLTSL L*IRTAYPRFRYDQLIHL
3239	17140	A	3261	2	400	ISDLSEK*FKRLVVKVIMEAPERGAQC KEIQKMTQEVKGGEI FKE*IA*RKKS QETLDTLIMQSALESFNNRIKQVEERN SELKDKIFELTQSNKDKGKIRIRKYEQL *VANDYIQ*PNLGIIGPEEE
3240	17141	A	3262	450	129	NNLAFN*V*EFCVLAIKLLVKRYPIEW EKMFANHISDKGLVSGIYKELFRLSNKQ AIDLTF*KWAAGHGSSPL
3241	17142	A	3263	238	3	KEKKIGLKKCLQSSHPSTHTAWSIIYIM FSPILTIIISKRMRGPGIYAHTCNPST*G G*GRWITRSQVGRDQTQGHGKT
3242	17143	A	3264	350	3	SPTLGSKPNLLGFRRPLKWKKGKIIIRA PLSLGLN*RFPSSEVVLIP*KPPKNWPGG TFLVVCFLKRGFPFLSQKKKKKNPGAVA HACNPSLGGGRGSGGQLETSANTV KTR
3243	17144	A	3265	69	200	RLECSGVISAHNCNLNLPSCGDSFASAS* LAGITVMVKLPVIAK
3244	17145	A	3266	223	408	GGGFFFPFGSGEGNFGELLEPLPGLRK FFCLGPPRRGD*GPRSSPSGFWVFKKN GVSP
3245	17146	A	3267	185	420	DQQLWGFITYFYRQSLA*VHWNHPSLS* PRTPGKHTPVPSSLTISNDYGRTPPHLT NFCIFIFDRGSGFF*DRVSATHA
3246	17147	A	3268	3	392	TGCHSTPOAGVOMHNRGLLQPOFFGLR* SSCLSLPSSWHY
3247	17148	A	3269	1	398	KFSCTSSKHQKLLTKPKPKPPFKKSPL VLPIGKKIRETFWAGFKGPPNPQKGAQ TLPLKIWDKMGGGGGLALVV*KAPPGN KGPPGGKPMQOP*LGPGPLKWKGLPH QKGGFSKAPGEKKGGEGRL
3248	17149	A	3270	422	183	ETEVSLSLKVITTEKSPNLEKDTNIQVQ ESYRTPSRFILMKTSTRHLIIILPKVNN TERIL*MQQDRGNNTQWSSGCSA
3249	17150	A	3271	3	35	KNNSLIIPITIIITLLNLYFYLSFLLY **SSSSPS
3250	17151	A	3272	155	1	KDFFFFFLQSQFTLVAQAAAEWCDLCSL QPKPPGFK*FSYNSLSSSWDYIG
3251	17152	A	3273	413	71	PPSTGLFLTEEYVSFPFFPL*KFFFPF SGLFFGGGVPPFFPPPKGFFPKYPRLV FKGPLLGGGLPPPPP*ILPLGSLFLPA PPLFFFLFFFL
3252	17153	A	3274	336	45	DRVLSCSAANRAMARSHDFG*LQLPPPR VKVPSCLSNPSSWDPRHVPRKGNFVL VKTGNPNWLGQGGCRERRLCPCIPANGT DRDVSKKKKKS
3253	17154	A	3275	206	366	SVFFFLVFGFFYGALLCFPNPWLCESGT ILVHCNHLHFGSGKSSASPS*VAGT
3254	17155	A	3276	334	75	ENTRRVERRRRTTHIYYNFF*EFFNRRFF FFIIFDGRFSCVFFFFLFYTFFFFF FFFFFFFF*FFFWPSARSFIYFLPRH VT
3255	17156	A	3277	144	17	KAPLPLFFFLFFFLFFFLFF*FRG* HWNGDACMNLTKS
3256	17157	A	3278	2	109	YHVKRPS*PLTGALSALMTSGLAM*F HFHSITL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
3257	17158	A	3279	404	65	NLVSSPKRSVVFISPSQKIFFFFNWKE SKISLPKEGGGLLLIRORTPIFFFFF FYFFFFFFFFFFFIFFFIFFFIFFF FFFFFFFFFFF*TACLF*TFKFTKTK R
3258	17159	A	3280	226	383	GI*KNSMDGCCLGPPVVFETGSHSHPGW SIVWRNLGSLQLLPKPKRPSCLS
3259	17160	A	3281	91	26	LFFFFFFFIFFFIFFFIFFFIFFF
3260	17161	A	3282	3	321	HTVIYIFGKNEFFGYIGVA*AMISVGS LFMA*AHHIFTGGIDVSPAYLTATII VAIPTGVKVF*LATLLGSGMKRASA V*TLGFI*FLTARGLTGIVLSNS
3261	17162	A	3283	393	112	PPLRVFFPPFLKNNFFSSRRFFFWGGV APFFPPKGGFSSKIPGFFPPPLKKK IFSSDP*FWAPGGFLKGGPPFFIF FFFFIFFF
3262	17163	A	3284	360	47	BDLHRWVPPDP*KFFFSQTKFFKGVF SQNPFPKKSFPKKNPPGVYSPPKKKK KFLELPIFFPPPPFFFTTTPPPFFK FFIFFFIFFLDFFFWVSF
3263	17164	A	3285	386	157	FFSNPLIFWGGGGPKFPPKKRFFSKN PPGVFSPLKKKKFFPP*NLAPRD FLKGPFFIFFFIFFFIFFF
3264	17165	A	3286	3	385	DAWVECKLYLGVFRCFVKISALILIKI LIFNIENKSI*YLLKKKKKKKKKKK KKKKKKKKKKKKKKKKKPTPKKKK KDSR
3265	17166	A	3288	81	270	ITLEKKKKKKKKKKKKKKKKRS*KGNE KTRGPKKKVHRDVTKKILCYICPFNG ISLIGT
3266	17167	A	3289	3	145	LGRLRQENHLNLGG*GCRFPKSHHRLA WATEQDSISKKKRIGGPV
3267	17168	A	3290	404	47	GGGGKIFFKKNPEEKIFSTQKKKGFFP FPPKNFFPPGGFFFWGGGGPIFPPPK GFFPKIPRGVFTTPKKKIYFPDPREI WAPPGIF*KGPPLFFIFFFIFFFFLV LNDILLA
3268	17169	A	3291	106	362	KKKKKKKKKKKKKKKKKKKKRKMKN KKKKKGGGGKKKPRGAQIIIRGKKKII FFFKVKF*KGGGD*KKSPCGENNLE NTHKE
3269	17170	A	3292	3	226	NPLVNLNLGLLFLATSSSLAVYSIL*SG GASNSNYALIGALRAVAQKKKKKKKK KKKKKKKKKKKKGGGVL
3270	17171	A	3293	337	2	FPNRELLKSNKETEKNHDYHKERIWHP DRPKFFMLFCRQVLIFFLYLFFIYF FFFFIFFFIFFFIFFFIFFFELNI*F FSINTHKCNRGCGGAGPRLNGRV
3271	17172	A	3294	327	21	KFFSF*PNKYFFVFPHKFFPTPKMFL* KIPPPILSPDPKENHQCPDPPIFADP SHFFPGPHFFFFFLFFFLWRTGSRV IAQAGLELLGSSYDPAS
3272	17173	A	3295	367	101	FFFGF*KKKNFFPPPLWPPPNFL*N PPPPFFIFFFIFFFIFFFIFFFIFFF FFIFFFIFFFIFFLVNSLCRRYR*SLY YAWL
3273	17174	A	3296	178	2	KGPPFFIFFFIFFFPDSITLFIITNEK KTRCTSIGE*ITWYTHGEYYSVMKRNE

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3287	17188	A	3310	1	364	LYITGPTLALITALL*TLFPIPNPLVN NLGGLFILATSSLAGYSIL*SGGASG NVALIGALEAVPOTISVETLATILST LLIRGSFNLSTLITTOEHL*LLLP*PL AII*FISTL
3288	17189	A	3311	215	2	GMAKLKARFLPKKGGKRSPLLWGS PTSGTGETFFFF*DRVLLCQPGWSA QS*LTASTFWAQA
3289	17190	A	3312	153	3	MNKICMCVCMCVCFRSHKHTVCAMVCV Y*V*TYTVCCVCCVCCVCCV
3290	17191	A	3313	149	1	KTPFGFFFGKGF*FKGPPFFFF ETEDGVLLCRPGNSAVSRDRA
3291	17192	A	3314	282	69	KIGKTAPFFSWFRVPLFKKKKK*GL TLSSRLYGGMISLELGGSSDTLASASR VARIIGQCPHAWLT
3292	17193	A	3315	479	60	MMQHSIKHALVEITGVWRVLRPVPALW EAEVGEFNSISKNNRKNIVMKSLF NLIYRINAPFFKFLIALNKNKSXS NLKS*STQ*SSRNNVGGITISDF*THQ QATELRQFLHTGLVHRSTVSRFRFA
3293	17194	A	3316	129	3	SFHQKVPDAVAHACSPSTLGG*GGRIT GSGDQDHPQGHGE
3294	17195	A	3317	3	156	EFHRVSDQGLDRLT*STLLGLPKWCNDY RCEPFRPASFPFLTVRISPL
3295	17196	A	3318	36	340	TGLVIAEHLFFFKGKGFPCPPGGRAG PQGNLMFPPVSGGKIFCPGPPKSGE* R APPPSRGKFWFFKKKGGLFPVGGV*TS DPRGTPPLGPKKGGEYR
3296	17197	A	3319	326	2	KAFFLNFKPHPGFA*GLKFKPNSLLPT* SFIRKT*AFLICL*IQLNADGKIPKLP GVIPFKKCPNTPPLFFKNCSSSTPNL FFFFFFFFFFDGLICRPGWSAVA
3297	17198	A	3320	175	312	QAGVCWCDLSS*YXFFPSGLT*FY*CSLP RTWBYRCPPSRPCNPISL
3298	17199	A	3321	363	51	RWGRLVAVKLPVSRRAECSRGRAG GOGGOGGQAR*REGPDWGTGAPVGMG SPSLNREGAGRGPPOGPPSSKSRGRVRC TPHSCILIGCLSPFICKMG
3299	17200	A	3322	344	187	LROETCFNPGGKNFG*QKLPPCPPMAT RGWVSKKKKKRKKRKEIRICVLT
3300	17201	A	3323	3	313	TRRRERERERERERERERERERERER RERERFFFF*KNLSPPPGKKRGGGG FHSPPFWGEKDFLPPRPKGGRGRGPP PPVFFFFFKKEGAPDGGV
3301	17202	A	3324	365	1	SLGWRVTPPPFPLGPRGSGPPRPDKRG SPGRVKFGVKPFFKVKP*PPPKRLDPS GA*FFFSPPKKICQPPPPKKKKKEALS ILCTKFLQEEVMOVPPPTCSSEPG INCICKRHC
3302	17203	A	3325	1	269	ARATLSLSLSLSLSLSLEFFFFFLAPT QILGGGLFYPPKGGAHLSNRLGGGRVFF GPPGKKTAPLGGGRVKKKTPGPTL*L SPPPGGPFFFGQKKLSPPPAGLTGGP PPWGGKAPPPKFGSGPKKKKTLERER ERERERERELV
3303	17204	A	3326	1	316	ARGERERERERERERERERERERFFV SPPGPDTLQDRGGVLFASDPHTIYLP CPLRGLPSRDEELHGVCFSPSHRW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3304	17205	A	3327	2	369	FPFEEGVGDIQQC*HRGECGSP ARGDVTRESTYQGHHTPPVQKGLRGYII LFITSEVFFVFFAGIF*AFYHSSLSPTPQL RGHWPPGTITPLNTLEVPLLNTSVLLAS GV*IT*AHHSLENNRNQIIRALLITII LGLYFTLLQA
3305	17206	A	3328	1	259	GTRKKHSTILIREIDIKFMRPFHISPI RLVKI*ALANIRC*QQCKVGNLLHC*F SKLVQSTGRAIWHALVLSLARSRLSL LH
3306	17207	A	3329	2	352	ARGTLLLLCLLFALTIYPRWCDVTRKS TYQGHHTPFVQKEPLVLGGKLFITS*VI FFAGFF*AFYHSSLTPTPLLGGHWPPTS ISLNFPLKKPLNTSGLLASGVSI*AH HSLLO
3307	17208	A	3330	3	361	HEEPLGYIRMA*AMISIGPLGLIVRAHH IPTCQIDVDSRYLTLSATIIAPPTGGK VFR*LATLHGNSNMK*SGAGL*ALGFMFL FTVGGLTGIVLTNS*LDIGLHDYIVVVA HPHYVLS
3308	17209	A	3331	1	340	GTSGDTRAVFTSATIIIAIPTGVQVFS* LATLHGNSNMK*SAEL*ALRFIFLFTVS GLTGIVLANSSLDIELHDYIVVVAHFHY VLSIGAEFAIRGSIH*FPFL*GYTLDO T
3309	17210	A	3332	2	352	ARGDVTTRAVFTSGTIIIIAIPFGVGFPS *LATLHGNSMK*SAAVL*ALGFIPLFTV RGLTGIALANSSLDIVLHDYIYGGAHFH YVLSIGAVFAIIGGFH*FPLFSGYTLD QTYAK
3310	17211	A	3333	85	370	QVSHRVKPCFEREREDRYRHTQRECE AKEIYSGFFLSASEMESCSLAQAGCKE LRMCHCTPAWVTQGDVCS*NKK*HNEKK GLWFLGVNIST
3311	17212	A	3334	362	3	QEVKVSMMNRDHTSLQRGEQKRNVSCK KKKSSQEKLRVHTQTHT*IFIAVLIV ARNGKQFPKFPSTCEWINNM*YIHTMEY SATKQQLHVTT*MNLNNIYTKFLKARQ KMTYSC
3312	17213	A	3335	3	351	HGGTILHLLFLLETTGSNNPLGITHFSKD KTFHPHYCTKDALGLLFLLSMLTLL *PDLLGDDPNYTLAHLNTPAHIXPE*Y FLFAYTILRSGPNKLGCGPALLLSILIL AIIP
3313	17214	A	3336	17	350	FIFTLTETNRTPDLAESESELSGSLKI KYAAGPLALLFTTETYNIIIDTSTTI VLGTTYDALSPELYATYFVTKTLVTSLS FL*IRTAYPLRLRYEQILHLL*KNFLPL
3314	17215	A	3337	2	349	ARDSLISPIRLHPRFNLRQNAFYHIIH RGKSNFLPTTLRPIRNAPTLGLRPCI HMKHPICRLIH*FPLFSGYTLDTQYA KMHFTIIFIGVNLTFPPQHFGLSGMPR RYSYDPDAYTT*NILSYVGSFISLTA LIIIFM*EAFASKRKVLIVEEPSINLE* LYGCPPPYHTFE
3315	17216	A	3338	2	386	ARAILNMAFLILTERKILGYIOLHRGP NVVGPYGLLPFADAIKLFKEPKPAT STIILYISGPTLALNIGLL*TPLPIN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PLRNLNLGLLFLATSSSLADYSIL*SG*ASNSNYALIGALRAVV
3316	17217	A	3339	175	16	ILGDLFFPPAWLHPFLFLLLLFSRPSLAVTEAAVQWRNLGLLQPLPGGY*SSWC
3317	17218	A	3340	1	369	GTSNLSLLFIVATCGLAAN*ML**GGKIN*YTLARVALAAIHTILYEITLSIILL*TLISGSENLSTLTITQEHL*LLPS*PLAII*FISTLAETNRTFFDLAEGESEL F*GLNIEYSAR
3318	17219	A	3341	1	363	GTRGGTILPAMVLMILDVBSRLRLYYITNKVNEPSLTIKSNHGWY*TYQYTDYGGILNSYILPPLFLQPGDLRLDLDVNRVVLPIETPIRIINT*QDGLHS*AGPTLGLKTDAIAGRVNQ
3319	17220	A	3342	181	315	PKSFPTPPFPPTXXXPGGNPFGPFL*GPFYWGGERGPPF*TGGP
3320	17221	A	3343	3	183	HEVQSQCRLLTSGDPPASASQAGISGMHHRAPVPS*TFHFNICYGPGVLKPYLNL
3321	17222	A	3344	83	354	VLGARCPCAGVSRVSMEPFWLWQOACLLPWRRCCLSTLYANRADRDVP*TSRTGPVMVAHACSPTLGGGGGVWTRSGV*QDPGQDGETP
3322	17223	A	3345	124	379	GGGICFMVYVSLGSLSHRLAHCRTYVGVNNLLCSSLPLFLPLPLPPEPGPWDDINIIIFIFIRDKVLCLCLGWSAVT*SQLTTA
3323	17224	A	3346	3	368	YEPYP*PLTGALSALLMTQCLGAM*IHLHSITLLILGLLSNTLTIYQ*WRDVTRESTYHGHT*PPVQKGLRNGIILLITSEAFFAGVF*AIYHSSLAPT*QLGGHWPTTGMTPLNVPQGPILL
3324	17225	A	3347	1	352	GTSAGDVYGG*IRYVLHADGAKIFLRCLFLHSGRGLYGSVYYSKT*NIALLLLATIAATFYGVLAA*QQLL*GATYSTNLLSDIPYIGTDLISQRI*GGYSVDRPTLTRFTTFHF
3325	17226	A	3348	2	360	ARAETISPLHSNLGNESETPSQKKKKKPKPGGGGKNWNPYPSGT*PPNP*PKGE*REPPPLTKRVF*KKVFFEGPRVKKNLGGKGGKKRGFPAR*KNPVPKAKGGRNFGPQAFFFKK
3326	17227	A	3349	226	366	PQSFCVSASVWPGDIMEI*AWQKFYEYKPKVPMDFEGCLLPLAKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELV
3327	17228	A	3350	2	374	ARGGGYSPHRATLTRTVTFHSILPFTIAGLAAIHLFLHETGAYT*PL*ITSHSEKTFHPYITMKDALGVLLFPLSLTTLTLCSPNLLGEPHIDYTLTNPLNTRPHIKPE*DCLFAYTNMRSGPN
3328	17229	A	3351	1	266	LGLVEHFLTLTKLTSSNSIDAQEIQSV*NILTAIILNLMVLPSLRMLYITNEVDFPSLTIKSIGHQWY*AYETDFGGLIFNCYILP
3329	17230	A	3352	207	362	ILFLLKQKRYVLPFGSN*GSSIPELAHSDAYOTKEICSSGKVKYKLCQWCK
3330	17231	A	3353	178	365	NHGIDKGLRYRTYVQGEDNSVKR*LKD FNQHLSDKNIRSADHKRCRCPTSLVNI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
3331	17232	A	3354	359	3	MPKFP LQVRSMLPGLQGFHPF*NFCCSFFFKPKI PFFFLFLKGVFVFFPGWRARGQFVFG PPPPKFKKFFFTLLRNWGRDFPSSRG KFFFFFWYF**RLRFTMLTRLVFN* QVISC
3332	17233	A	3355	2	354	AREPSP*PLTGALSALLMTGCLSM*YHL HSITLLILGLLNTLTLYQ*WRDVTPE TFQGHHTPVPQGLGVGIIILFITSEVFF FAGFL*AFYHSSLAPTHLGGDWPPPTGV TPLNAL
3333	17234	A	3356	1	364	GIREMCCSALSPIRIHLSFHRRWPDWHC ISKLTIRHRTTRHVLWRSPLCPINRS WICHRRRLHSLISILRLHPKPNLRQNP FHTHIGRK*SAAVL*ALQFIFLFTVGG LTVIVLANSLLDGLHDTYVGAHFHYV LSIGAGFAIIGGFH*TPLFSGYTLNQT YAKIHFTIIFMGVNLTFPQHFLGLSGM PRRYSDVDPDAYTT
3334	17235	A	3357	2	376	ARGGQFEDYIILPSPGIIPIHIVYYSY KKEPFGYICMV*AMISIGPLGFTA*AHF IFSVGIDVNTAYFTSATIIIAITPGVSG VFSWLATLHGSNMK*SAAAL*ALRFIFL FTVSLGTIVLCN
3335	17236	A	3358	357	139	AQWFFFLFETVFCARQAQGLKSIGSSDL PTASQSVGTTGMSHAWPERS*QNTF TYVQSYSDDIRKSMF
3336	17237	A	3359	277	1	SCQKDISIGFLFVPGFRVKGVAQEHV VRMYVLVPTVGGDGKERER*RGIRHTPP PSERVORERERGRDRDEKERASQRKP EMDRETS
3337	17238	A	3360	261	2	TICSKCAWLCSFKSTLLTNTCASRDLAH GP*CPNLCSGIFSSAWTIDISRLFFCL FVLRQSLTVAGAGVQCNLCSPOPLPG SC
3338	17239	A	3361	199	334	HLFPYWMFMATFNFFFPETEFHFPFQA GGQWGDGF*LKPPPARLKQFSCLN
3339	17240	A	3362	3	364	HEDRDTPAYFTCANIIAIPGVKVFN* LATLHGSNMK*SAAV*ALRYIFLFTVS GLTGIVLSYSSLDIVLHDTDYVVAHFHY VLSIRAVFAIIGGFH*PFLFSGCTLNQ TYAEIHT
3340	17241	A	3363	3	360	HEETVYIPKQKYSPLADSQTSFCFSNSI PTPSNMEETQKQSVSGCRLP*AGWETC GQGSRAAQPLSPLOQLKLLRISLLLI EAWLEPERVLKSMFANNLCYDTSDDSY HLLKDLE
3341	17242	A	3364	352	27	VYLSSQRNSAASVNRMTVVDRSLSPYT LGMHRPDRLEHFVPSLFVYTVFVERGSQS IAQAGVQWCHSSL*P*TPGLK*TCSC LP*VAGTTGTHHYTGFLILLNLFN
3342	17243	A	3365	347	99	GGPPLPRGFSPPGARPLAPPWGPQES PPPPPKTAPQKKKAPSI PAGQWLVQ NRPQPQFKKPPGVGF*NPPPLNMGF
3343	17244	A	3366	3	319	HEECLAHTLCFFNLMS*RTTVILHRMFS IVTAI*YLLSQVYIGYIYVCIHHTH MYIHTHRHRTFCVCCVCIYITSIC
3344	17245	A	3367	3	474	YELLNLNGPILNARAFILFERKILGYI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QLHGGPNAVSPVGLLQPPADAIKLFTKE PLKPAATSTITLYTAPFTALTIDLL*TL RLPTNPLDNLWLSLPLTATSSLPVYS IL*SG*A*NSNYALIGALRAVAQTII*EE VTPPTIILLSHYVKKLNR
3345	17246	A	3368	2	348	ARGLQDATFPFIEELITFHHDHALIIVL ICPLGLVALFLTLTKLNTNTHSHAQEI ETV*TILPAIILVLIALPSLRMLYITDE VNDPSLTIKSIGHQWY*TYQTTYGGLI FNS
3346	17247	A	3369	64	363	KKWGFVPOCKKGGGRISVNG*PFIFKGG NFPF*PPGEGGTGPGGPKK*IWIFKKR GGLIFWPKCFPTPGPKGTHPPGPPKGGK *RGGPSPGGFNFKRG
3347	17248	A	3370	34	355	AKGKEYIETVAEKKKKKKKAPPI*KAP *NPGKKPLALKPPPPSQKAPPALFCP *KGPPIRVFVKKKKKFPFGKRGFTG GKPF
3348	17249	A	3371	1	374	FLNSLHLSRLLYLF*KFSMFITLLKAY YTLCVCVCVCVCVCVCV*PLNKHINHF TCSTVRGRSNPIFFPLLN*RPYFT
3349	17250	A	3372	429	3	FFFFLLKKQKISRVFPRGPEFFGGRKFFW AKGPPRAPCKGGEKGNPSPPPLIFPK KGKPKQGGPLFKGLGFFSPKVFPPKK VFKSGPGGP*NFGRGFSPSPPKKGGK KRKPSPGFFFFF*FELGCSGRSRSR T
3350	17251	A	3373	2	404	LGTDLSLIIRADLQGTGDLGNHDHINYA YTAHAFETIIFETIPIIRGFON*LIP LIIGAPMAFPRINWIS*LLDPSILL LASAIVAGAGTSGTDPPLSGNYSHPG ACVDLTILSLHLAGVSSILGAI
3351	17252	A	3374	2	417	AFV*TAHITRDVYVY*TIIRYLHAGKARI FFMCLFLHIGRGLVYGTFLYSET*NIGI ILLLATIATAPIGVLL*GQISF*GATE ITNLLSAIPYIGTDLIQ*I*GGYSVDSP TLTRFFTFHIFLPIIAGPNPLHLIT
3352	17253	A	3375	85	1	FWPGAVAYACYSPSTLGG*GGWIMRSGVR
3353	17254	A	3376	396	1	KEGYIKGPRGENFF*KNPERKISRQRK GGVFSPLPKKFFFFPKGLIFLGGGCP FPPPKKRVFSKNPPGVFNPP*KKKKIF SPPPENWGPRVFLKGPPIPPPPFFFFF FFFFFQTLFGGCGYNTKLR
3354	17255	A	3377	3	118	LLFPSLLLLLAYALLVAGAGT*TDYPP LTGNY*KTKA
3355	17256	A	3378	301	82	ERKGGPPRGGKGPKAQPKKKKKPKKRP PPPN*FFSNPPKKKKGGKDPSPSKRGG GKGVPPRKKKKKKKE
3356	17257	A	3379	2	195	DR*LFSTNHKIDIGTLVLLFGA*AGVLST GLSLIRAEGLGQPNLLCNHDHINYVIVT AHAFVIIIF
3357	17258	A	3380	21	411	VFTNH*DIGTYLLFGA*AGVLRALS LLIRAEGLGQGLLGNHDHINYVIVTGH FVNNLFIPIIIVGSSGN*LGPLEIGAP DMAYPRINNIGF*LLFPSLLLLLAYAIV EAGAGTG*TVYPLAGNY
3358	17259	A	3381	2	421	GRVGRVGSNTNRDITGLYLLFGA*TVG LSTALSLIRAEGLGQPNLLGNHDHINYV

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						IVTAHALAKIFILVPIIIGGGFNGNLVPLIIGAPDMAPFRISNISL*LLPPSVLLLLESVIAEAEAGTGRTVVPFLAGTYSNPG
3359	17260	A	3382	3	185	VIYSTIFAGTLITLSSH*FFT*VGLEYNMLAFIPVLTKKINPRSTAAIKYFLTQATASIIILLIAILFNNILSQ*TTITNTNQYSSLIIMATAIKLGIAPFHF*VPEVTGQPLTSGLLLL*QKLPSSISSRKQHPF
3360	17261	A	3383	5	398	FFGHPEVYIILPFGFIISHIGAYYSKGKEPFGYLGMA*AMISIGFLGFIA*AHHIFTUGIDVHTRAFYFSTATIIAIPGVKVFN*LATLHSGNK*SAAL*ALGFIFITVUGLITGVLANSSLDIUL
3361	17262	A	3384	1	250	LKNTGETLSLQKN*KLRCGGTCLRSQLLRLK*EHCLTPGGRGCSPPRSCHSSP AWATQODLSOQQQKQYPLRIPSAIKS
3362	17263	A	3385	456	0	IPFFSQVETGTHHIGQAGLQLTSGDAPCVGLQKSWDYRPEPLHLAWL.IHSLSNFYVC*FGCKLSVFILINVCNKTCNSSMFLFSYS*NPCAQ*KNEGPLLKNPCRITDAWADANVAVPF
3363	17264	A	3386	1	225	PSRNFLVLVDKLLKFT*KYRGPRRTAKTLKKKKKVRLTLLIFKSYKTTIVITIGWYGFQDRQVD*WNRISLE
3364	17265	A	3387	3	400	LLILGLLTNTLFIYF*WGDATRESTYCGHHITPVQKGLRYGILIFTSQVFFAGF*AFYHSSLSPTPLQGGHWPFTGITPLNPLEAPLNTSVLLASGVST*AHPLGIE NNPNPIFRALLITNILGLYF
3365	17266	A	3388	24	407	IASGRFFFFFFFFFFPGKFFISRGGGPFSPPKI*KNWGKGSFPFPPOREPCKRGVPPKNSLSFYPPGGKPLGPPKLVPPSS*PGKKAFFFF*TPPPGFLTPLGGGLSPLKGGYLLAPHFVPTGEL
3366	17267	A	3389	148	413	LNLNNNNNKNNHLLNTYSCT*LEEKKKKKKKKKKKKKKKKKKKKAPGGGFF
3367	17268	A	3390	157	14	RVSACQGVNW*MPVVPATREAEARESLEPGRHRLSCCHDRDPVSKS
3368	17269	A	3391	2	398	LFSNTHEDIGTLVLLFGARAGVGRGTALSLLIRAELEGQGNLLGNHDIYNVIVTAHAFVINFEIVPELIGGQCN*LVPLIIGAPDMAFFRINNISF*LLPPSLLLVAIVAEAGAGT*TVYPLAGNYSH
3369	17270	A	3392	2	395	DQKDIGTLVLLFGA*AGVLGTAVSLLIGAEIAGHPGYLIGNDHYVNVIVTAHAFVIIFFIVIPILIGGQCN*LVPLIIGAPDMAFFRINNISF*LLPPSLLLVAIVAEAGRTG*TVYPLAGNYSHGA
3370	17271	A	3393	396	54	GYPNLTFTVTSLSLTSVPSPSHPHSVCSPTPAIPQTPRSPSPSETPPTVEUSLTPTLSLGAISSLASAGPGASPASPGFWGTSPP*PYS*NRPQTAAAGVFSQLFFIRPEVP
3371	17272	A	3394	417	60	KGVWFQRLWPGPGGSPPRYSRPFGGPRGLIPLGSGV*TPPGHWETPFFFNQPISSGQGGGGLIPLGGVKPEKIFYPGNQSFH*PKIPPHPPPLGAKQNFPPKKKKPKCN

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						TRGFVV
3372	17273	A	3395	417	3	FFFFFQQHFGQFEAAA*YWHFVDVV*L FLVVSIV*GSYSFINS
3373	17274	A	3396	229	1	KSFWKTKMGFSCKDFF*TINGNKDTTYQ NLADTAXAVLRGKEIALNVPINKLERSQ ISNLSQVKEGQANWMPVI
3374	17275	A	3397	344	165	ELKSPQPRKRNCGFFLAVDPEDEGF*NLN PCQNGQGLNAPGGYPCEIPMGFVFNAYG KTF
3375	17276	A	3398	1	409	RKDIGTLVLLFCARTGILGTALSLLIRA ELGQPCNLLGNDRHYNGIGTQALVRIL FIVIPITITGGFON*LIPLIIGAPNMAVP RINNISF*L*PPSLLLLVAYGIVEAGAR TG*TGYPPLAGNYSHPGACVDLTM
3376	17277	A	3399	3	396	KDIGTLVLSFL*AGVLGAALLRLLIRAK LGQPRNLLRNDRHIYNVIVTAHAFVIIFF IVIPIIIGGFGN*LLTLIIGAPDMALPR INNISF*LLPSSLLLLLAYGIVEAGART G*TAYPPLSGNYSHPGASV
3377	17278	A	3400	49	350	KSNSHTEVQAGOEKSFRRSKHKAGRAG SDPAPYVLAGLCRSISSFLFFFSLFF FFPFKRGDV*QGYSSGNTPGVKQSSCL GLPKYWDYRREPLHPA
3378	17279	A	3401	1	398	KPFAITQYQTPLFV*SVLITAVLLVLSL PGLGAGITILLTDRSLNATFPDPAGGGD PILYQHLF*FFGHPEAYLILPGPGIIS HIETYSGKKKPPGYIGMG*AMISIGLL GFIA*AHHIFTG*IDVDTRS
3379	17280	A	3402	388	42	TPLFNPPGAKCVNPPFPKLLKKNFPSRA MGGPPLFPPLWGGKPKGPF*NRKSGAPV THFAPPAPPPGKKREPPPKKKKKKKR EEKESNRVQIKKRGNKGRPLPVLDAE ESQ
3380	17281	A	3403	413	2	SHPLKNFFLPFPKPPNSGGGLAPFVPFQ K*GSLPKIPRGYKSPPFKEKTNALPPR GKGPBRASSKRPPLFFFFRGRVPLCH PG*STVQCQVQACTLELLGSSNFLTSS PVTWGHRRGQPPRPINFFIFFRGRVP
3381	17282	A	3404	433	274	LGVVAHACNPSFLEG*GGRTAWSPGVQD QGOHSETPISTNFFWYFRISYFHI
3382	17283	A	3405	131	427	GPFPQPPFFWGRGGGNPPFFFFSEKRD VF*QFLLRRRGPKQKFPFFCLQKTS FSEKKKKKGGFPPLFPQKKGCGGGH KKEGFTLNSFLFQGDGVSSVAQAEVQWR NISSLQALPPGFT
3383	17284	A	3406	413	137	SPPPPPQGGIFFFFFKPR*ETFSPPPNLG FFSPPSPLKFFFPFKGFIPLGGGGPKPF PPKKRFFQNSPGGFFFPF*KNFFFL PPVILGPPRVF*GPPPPK
3384	17285	A	3407	319	540	IVFKDQCESTTTLNVDIRNHQNLDSL EQHGKDLL*GANAYHCEKCNKVRVAVQ LCLILITFNQFRKNRFFW
3385	17286	A	3408	2	403	SLHLGGGSCIVGAIYFITTIIINIKPAGI TQYQTPLFV*SGLTIGILLLSLPVLAA GITILLTDRNLFTTFLNPGGGGDPILYQ HLL*LLSRPEVYILILPGPGIISHIGTY YSGKKEAFVYIGV*AIISIGC
3386	17287	A	3409	2	142	KKENYRVPVSLNRDAKSLNIGLHI*KII

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3387	17288	A	3410	407	48	HCNQVGFIFGMOQGFNLL PPGGKIFFYKNPEKKIFPTQQKKGVFPP PPLKNFFPPPRGKIFGGGGQNAPPKK GFPPKIPQGV*SPPKKKKNFFPPGKI WAPQGVFLKGPPPPPPPPPPPPPPPP FFFLGVR
3388	17289	A	3411	3	402	SYRL*QLEDKAAFPQDFTQQLRWFEQ HRMVWDKEDMHKQLEASETLLKSQAE L*DAHQQQKLALQREFLEFNEMLAEYLSH NHKVDKKEEMEVAMHKADMWQEI*RS KKLTKRMLTQMRRTIPVIPS
3389	17290	A	3412	1	224	LLFQLRLRLRQENHLNLEGRSCSELKMH HWTPPWGTE*DCI*LLKKQSAYLFPNNTI KKLTGSRITIEDICTEYNK
3390	17291	A	3413	202	1	IVMSVPGVWTHA*IPSTLGGGGWITRS GVNDPLASAFQSGAGITSVSHCSQLIFVT VFVLSPLSHLY
3391	17292	A	3414	407	309	ESFKASDRITLLQANNAAGDLKFTBHF IYHSENPRALKNYTKSTLPVPLCIRNI KAWMAHLFTANLNEHFKP IVEVTHCSGK KISFKILLINKAPGHRRAQMERHKQNV VFMLANITPILKLMQGV*TFILCLSI
3392	17293	A	3415	404	46	LKKPPFKLKLKLLKKKGGGGGPPP* T PPFGGGRRGVDPRAVGSKNPVPQGETLF FFKNPKFPVGVPAP*FPLLRGVNKNF FNLGGGFGKKRKFSPPPPRGKFFFPK KKKKKKE
3393	17294	A	3416	23	404	SVLITGALLLLSMPVLGAGITILLTDNR LKTTFDPAGGGDPILYQHL*IFGHPE DNILILPGFGIGSHIVYYSKKKEPPFG IGMA*AMKPIGFDIAGAHVFTG*ID VNTRSYFTSDTINMG
3394	17295	A	3417	38	469	SGTHASALFDPAGG*DFILYQHL*IF GDPEVYILLPLGFRIISHIVTDSGKKE PPFYIGMA*AMRSIGLFGIG*AHIFT V*IDVTRAYFTSATIIIAIPTGVKFT *LATLHGSNN*SAAVL*ALRFIFLFTV GLIT
3395	17296	A	3418	1	419	FSINHKDIGTYLLFGA*AGVLGTGLSL LIRAEAGQGNLGNLHINIGITAHAF VIFPTVPIIIGGPN*LDPLIGAD MAFPRINNIS*LLPSSLMLLLASAGE AGAGTG*TVVDPGLGNYSHPGASVOLT
3396	17297	A	3419	397	107	KNSAPFSPITFLP*GEKFAFFPPKKVG KKIF*FKPAPGPGQGVLRGGGSPSPPO TPNWNPKAAFLVPPPPFVFNPKKKK KKAVAFSSPNRR
3397	17298	A	3420	3	253	RGCREMRLCHSSAWAIAGVSEKKKKK KNWQ*CLLGICSYLDLWPLGLFKMLSQI GRIVELQLELKQYLRGITKTKILILH
3398	17299	A	3421	1	393	RTRITKTPAITQYQTPLEVCALITAAAL LLLSLPVLAAGITILLTNRYLNTTFDDP VGGGDPILYQHL*LFVPGDYIVILPG FGIISHMVAYSGKKEPPGYIRMD*AMI SIDFLRIIV*AHIFTVEN
3399	17300	A	3422	142	377	LSKNCKPSYVGVFCQCKFFNQLSKFL VKLLYCMVKLC*EG*MAQPL*QKFLV ALKNLIVLPYNKAISLPGIYSTD*KTYT

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						DTQNLHTTVYSSSLITIKN*KQQRCPFSV GE*INKCFIYTTTEYYSLTKRNLSSHMK A
3400	17301	A	3423	2	435	LTLPGFGIISHIVTYYSKGKEPFGYIGM G*AMISIGFLGFI*AHIFTVGVIDVYT RAYFTSATIIIAIPTGVKVF*LATLHG SNMK*SAAVL*ALRFIFLFTVGGLTGIV LANS*VDIVLHDTYYVGAHLHYVLSIRA VFAI
3401	17302	A	3424	2	436	LNTTFDPAGGGDPILYOHL*FFGHPE VYILILPGFGIISHIVTYYSKGKEPFGY IGMG*AMISIGFLGFI*AHIFTVGVID VTRAYFTSATIIIAIPTGVKVF*LAT LHGSNMK*SAAVL*ALRFIFLFTVGGLT GIVLS
3402	17303	A	3425	1	193	PTKPTRPACSELRSRCHTPAWVE*DS VSKKKKKKFSFARGAHVCTPTPLGGQR GKKKCFAP
3403	17304	A	3426	3	446	HKKPLFPKSPFNRFVPTTKKKNRPGPGF FFFFLKKIFFFFPGGI*SGFGSLQLFP PRVKKFFSPPPEKGGFKAPPGPGNFF FFLKKRGSFSGGGGFLK*NPGFPPPPPF KKWGVKGGAPPPPPF
3404	17305	A	3427	202	1	FSQGMGNITKLPIYTHSPILMNSQNL EYKVCIGIPLSNFKNTYKATAIKTMWY HNRVND*WNR
3405	17306	A	3428	159	1	NPPHEKNFCSFFQMESHSADQGVQWCD LSSLQPSLRGFKRFS*VSLVSSWDH
3406	17307	A	3429	22	298	ESYASTAKATERHMSDRKLSASGMPRRY SDYDPDATT*NLSSVGSFISLAEGILI IFM*EAFASKRKVLIVREPSINLE*LY GCPRLRGR
3407	17308	A	3430	267	26	GITFFFFFWLEI*LYYWLFLANKLYFHE QIWGLVFFFGLLLFDSFYSDYFPLLL CLGFSNF*CLIHCFSVIIVLLF
3408	17309	A	3431	274	376	NKG*ISCSISPPORTVRRGLTSPRLEC SGVISAHCRLLCPGSSDPPASAS
3409	17310	A	3432	177	47	FVYFFFFFFFFFFFSSLLFFFFFFF FFFFFFFQINRSFIASFYKHK*V LIFKKKK
3410	17311	A	3433	379	83	FKRHFTKEDLRMTVEHKSCESSLATRA MQIETMAHCYTFMRLAKIKKYQTKCC *R*RVGTGLTYCWCECKMTQPFWKTI RFLKQYIYHIGYV
3411	17312	A	3434	214	3	AASTFFFFTRSTYYVCFILKSKRMINK* NYIKLSFCTTTIKINKMKRQPTDWEKM FANHINHLEGLLK
3412	17313	A	3435	1	353	GGQGGPQ*SETLSQ*KVSWAN*LQLHR RMRQDNLSPGDQ*SEPC*CYTTPAWA RVRLCQRSVNEKSLHDICNDKK*ONI* IISVPBGQRMKGLNLFNEILDENYPS LARDL
3413	17314	A	3436	29	394	VPMVEDEFFFFFFFFFFFGKKNFFFPKR GGGGCP*IPGPPPPRKGKNNPPPPPK GGKGGPPPPPGFFFF*KKGSGPGGG LFTPLWDPPPPRQGGFGV*TPWPGP GSDFLNFFF
3414	17315	A	3437	108	2	PVAVAHSCNPNTISGGKGGWIS*GHEFQT

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						SLANTVK
3415	17316	A	3438	215	3	LLLLREFFLPKHREVFIFVFYFMROGLT LTEAGVQWRSHGS LWPQTPLGK*SSCLS LPSIWEYSAYHHIR
3416	17317	A	3439	1	186	QTSSFSFRSIVITNPFKLLKDDV*TH*KE AKNLEKRLDEWLIIRIKSVEKTLNDLMEL KTSTRP
3417	17318	A	3440	290	3	PGLGGGPRYSRFSGGLOPKIFLNPGE SILKNPPAPP PGGPN*DSFLPPPKKK KKKTHVLFGSGNLQLQLPGGAFTTEVN GGLAQSPKVL
3418	17319	A	3441	163	2	PAGLVKPRFQDKLNFPPGPFPPPPPP *I*DKVLLCHPGESATVHSSLGDR
3419	17320	A	3442	131	1	RKRPRLTIKSIGHQNY*TYETDYGLLI FNSYILPPLFLEPGS
3420	17321	A	3443	162	2	PGAHSTGHLPLRFHLRGAUTHAGNDR TLGGQCRWIT*QGFKTSLSAKRVRP
3421	17322	A	3444	2	130	WKEITFANHVSDEGLIYRIYNELQQLYK* KINGPIKKRPSKTRP
3422	17323	A	3445	2	117	LALLGLKPSLK*ATCLGLPRYWDYRHQP PHDAPCSKGI
3423	17324	A	3446	350	101	KAFSSSGLGSRKKGDDSGCFTHFTV FGFFWTELEKKGIPFPIANFPFFFLRLV KGSKNPF*KRGPFFFPFFPNFYIWN
3424	17325	A	3447	106	1	LLOPNGOLPGTVAHGCNPFSTLGG*GER ITTSVGR
3425	17326	A	3448	28	333	GQOEONSISXKKKKKKKTPFKKGKRR IPGKKKPLGKSRAAPPPLGGGKNPPPG KRAPEKI FKKKPRGNWETFKRMKGFLK GO*PGNP*KVKPLWGGKK
3426	17327	A	3449	81	339	PIVSSCPGVAGALKQAMTLEFKVYQHHV VANCRLSEALTELGYKIGTRDITDGVQ QALLVVGRLAS*PIVSSCPGVAGALKQ AMTLEFKVYQHHVVANCRLSEALTEL YKIGTRDITDGVQALLVVGRLASQV QPGCGPGSAAAAAMM
3427	17328	A	3450	166	322	RDFSSTVLITDRSQRKIPTDVSQNL DIYKLT*PTIGKYTFSSYRSLR
3428	17329	A	3451	257	354	KFLSFFRDRLVLCPCGWSAVV*S*FTAA LSSW
3429	17330	A	3452	286	3	TDPPFIKRAKEREMQITKIRSIRENFI TDQQTKEK*EEQLYAHVNDLDEMDFK LEGK*PSMTHGKIENCRPITSKDIES VINKLTDPP
3430	17331	A	3453	358	353	R*KLWMGC*IEINKT*NTCTVIKEEK GQPTVAHACNPSITLG*GGRT
3431	17332	A	3454	108	353	THLGSFVRLVALLLHVRSYRISVS HCKDQYTLPLL*NFLMELCTVANTNP SILGGGRRIT*VQFETSLSANMVKC
3432	17333	A	3455	342	50	GPVTNPIPVVPLGSGKLEFPFKKKK* KFWGSPPLPFKKPKNPRETPPESCPKP KKTPIPVKV*GKTP*TPSKKKKTPPI ELFLKKKKKLIN
3433	17334	A	3456	343	2	KAPFFFFFKFWSQKRGLEFFFFKINF IPGPGPTFFFWGFFFFFKGPPV* LKK FFGGPLPLKDDPGVFFSPF*FNDPDP PPPPPPPPFFFTVSLCRPGWSAVSRD C

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
3434	17335	A	3457	2	259	LTKPTESGTEDEKGRDSKESGKTERTE SLRSQNGGSENV*SCPSTSSTAALNTAA AANPLALNPQVLSLSLSCCPISIKGSFV P
3435	17336	A	3458	186	334	AGGNKKMEKRN*KEIF*WFKKNWPGA GAHACNPPTLLGGRGRRIRSG
3436	17337	A	3459	207	1	YFKPTLKNIDKGYLNETIDKDPDRDNR TSNLT*EHALFPSTCGIFMRDXYIEGH EVNLNQFORIRTO
3437	17338	A	3460	268	3	PLNPGFKQSSPPGLPKFWPFGEPLPLG PWFFVVKNGRP*AFGFTNPLAFLFL *DRVLFCFHGWSVVVQSLTVQPPFLRL KQPS
3438	17339	A	3461	350	2	AETAHNINNAFGPGSANKCTVRWFK*L CKGVKRLKDLGKWPSPKVAINQLRAII KGAPLKPTRKVAKENIEPSAVIQHLKR IGVKVKKLHKVPHLHENKRNRFVWSS LIIP
3439	17340	A	3462	312	1	HIVTYYSCKKEPFYIGMV*AMISIGFL GFIV*AHHIFTVGIDVDTRAYFTSVPII IAPPGVKVFS*LATLHGSNMK*SAVL *ALGFIPLPLVGGTLRIVLA
3440	17341	A	3463	181	3	PLFLAAPSGLLPSGLGVFLFCFFET ELPRLECCGTISAHCSI*LLGSSDSCAS GTH
3441	17342	A	3464	176	263	VGHDAHNPSILGGPGGWIT*GQEFKVD A
3442	17343	A	3465	239	336	EPGEVAYSNCNPTLGGREGWII*GQEFE TSLT
3443	17344	A	3466	88	326	QTSLLNTI**PLH*KNIPLEPPPLPPTL TPPSPPPPPPPPPKKKKKKR
3444	17345	A	3467	4	345	EEERRRERKKKKKKKKKKKEEREEREE ERKKKKKKKKKKRRGRQEKRG*IE RKO
3445	17346	A	3468	265	335	QMPNDRHLQF*DKVLLCHPGMGTVARS* LTATSRSSCLSPFSGWDCRRVDPCLASF
3446	17347	A	3469	115	342	INQINKIKPTSYNILLQSLL*FKAL TLINSVQAQGEKATREKFEGIS*PMR FKQINHLNLIKQGEKPTSD
3447	17348	A	3470	56	328	RTYPTFKQMRDPEDPTSRPRYIPRHLY ITDEVNDPSLTIKGIGHQND*TYEYTDY GGLTFNSYILPLPLEPSDLRLDVNDR VEPATRA
3448	17349	A	3471	3	329	RIGARDESSLAVTHKPKRIHRKLTLLWVF VNDLSLMPRPDKNKHQWAFNKNCFPLVDV GIDPYLVYHLRPHQAQGIIFLYECVMGM RMNGRCGAILAD*NGLGKTLQGISL
3449	17350	A	3472	154	2	PNLLYPSKYWKKKDIWTFMFIVALTIV KIQKQPRCPLMDKSI*L*YIH
3450	17351	A	3473	132	340	ALKTENITTLCLDF*LIETVR**MCVFK KKKKKKKKKKKKKKKKKKKKDPKKKKK IK
3451	17352	A	3474	3	345	VYSSIFAGTLITALLSS*FFT*VGLEI NMLAFIVLTKKINPRSTEADIKYFLTQ ATASIFLLIAILFNILSGL*TI TNITN QYSSLIIMAIKLGIAFPFRRRRGREFQ IY
3452	17353	A	3475	1	254	FHHVQGAGFTPDLR*STRGLPKCWDYR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown; *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REALCLVHILLYLPMIGPFRIOKLLKAA VFVFLQLHQAFIQSLTLTFYFISFP CNS
3453	17354	A	3476	351	186	SVLSADNTMGFHHVQAGLELLSSSDP LAPAS* SAGIRGVRRHNTWVLTITLN
3454	17355	A	3477	330	3	GEKVFEIPLTRDNVSEILRCFLMAYGVE PALCDRLRTOFFQAQPHOOKAAVLAFV HELNGSTLIINEMDKTLEMSRYRYKEW NVKERLRRLKARA*RLGRSQQVK
3455	17356	A	3478	373	248	NRLNPGGGGWSPEPSQHSPTPTWTEYDS VSKK* INKNKNK
3456	17357	A	3479	3	92	EGQGCSEPS*SRYCSPA WITE*DCVSKNF F
3457	17358	A	3480	380	2	VEVPLLNTSVFFASGVSIIT*AHHSLEIN NRNQIQALLITNLGGLYPTLLQASEYL ESPFTISASIVGSPFVATGPHGLHVI GSPFTLMCFIRIQIIPHFTSKHHFGL EAA*CWHFVDVVCIFL
3458	17359	A	3481	225	1	ERERVVEQVMIALFSPNVIILSFPISP TPVVRHKFRHLKGVINPOTVAHTCNPS TLGSGGGQITRSGD*DHGP
3459	17360	A	3482	332	1	IKVPLTONTASTILLLAILPNNILSGQ* TITNTNTQVSSLIIMAIAIN*GIAPPH F*VPEVTQGTPLTS
3460	17361	A	3483	277	1	LSMSSFSSTISIPASINS*ALLSSAES NSLECTFSSTSPNSSSEFSSTSPSCC AS*FSNSQSLIKASSSTEASPLNSSASC FLPLPLVG
3461	17362	A	3484	404	209	ALSQQLWRPQEBNGVNGPKASR*PRF PPCGPANATKGELVPKKKKKISFLGHD QSLELLLR
3462	17363	A	3485	31	347	FCILERKAFLYV*CWKFFFFFFFLE KGFFFLPLLFFWCYHKGASLP*VFL FFYLHCYSSLFTLFFIFLQSLTPHFFLV *TFYFYDPLMFFFLTFLLELV
3463	17364	A	3486	327	161	QKKVRDPYEQL*ANKFN*EMPRFLEK HKLKLTQEEIKNO
3464	17365	A	3487	311	3	PRRGRFQLTQNFALPNLGNKTIPIFFKK KKKKTPLCPCCTCVCAAFVCLFHLCT* PCDCAHDCDNICVCVNI CVYVCVTHLH TGLCSCVDCDHICVGTCC
3465	17366	A	3488	245	1	RPRRLALLLLITIT*LPQLNGYIEKST PYEGGFDPIPARVPLSKFFLVAITFL LPDLLEIALLLPL*ALQATKLPLV
3466	17367	A	3489	2	400	APLILGLSLQRGKTRQRQRLCLMSA TLLFLYFLNKLIL*TKKKKKKKKKKK KKKKKKKKKKGGPQGNPQLKQKIG KPPGGFFKGGGGPKLIPFFKNALFFK KCPQKKNLGPGPGLKNFLKEKKA
3467	17368	A	3490	57	366	INVFAGKDLQPLCACPSPTTIVESDR PDMVQCGNLNHFYLI IYLRNSALVAQA GV*WHHLGSLHPLPEPKCFSC
3468	17369	A	3491	25	384	IRGTF*FWGGLGGLSGXNPL*KNPSF PKLGVLPPLFFPGGGGFFFPAGAPGF KKKKPPPKKFF*KKGAPPPFFFFFF FF
3469	17370	A	3492	170	41	AGPDORGETTFLKLQKLTTRHGGL* S QLIGGLSFIQKITC
3470	17371	A	3493	1	240	VLSPADKTNVKAAGKVGAGHAGEYGAEA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USNN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						LERMELSFPTTDS*FLDFFFLERKIGFH HVQSSGLFELTSRDPASAYNSLGS
3471	17372	A	3494	359	204	TQWLMPVILAPWEVEVGR*PEVRSRLRPA LNSPPFFKRLVVMIMYIMNIIILS
3472	17373	A	3495	1	178	DRLSGV*GSEEL*LCHTFGWATEPDH VSRKKKKRKKVGLGKNKAKQKHPRGYYR AEL
3473	17374	A	3496	361	1	LGPKLKKKPFWISGIGKVGAGLPGFFFT PPQ*G*NGFLKRGGFFFYFFFAKGWNT PGGKRGPFPSRLPEFPFVVLFFFPNLP NNWGHKGAPPKPPFFFFFLRNSPALVAQ AGVQWCDL
3474	17375	A	3497	276	79	AEVYKIKCELGAVAHACNFSTLGGQGG ITRS*VSASFTEKKVQLALMKELLNE
3475	17376	A	3498	3	476	FGTSMNIIITLTPRLARGNNLFS CPPT FTFDHLATPLLILT*LLPLTSMASQRH LFRFPLSRKKLYLSIQLSQSLIITPT GTLLIIFYIFFETTLIPTLAIITR*GNQ PERLNAGTYLLFYTLLVGLPLLLIALIYT HNTLGSLNILLTLLTVAQE
3476	17377	A	3499	581	2	AHACNLNTLGGRGWRIT*GQEPDTSLAN K
3477	17378	A	3500	380	135	RHSGQIGKTPSLVKIPKLTLPFGKGV *SHLTKRARQEKGLNPKSRGFN*PKLRPC PPTIVAKQNPVSKKKKOTROEPSA
3478	17379	A	3501	1	386	GSR*GNHPERLNAGAYFLFYTL*GSLPL LIRLIYTDNTLCSINYLTLTQELSN S*AHNLI*LAYTIAFIVKIPLYRLHL*L PKAHAQAP IAGS IVLA AVL LKLCGYGII RLTLILNPLKKHIDYF
3479	17380	A	3502	2	389	EKOL*KDKOVYRATHRLVLGAGESGKS TTAKMRILAVNGFNQEGGEDPHARS YIDGKATKVQDILNLLKEGIIETIGAVN SNLVPVVELANPENQETVDYILSAMNVP DEDFPSEFYEHAKALNE
3480	17381	A	3503	2	379	PGYIGMV*AXISIGFLGFIG*AHHIFT VGIDVYTRAYFTCATIIIAIPTGVKVPFS *LATLHGSNMK*SAEL*ALGFI FLFTV SGLTGIGL TNSSLDIRLHDYTVVVAHFH YVLSIGAVFAIIGG
3481	17382	A	3504	281	68	FKMRFGWGHSGTQSVENYKPLLKEIRENP NK*KNIPCSWIGRISIVEMPTLPKVIYR FNAFFIKLPSPPFTL
3482	17383	A	3505	139	263	ETGSHYVPOAGL*LASSDPFATASQNI GITHVSYVQPL*PIFEAVAGGSLEAR S
3483	17384	A	3506	2	427	LKTSMTMISTITLLT*LRPAWH*AQYQTP FFV*SA LITAGLLFLFLVLAAGITVLL TDRNLNTTFDPAGGGDPIYQHLF*FF GHPEGYILILPGFGIISHIGTYSKGKE PFGYIGMV*AMISTGFLGVIG*AHVFT GG
3484	17385	A	3507	343	3	GWHSRSSGGASSFSSPSHRSRLRVSSGS LGRIL*WSKSSKTSVSCGVVARDTEKPLP SKIEASSSDSCSVMAKANAVFTTGTG EKPASSASLSLVWASGSSPPGAANSS S
3485	17386	A	3508	3	363	GPDKAARRIALENLDIT*KGMRTHKC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						AKQLLSKQFF*SSRTGDLKLELOIELVR ETKRKC*RVL*IDRALTSHLYSLLQTD ALGDASADLIQKTS*LQEEFGYYAKTQK LLCRNGET
3486	17387	A	3509	3	434	GGPDHVARGISGKKYDIOGKMGMTYK TKELLSQRFGLGSPTVDLEL*LQIELLR ETKRKYESVLHLGALTAHLYSLLQTOH ALGDAFADLRQKSPOLCEEFQCYAQTQK LLCKNGETLLGAANLFVSSITYTLGKTMT EDTL
3487	17388	A	3510	1	401	GTRKNSFLHDSQTSFCFSDSIPTFSNME ETQKNSLELLRISLILLIEPWLEPVRFL KSMFANNLYVDTSDDVHLLKDL*EGI PTLMGRLEDGNRRGTGQILKQTSYKFDTN SHNHDALLNGYLLYCFKRCMDN
3488	17389	A	3511	117	2	KFFTFSEMHSSVA*AGVQRNLGSLQ LPFAWQFSC
3489	17390	A	3512	491	90	KKVXIVLAGFFPKFPFPFN*KKGLK*R KGVGPRYTVNPHDCVYKFGGPGVQNP PQQRGETPFPQKKNKKPGGGGALLP KGGRGVPLSPKFKLFPFGPPP*CKK KNRFQKKKKKRON*PQKSC
3490	17391	A	3513	2	31	GKGAPTTSLINAVGKTITAKRVEDNKL GAICSLTCCGAHIGTPMARDERVNLISF TGSTGGKQVGLMVHERFGRRLVLEQGN NAIIAFEDAHNLNLYVPSTLFAAVGTAGP KCTTARRQLIHESIIDEA*NHFFH
3491	17392	A	3514	2	390	KEFEKTHPLENITLAPDEPGDGLPVA YNPMDIRQREDGQTLNIREPYGPIPD F*RKIRQSYFASGA*LDTDGRLLSALD DLQLANSTIIAFTSDHGWALGEHGEWA* YNNFDDDDHDLPIFYDT
3492	17393	A	3515	3	410	RGTGNWAGGHYTKGAELVDSVLDVVRK ES*SCDCLOGFOLTHSLGGGTGFGMGLT LITKIREEYPNRMNTFRVMPKPV*DT EGEPYNATLLVHQLVGNDETYSIDNEA LYDICFRTLKLTPTTYGDRHLVS
3493	17394	A	3516	1	396	GEDAANNIYARGHYTTGMENIDLGLDRIR KLADPCTGLQGLFLVHFSFGGTTGGGFTS LLMERISCDYGGKKNLEVISYPAPQVCT AVFEPNITLSTHTTLEHSD*AFMVNDNE AIVDICRINLHIERSTTNL
3494	17395	A	3517	2	399	EKGYNPDTVAVFISGWDNMLEPNA NMPWFKGWVTRKDNAGACTTLEALEC ILPPTSTRDKPLRLPLQDVKKGGIGTV PAGRVETGVLPKGMETVAFVNGTTEV* SAERHHEPFPREALPGDNVGF
3495	17396	A	3518	1	402	GEDAANNIYARGHYTTGTETIDLLDRIR KLADORTGLQGLFLVHFSFGGTTGGGFTS LLMERISIDYGTSKLEFSIYPAPQVST ACSEPNYSILTHTTLEHSDCAFMVINE AIYDI*RIINLDIERSTYTNLR
3496	17397	A	3519	1	408	GSCIGQLKLYNSTTKAT*WSSNHTKKNP FSKFPKLQNVWTHPESHDRWTAPRILY ICGHRPVYKLPNQWAGSCIIGTIKPSFF LLPIKTGELLGPPVYASHAKRSIAGNW KDNEWPPERIIQVYEPATWAGDGL
3497	17398	A	3520	3	162	ETVLLCCPGWL*TLGLRQSSCLSLPKCS

SEQ ID No: of nucleotide sequence	SEQ ID No: of peptide sequence	M eth od	SEQ ID No: in USN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleo- tide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
3498	17399	A	3521	184	354	DYRHATVPGQKYRFNRYYSYS ETGSSLLP*GSSELPVSHPYFFNTHLS LSHTHTHTHTNNSISNHYCLPTNMS CQRLVAVYRQKGSFADQCTDI
3499	17400	A	3522	2	313	YYLSPPMGDQPGQHGETLFLQKLAG*GG ARLSQLLRLRLRQENCLTGPQIACRELL GFKNSCAFCQKQKQLCLNTLYSSLD DKARDSVSTKTREREK
3500	17401	A	3523	13	127	LGLQARTTSMSS*CYRRAPPCCPALLY F*VETGFHHVGOAGLELLTSTRP
3501	17402	A	3524	148	1	SCVFLSESCSVAQAGVQWYNHSSLP* T DGLKRSF*LSLPSRDHRLMT
3502	17403	A	3525	1	98	VNFGEGCS*EPRSHHCTTAWTE*DSIS KINK
3503	17404	A	3526	138	3	AASTHDLG*LQPPFPGITPFSCLRLSS WDYRVPDLRANFLYP
3504	17405	A	3527	10	206	PTTSLISFTSYSPCLKCSNVVEQVNRMR VLFYKSKQRLGMVAHYDSTLGGRGSK IT*GQRRG
3505	17406	A	3528	345	3	VTELYQSNKAKKKKSKNNEQSLQKI* DYAKQPNLRISGVLEEEKSKLENIFE KIIENFPGLTRDLEIQIQAKRPFKI AKRLSPRHTVIRLSKVKTGRILRAERQ K
3506	17407	A	3529	3	90	AVL*ALGFIFLFTVUGLTIIVLANSVDA A
3507	17408	A	3530	3	90	AVL*ALGFIFLFTVUGLTIIVLANSVDA A
3508	17409	A	3531	354	3	AVINSLPTKSPGPDGFTAKSYQRYKEEL VLFLKLPFQRIEKGLPNSFYESSVIL IPKPHRGTPKESFRFISLMNLNAKILNK RLAS*NHQHIKKVIHHGQVGFIPRTQGW FNQ
3509	17410	A	3532	2	357	FTRPRFSFTFFVLIRKYLSCGKISIQH SY*KKSKGKGLG*GINFCEFFERFHS VTQVGQKHDGP*LKFFPPGFRGFSRLS LPSSNNHKGRTPLRANFCTPNKNGGRRG RKFOY
3510	17411	A	3533	76	365	KKKKKKKKKKKKKKKKGGAGPETHK MKGSEKPPGVFLRGVGEIKFFFLKKG PPF*KKKPLKNKNWAREPSFKKIFKKKK KKAHFFGPKILKK
3511	17412	A	3534	7	353	FFGFGGVFLVFLFFFF*KYPPFFFPPL FFFPFFKMA DPRPPPPFPSPFNFFFP FPDPPPPFFFPQNFPLFLSPFLFFFS PKFFFFFLTLTKKKKKKKKKTKPKI HPQTRK
3512	17413	A	3535	354	41	AGGVPPGIPPPWGGGRAGSPKRGSGPFP WPKRGTPPPFF*KKKKKKKPGGPAIPA TREGEKSP*PWKPRVQPT*NAAPPSP PGEKAKPPQKKKSMFHR
3513	17414	A	3536	174	364	TFNSLAFTEFFFF*RETGSHFLEAGVQ GNHSSLNP*PPGLRGSSCLTLPKC*DYR REPLPA
3514	17415	A	3537	38	368	PGRLRLQEA VNHCTLEFGQGSV*KKKK KRGAFFKAKLTLGAKGKKKKTGVFF *TLKIRPKETRNQGSQQRKKAELGKLG QTYVPLNFKATFYGEQGDIY*TFKFP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, =possible nucleotide insertion)
3515	17416	A	3538	107	349	SVTFPPFFFFFLKQTGSHFVV*AGGOGGN FD*LEPKPPWLRSSLLTLPSSLDYGGP PTGPNFGIFFEKRGFCLVPQASFE
3516	17417	A	3539	274	3	PRRWSLPLTOMGFLPSRMGPKTCLCPKK KKKKIPPRKILEPVDVTGQFYLMFKEIT SIFLKLQCCCEEGTFSNSF*EARIALK TK*DKN
3517	17418	A	3540	1	374	ACALVRNDHIYVVVGPTALGELFFETET PIIIG*DN*LGPLVIGAHVVALTLINY ISL*L*PPSVLLLLACAIPEARAGTGCT AYPPLAGDYSHRAAYVNLITLSLHLARV SSLWDWDSITT
3518	17419	A	3541	427	76	RGSLSPGV*K*PGGQNTFPKAPKLRRP APRCFPAGKSGTKPTGSPGGRGRTPC SKKKKNFRETPSPFFMGPPFLKNRGGF MFWASKTNGLNKLTGPNPGPLGGRLS DFWVG
3519	17420	A	3542	234	88	FFFFFFFFFFFSSFFSFFFFFFFFFF FFFFFFFFFFFWM*LLYFV
3520	17421	A	3543	30	419	TGFFFFFLFFFGFLVLGGEGKGMDBKP GPAEKPTTSPPKI*KKGAPDPVRNFK KF*KKGDLPSPGGKNLKSFWGIWSIGN PLWVTPKPNQKPPFFKGPKKNFFFKG PKPGGKTKIFFFFLEWK
3521	17422	A	3544	159	411	VSRDPSVRLSPSSCF*PFLHISSSVE GRFSSFAQFLSLCNFTCPPLLFLLLRF *DRVSLCHPGWSAVA*SQTATSTFWVK
3522	17423	A	3545	2	351	CLARTSGVES*ASLPCGQNSYIHYLKL CMELSFPPYLLIYSISYLY*HTIMVIY FILVL*SILLNLIYLVFTQIPFALASGS SFNWLCLFNTTILAVHVCVCVCVCVR VCAC
3523	17424	A	3546	397	1	KPPPPCSYGGKKKIFLLVFFRTLPKFP GAGRKIFPRGPGFFLNKPKAL*TTFAPP PFIQKGPFLLOQA*IPFPVFFLFKKKP FLCSP*GGIGVSLFFFFSETESC SVTQ AGVQSCDLGSLQPLPGLKR
3524	17425	A	3547	76	354	FLNFPMGKIFPMFRGGVFFFPFGGNYI FLVLKIFPFFFGGFLDPFFFLKKFFF FLGFFFGKISQKIFFFVFN*IFLLXXGA PPLFFFFFL
3525	17426	A	3548	197	1	YNKNGQRM*EKIPAKHVSHKGLISQI CK*LIHLNSEKTNPRKWAEDLNHRHS KRDTHWNNM
3526	17427	A	3549	175	309	KSTLKVMLISISIFNYFF*DRVLLCHP GWSAVA*SLTAASTRP
3527	17428	A	3550	3	196	GFHRVSDGLDLTTS*SACVSFPKCMYD SHEPPRPAHKTSLKXNKRVRRIIIMMTI TYPAPVVC
3528	17429	A	3551	3	360	RAVEIFCYDVCVSGGACDIQLLLCPTS IKVCFSSLSLDIVTIPDIYICIIYII FFFFFKQARS*COCLNDKE*YCSLWPTP PGFKKLSVSLPSIWDLCAPSHPPNFC VFGKNGV
3529	17430	A	3552	326	1	KDNHRILKMLAKSGKVRHYVDFGKQY SKMSEKNIGVKPPIGKEKTKNPKKPSR TEDPKICTYVL*PDKKWRRLNT*GIQ LG*KEIKLSLFDADMIVYLENPV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
3530	17431	A	3553	186	1	KPRLRLIKLPMFTTFTELEKTTFKPI*NO KRVRIAKSILSQNEVGGITPPDFKL*Y KDTVTN
3531	17432	A	3554	3	366	KTSLGNMVKPYNFV*FPYI**KKEIKK NSIGVL*FGTEQSKHEFKKILPSSKRNKI ASKRIKYL*INLT*EGQDMYTENYKTLT KEI IEDLNKYKDIPCS*IIRLDLVMMAV LTKLIYREN
3532	17433	A	3555	239	1	GRGKMLPVSLINI*TVTFAPCSGISILV LIALPSLRILYITDEVNDPSLTKISIGH QWY*TYEYTDYGGILFNSYILP
3533	17434	A	3556	3	123	QAGLEV*TSDDLPTSVSQAGITGSGHR ARPANI INSVF
3534	17435	A	3557	237	2	KGFSPTQKFGFLGVFPPOKKKTKKNPR PPKGLTPVS*KGMLTEPLEFPFFFLRQ SRSSVAGQVQWNGLSLQALPP
3535	17436	A	3558	87	379	KKKKKKKFTLQKPVGFLNPNNGEAKSOI INELLKIATKKKKLKLKKKGKDLF RGNYNPLFKKIKDDPTNGKNFPCS*MGK ISFEKMTLLPKAI
3536	17437	A	3559	390	181	KKKKKNPGGGGPPFFPTFRGG*GGGFPQ PGGGGAPKV*ISPPPPPGGKKSPPOKK KKKKKKKGPFPLPHL
3537	17438	A	3560	2	101	VIVTAHAFVITIFFVPIIIGGFGN*LV PVDAA
3538	17439	A	3561	2	126	INTLLALLLLIITF*LPOLNGYTEKSTP YECGDFPISRRRG
3539	17440	A	3562	16	349	FAFOKITLAMEKATEAQTGAKKACQGT NNIMKPLKKKCIPTTIFWISFFSFLFFF FETKPHFNWPEGKPNLG*LKPLPLGL KQFCCLTLPRKGNRYRHLPPVNGFFFF
3540	17441	A	3563	6	130	TLRRILEDHFSLRS*GCGEPLCRHCPMA WLTE*DPVSKNIY
3541	17442	A	3564	3	152	GFHCVRQDGLLTS*SAHLSLPKCDYR RKPFPAGKGTFFIDYSTIE
3542	17443	A	3565	241	3	NLVSIVSHRKVNLVQGNVTSSNRNSH TWLSFVILYPIIISIVFQGVFGVYA KFSSDDE*DFGVPIITQVYTAHP
3543	17444	A	3566	71	256	SVFLTLVFLYPLATSEFFLNKVSLLCCP WL*TPGLKQFCSCLSLPKRWNYRHEPLTP GSNFF
3544	17445	A	3567	1	392	AGAGTSGTDYPPLSGNYSHPGACVDLTI FSLHLAGVASMGLAISVMTVMNIEPPA IYOYQTLFV*SGRNTAGLLLLCVPLA AGITILLTDRNLNTFFDPAGGGDPILY OHLGKRGIIICSHRDRI
3545	17446	A	3568	334	409	LGTVAHACNPSTLGG*GGHITRSGV
3546	17447	A	3569	3	467	PKNPGGGFFSPL*EKKYILPPP*TWPP PGFF*KAPPPPPPPPPPPPPPPPPFIQI YFIF
3547	17448	A	3570	3	420	FFDPAGGGDPILYQHL*FFGHPEEYML ILPFGILSHIATYSGKKEPPGYIGMV *AMISIGFLGIIV*AHIFTG*IDVDR AYFTSATIIIAIPTOVEVFS*LATHGS NMK*SAVLSALGFIFLTRGLTSIV
3548	17449	A	3571	1	418	NLIHNSFIDLFTPSNIFA*NFSGSLGA CLILQITTLGLFLAMHY*PDASTAFSSIG HITRDVHYG*IIRYLHARGASIFPICLF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
						LHIGRGLYVAGFLV*ET*NGIILLLAT IATAPIGVYLPGGQISF*GATVITNLL
3549	17450	A	3572	3	414	SSGLAM*FHFHSITLLTLLGLLTNTLT Q*WRDVTRESTYQGHHTPPVQGLR ILFITSEVFFVAGFF*AFYHSSLAPT LGGHWPPTGITPLNPLEVPLNTSVLLA SGVSIT*AHHSLIENNRNQTIIQALL
3550	17451	A	3573	2	423	GTLYLLFGA*AGVLGTALITLRLGQ PGNLVGNDDHIYINGVTAHAFVIF PIIIGGPGN*LVPLIGAPEMAFPRIN ISL*LLPPSLLLLASAIVEAGAGT* VYPPLAGNYSHPGAVDLTIFCLHLAGV
3551	17452	A	3574	411	117	DGGPLQLQLRRARQENCFNPRGGCS* RLCPCPAMGAKLNSLSGKKKKRHRVE KYAQHDYIINVLVCVVRHKWLSLYMYS ITKSIDKICKKAS
3552	17453	A	3575	2	394	ALANMWEQIRSLHQYAVHRIISLFSLLS KKHDRVLEQATQYLRGSLNTNDVPLPDY AQDLTVIEELIPMLLEIINS*LTNSLHH IPNLVYALLY*RDLPFQFTRHPSQDIM QNIDLVSVNEDYVDSFSL
3553	17454	A	3576	262	418	GKREWTLLIFTFETTLIPTLAIITR *GNQPERLAGTYLFTLTVGSSFL
3554	17455	A	3577	232	443	PSVQTFPCPLSEGGFWLLCVMTSPSG VVPVTERALYSMECAFHLFSLTSGACR LDYRTPDNR*VQLP
3555	17456	A	3578	48	410	GGLLLHRAGCRCGHAADRADQPDSSDPH SLHAACLPPIPGGAARAAGAPSTA*TPAA CPAPVPAPCSEHRC*PGLSQRPCLPGL PDARPPGAAAHGWSLPTRLVMDRSH EAPRRHED
3556	17457	A	3579	422	186	VYSKFL*SQLLERLRQENRNPFGSRGCR EPRS*HCIPAWVTQDQSLSSISSTSH CGSHCSGYLTVHICDQPVFSL
3557	17458	A	3580	442	3	GSATSSRCRTOESTYQGHPTPPVKGLRY GIILFITSEVFFLAGFL*AFSHSTLAPT SQLGGHWPPTGITPLNPLEVPLNTSVL LASGVSI*AHHSLIENNRNQTIIQALL TILGLYFTLLQASE*LESPFTISDGM YCGRSRG
3558	17459	A	3581	428	1	IRDFMNASLGM*FHTPTITLLTLLGLLT TPLTIYQ*WRDVSRESTYQGHHTPPVQK GLRYGIIILFITSEVFFVAGFF*AFYHSS LAPTQGLGGHWPPTGITPLNPLEVPLN TSALLASGVSI*AHHSLIENNRNQTIIQAA LE
3559	17460	A	3582	160	415	RLSHCLAPFMLSILFIPSQLLSLPFHV KNIFFFFLNKKFNCVPGAGGGQGNLI* LHPPPRGLKKFSLRITSS*NYGREPQ S
3560	17461	A	3583	399	2	STHLGLPKCWDYRCPEPRPALLATVLL CKTHIVRINNVCCLPLITGAASVIGLSA SLLFSVSPGTSLOLEAR*TFPWFMSST CVWRIFTSLGRAQPOHSDLOTCPRRDV DLAEPGLLFNGQMLVPPGRS
3561	17462	A	3584	215	1	KSPGLLNAFSRGSGQIYQASRAMGA*LNQ RFWPGTVAHACNPSTLGG*GARIMRSGD GDRNSKDGVSFCGRV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
3562	17463	A	3585	138	19	LNORFWPGTVAHACNPRPLGG*GARIMR SGDVYRNSKDEV
3563	17464	A	3586	262	3	GRPEVYKPPPPRGEFFFFFLLFFFFF FFFFFVLLFFFFFLLLLLLLLLLLLL*Q VRLYLLEKYLFFFFLFYQELSLCCPG WS
3564	17465	A	3587	381	1	KKFTPPP*PRKMGPPPGFF*RAPPPFFL GGGGGLFFLLGGPPPPGGGFFPPPPV FF*KSPPLFFSF*KKRGGPPFKRGGSPK TPDCFFFKKNPPKKKKKKKKKKKKK GRPSKSDAVRTG
3565	17466	A	3588	198	1	PKSFERPLARKEPNFFSKKKKKKSI*N LNTNSWLDMAHICNPSTSGRGG*PHL RSGVRDPOQ
3566	17467	A	3589	373	1	GIEFFPPKRGGFPPPPKKKFFFPFGFI FGGGGG*FWPPKRGGLFLKKKGVF*SP D*KGKKFFPPGGGVGPPRGLKGGDI IFFFFFFFFFFFPPFFPATIFLITYK DLTCHDGTHTH
3567	17468	A	3590	506	98	HTSRGPPPPKKKIIPTRPFFCCFWV FFPKKKFFFCSPRSFIHSPKKKKKN FFFPKGGGPPPLSPFLTPPPLFFFFFF FFFFFFFPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPP*LFVSLPSI FVLLIFFLYNAITTI
3568	17469	A	3591	407	1	LVRGQITNKKNLNFISELREWRVVF LPQORLFFFKL*LO*KEIYLI*MYTCS RGAGFKSSLYFFFRSPQVVLFFFFFF IFFYFF*FIFFFFFFFFFFFNCDFMI VLYISPLPLEKKKGGRSRSRS
3569	17470	A	3592	380	68	FRRGVGPQWPPPKKGFSGKPPGGFKRP PLKGGKITTPPGKFGPPKGPFRKPPF FLEGGKTLFLGDPD*NLGWWG*RGHK *GPANPRVPVPPFFPEEYSY
3570	17471	A	3593	394	45	ALMFSTGEGRQELKHPHPPHKKASRGE EPKGGVRKNYPKKKSKPPKNPPGVTP PKKKKAKLPPRPL*GQQRPPQKTAPP PLNFYPPKEPTKVLISFFSFFFSAND VELY
3571	17472	A	3594	402	62	AMTVLLHSSLGNAKAPCLFKKKNAKDLN KHSKEDSQMANKYMKRCLISLVIRNMQ MKITVRCHFILTRMAKKKQVNSKCRKE VQKITPLKHCWCKEKIV*ILWNTLAARV G
3572	17473	A	3595	220	425	FISGFLNQEEREIAFFKVNIRLGAUV HTCNPSLGGRRRIT*SPGV*DPQGH GEPCLYLNQKN
3573	17474	A	3596	13	412	AETAPLRSIHRARNCLKKKGRKGRNPG GDGPNPQIGPAFFGGGNGKTPGQKHPQ QTWQGRHLKGGGGGPKRKGVPKPKKTP TIWGTPLAPGVENWNGHTGNPGGADP KPGREK*SGGAQITGPHGTG
3574	17475	A	3597	2	293	CQLSP*ELGTPRERERERERERERER ERERLPRDLREKRAQDVATHPNYEFV CVIRHYRGCVVYTPLTTHASIDAHKMCV CVKKRPLYKKKK
3575	17476	A	3598	243	9	ILLRQEQCWSKGRFQLODEQVLNT*D RTWVMWPGAVTHACNPSTLGGGRGIM

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3576	17477	A	3599	1	329	RSRRDRDSRIHGGGSKPKSPR ESARRDWNIPKLPFPPRGKNPTGFFFLK PGGQQRGGKGGKGNF*SPGKPF*KGGG PPQFCPPPPRGGFFFPFGGPGGKGGG VKGPPPPFFFWPPPPNNLFFPPGA
3577	17478	A	3600	206	1	LRALGIMERAHAHTVRLVFQILGSL* YIF*RQDLSPSPRLCSCGTIAARCSLDL LSASNSPASASQ
3578	17479	A	3601	322	99	KRTGAFGFPFFFLFNKKKKVFLGPEGPK IVKKKKKKKKKKQNNRKKQTKK*KTN NKQNKKRETDIFGVEDBT
3579	17480	A	3602	410	25	LIFFKKKTGGGGGGPPFFHPFGVNGG VIRVGELSPPCPPGGTRFFPKTKNYPG G*GGFFPPPSGGGLGPKTSLPRGGS L*PNFGSLPKKGGGPPSKKKKKKKK QSRPRDS*SLRRGRK
3580	17481	A	3603	27	349	RSSIQCGILLFYFLYVMVFNDFVVL* GFSAITSLISMLPSCI*YVFFMVCLL FNRCHNIFYFL*MTKIAQIGN*IPFR DAYLGVFFLFFFFFGGKLYL
3581	17482	A	3604	88	435	RAISTCLQNEQKMLTTITSVEKSLNDL TELKTIW*ELHDKCTSFSSRPQLQERI SVTEDQNMENNNPLIHGFIYGSYSY STMVRKQDKLRVKDAGIKHRNQNKGFTA EKSA
3582	17483	A	3605	331	428	YGHYQIEATFLPAITTEKTELTKRKL* *SSINLLK*T*NVRPGTVGHACNLSTLG GRGGQIMRSGIRDQPNST
3583	17484	A	3606	3	294	GG*GCELSCHCTPSSLG*NTVRKKER KKGKREKERKREIIPGFGCAHHGA VTLGNLFPRVQVSQLVQRKIIITVIFD RLGEIVLSQSL
3584	17485	A	3607	263	426	RKLAGTFFFLWKSGFPOTILAAQRMGG NDPKETRVFHAGLSSSLGENK*VWKI
3585	17486	A	3608	213	439	LSWACAAXETVTQPANFLDYILPFFLL IRESSKF*RHMATQLETAASRPGVVVHA CNPTILGGRGGRITRSGVH
3586	17487	A	3609	2	441	MTDLESFPLESELSANSPVQCSGLCKPV LTIQVISHKGHCSSKYYLLNANYNVL HLSNSVLPRLLSQORTQKHFTAVLS VCLSYLSRDRVLLCYPGWSAVM*FYSL *PQIHGLKQSSCLSLPK*DYQHGISPP WCN
3587	17488	A	3610	102	354	EGGAWADRCWLGRVLLTHLWPCCLYFF YFIPIPLNSGDRVSLCCPPWSCLK*SSC LSLPECHDYRCQPLHPACAVFINSKR
3588	17489	A	3611	462	371	GLNFLTLL*SAKRLPKCNDYRHEPRPA WS
3589	17490	A	3612	463	319	RNSHDGLELLTL*SAHLGLPKCNDYRCE PPRPVLC
3590	17491	A	3613	49	476	PRNSTLLILGLTNTLILYQGVDFVTR ESTYQGHHTPPVQKGLRYGIIIFITSEV FFAGLF*SFYHSRLAPTQGLGHWPPT GITPLNPLEVPLNTSVLLASGVSI*A HHSLIENNRNQLNALLITILLGLYFTL LQ
3591	17492	A	3614	223	467	TPS*PLAIT*FISTLAETNRTPFDLAER ESELVSGFNIEYAAGFPALFFIAYNTNI

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						MIINTLTITITIFLGTTTYDALSPELYTTTFY VTKTLTLLTCLFL*IRTATPRFRYDQLIH LL*ENFLPLTALLLI*YVSIPITITSSIP D
3592	17493	A	3615	2	405	ARGLQEAGAVQNDPVSRLFDHMLQQRH AHQMAIVTYQRPGETYIPKDKQY*FLHE SQTYFCFLNIGIPTPSMMEETQHRSSLEL LRISLLIESWLEPVFRFLRSMNNNLVY DTSRDDYHLLKDLLEGIOTLM
3593	17494	A	3616	328	63	PSKF*KPCCLISPPPLGSGPPN*TPGFLK KPKFPPRGGAHP*SPLLFRVRPGDPLNP RGGGFP*PKLPPGPPTTRATKPNFVSQKK KKKE
3594	17495	A	3617	1	379	GTSVGIPTGGQEFSS*FAALHGSNVK*SA AAL*ALRIMILFTVRGLTGIGLANSSLD IVLHDTDYVEAHFHYVLSIGAVFAIIGG FIH*FPLFLGYTLDDQTYAKSHFTIIFIG VSVTLFPQHFLGLC
3595	17496	A	3618	494	17	GSANPRNPRRSGSKTRETSPRNVMSLMS PMSPTLPMRPTSPGT*PMHLTNSMGPMQ PNSSRPVNPASSATPVSPASPARPKPS CFPAQ*SPPL*SPEDRHGLSCLSVWK KECETWHVVSMMHIVEDRHSKPYHGPVMV AHACNPSTLGG
3596	17497	A	3619	350	480	LGSWDYVCKPPHPLAVLL*RCQSFVLLPR LVTNS*AOVIHLPPW
3597	17498	A	3620	2	400	AAAEPHGCTYAKVLDEFKPLGEEP*NLIK QNCFLFQLGSEYKFNALLGRYTKKVQ VSPFLVEVS*NLGKVSCKCKHFEAKR MP*AEVDYLSVNLQCLVMHEKTPVSDRV TKLLTESLVNRRPCFSALEVK
3598	17499	A	3621	3	476	LGVSVHPPOPLAQVLSPPFLGASRAQWL LRMRGPPSPHPPTTPAGLQAPHAALVPA RASPTPPCKLEWAPALASPERGSHSA VGG*RAPOMPMPKWEPRQRCQEQARALR TASMLSPLSFTHPVTLSSLNFFTSLPDR NSPSWVPVVSVR
3599	17500	A	3622	40	390	MKGALTPGRAGGLGSGSOMDASTPKP SPDDQGCSTHLWGFFLWSLLPSPSLSPS PPSPRRHSVGTCHAP*VLPRLGALRVP HSSVPRPHAVPVVGTTRYRSRGANPLSL DFRGL
3600	17501	A	3623	52	475	AVEFHLLFLQPLETTNLLSVMCLDPLILA NSPK*NQIICDLFWFPHLA*CF*DLFML EHVSVLHFMAE*FFFFFF*KGVSLSFPG WRAGAQFWLTKTPPHSPARLKQFSCLTL PGSWNYRRAPPSPANFFVF*SKRGFTIL P
3601	17502	A	3624	333	466	SIIGKIRLWKMRPWPFGAAQACDPGILR C*GKRITRSGVDRPG
3602	17503	A	3625	2	138	LRRGNRLNPGGGGGGCEP*SRHCTPASST E*DSVSNQKNTKNSQWH
3603	17504	A	3626	3	337	LSLRFPALPPCFRRRLPTFGQGHGPGSAG FPGRP*RLPPLDPDPPPSLGLSPGDDP GLAREELKSPCCWGPPLCHLPPF*CWA SSQPSINAYEWKKKKKKKKKKKKKK
3604	17505	A	3627	2	393	LGTDLSLLIRFELQQGNLLGNHIIYNV IVTAHAFVIIFFIVPIIIGGFN*LF

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						LIIGAPDMALPRINNISL*LLPPSLLLL IASAIVEAGAGTG* TGYPLAGNYSHPG ALVDLTIFYLHLARVCSI
3605	17506	A	3628	2	379	ODATYPIIEELITPHEHALITICLCFL ALDALFLTLTKLTNTNISDAQSIETV* TMLPAIILILIALPCLRLIYITDEGNDP SLTIK*IGHQWY*TYEYTDYGGIINSY ILPPLFLKPGDLRL
3606	17507	A	3629	1	400	PTRPPTRPPTRPMTNLTNSIHPLPR*K KKKKKKKKKKKKKKKKKKKKTAAGGGA *KCKNRGAKTHRSGSKLNFFFKRKNKIN PPVKIEKKTFFLGKKKKNNKPKQNNALK KKKNYFEGEGESLLLL
3607	17508	A	3630	416	1	SQLGYSVGRDPLEEATCLFSLDKLHAGR TTPLFOAVRQGHILQRLQFPFA*LCPA PRGGVYRGRQASLSCGGLHPVRASWPLC LPTQFSAMEGAPLPLPRSSSIDYCA SNEGQSVIGPSPPCNYLLVCHLL
3608	17509	A	3631	275	83	RWGSQVVLVGLQGLGSSDSFALASQSA GITGVSHCTQPKNVI*KISHLTVAGPAA DKTPQTER
3609	17510	A	3632	186	3	FFFFFFFFFFFVFVFVFVFVFVFVFVF FFFFFFFFFFFVLCVPLLCNL*HLVLY YMLV
3610	17511	A	3633	3	235	GITSLFLIR**YARADANTAAIRALYN RIGDIGFILALA*FILHNS*DPQQIAI LPHSPDSKKYLYLSHLQKKA
3611	17512	A	3634	1	428	RTLKTLFNPDDG*DPILYQHL*FFGH PEVYIILPRFR*ISHIVTYSGKNEPF GYISMV*AMISLGLGVIA*AHIFTV* IDVDTRAYLTATIMIAIPTAVRALS*L APLHRSNIK*SAKL*ALRLIFLTVGG QT
3612	17513	A	3635	2	129	PVIYSTIFAGTLITALSSH*FFT*VGLE INMLAFI PVLGWD
3613	17514	A	3636	2	422	DR*LFSTNHRDITGLVLLYGA*AVVLGT ALNLLIRAELEGQPNLGNNDHIYNYVIT AHAFGIILFTVPIIIGGFGN*LDPLII GAPDMAFPRINNISC*LLPPSLLLLLAS AIMEAGARTG*TAYPPLAGNYSHPGASV
3614	17515	A	3637	14	479	QNCINNFMYPFLPHQSEFPKRSCKQON TICFRLSNQNTMKKTENHALLWIRKQW T*KGQKSNQSYTPSPSRAKKKKKKKK KKKKKKKKKKKKKKKKKKKKPGGV LKKL
3615	17516	A	3638	2	449	ITTCFVGLCALVLTTLTKLTNANILDA QEVETG*ATLPAIMLVIALPCLRLIYI TDEVNDPSLTIK*IGHQWY*AYEYTDYG GLMFNAYILPPLFLKPGDLRLDGDNRV VLPNEAPIRIVMTSQVMHS*AVRTLSL RTDAIPGRL
3616	17517	A	3639	347	98	HFPLGGGKGGGFSPFPFKFFFLRQGF FGGGGPNFPFPKKGFFSKKPGQVF*TP PKKKKKFFFRGFWGPPGIFFKGPFP
3617	17518	A	3640	2	426	DR*LFSTNHRDITVLLYLLFGA*AGGLCT ALSLLIRAELEGQPNLGNNDHIYNYVIT AHAFVIFFGIPIIIGGCGN*LVPLII GAPDMAFPRINNISC*LLPPSLLLLLAF

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						AI VEAGAGTG*TVYPPLAGNYSHPGACA D
3618	17519	A	3641	94	294	GRGGGGVAGGRGAMMSKGRQRGRNGPVR GREGGKRSHFRKEG*KEGRKEPPPPPKK KSRGEKNOREG
3619	17520	A	3642	1	405	RTRGFDLRFVLFDVAQQMVESGYVCEG DBKTMANAIIDRVSLIKRKRQRQLVRE BOEKKKQESSLKQVEQSSASOTGIKQ LPADTGTPTASTTSASVSTOVEEPE AD*HBOLOYOQPSLEVLSDGTVD
3620	17521	A	3643	34	405	HILGRKONKATLEAEKKKKKKKKKKG GPLKNPFGAKNNRQGGKKIFSP*GGVK KTPDLGI FEKKPYFGGKKKWPAPPKIKT LKEKKKF*RGKGGKKPENPWGEDESS PK
3621	17522	A	3644	430	81	EFAQLSPQ LKGFSPPPNPLPSPFLGF FSPSP*KKFFSLKGFIPVGGFFPFPSP PKKSFSSKNPQLVFISPPFKKIFLFP PLNFGPRVFKRPPPPFFFFF
3622	17523	A	3645	399	2	AFFFTKKKKEFFPPFPKFFFSRVFF FLGGFFHFFPPQKIFFLKIPRGFFLTP PKKKKIFFFFP*FLAPGFFL*APDP FFFFFFFFFFFPPFFPSPCSWSCHQV EPHASNRINHNSNSYPLQGY
3623	17524	A	3646	49	326	KKKKKKKKKRGGFPKKTPGAQKNFGG EKKFFFL*GGHKPPRGIFKKKPPFGG KNWTTTPQKNKAFGGKKFLGGKSEKPP PKPRVKKN
3624	17525	A	3647	327	94	QKKKKKFFPPPPPPKNFFSPRGFFFGG GGPSPSPQKKGFFSKNPGGVFLPPPKKK KIFFFPPGGGAPGPF*RGPP
3625	17526	A	3648	2	301	TSSVASTFIMSFPPTTFMCLDQEGIIW N*H*ATTQTTLQYLSFKLDYPSIIFIPV ALFVWPTLIEVSL*YINSDPNINQFQY LLFLITLTLVTCG
3626	17527	A	3649	2	406	STNHKDGITLYLLFGA*AGYLGALNLL IRAEGLQPCNLVGNHDHYNVITAHAPG IIFVIVIPITIGGFG*LVPLIIGAPDM EPARINNISF*LLPPSLLLLGCAIVEA GAGTG*TVYPPLAGNYSHPGACV
3627	17528	A	3650	3	418	HAYADAWVHFHSITLLILGLLNTLTIY Q*WRDVSRESTYQGHHTFPVQKGLRYGI ILFITSEVFFVAGFF*AFYHSSLAPTPQ LGGHWPPTGITPLNTLEVPLLNTSVLLA SGVSIT*AHHSLIENNQNQITQALL
3628	17529	A	3651	526	2	WGGGEKGRAGGAGEETPHQESQRQGCAL PQEPPLYPCCPAIHPPPLPLGGLLLFPS LPPLP*AAWFPHQOQGRNLNGESPTTR EKRLWGPPLETPLPWPPTQPTPLSRRTG CPPCPREVPTSPPWAEPPPLPGPPSEI AHLTTVRGGAALANVNHNISDTDENKL NAPVTA
3629	17530	A	3652	464	297	RNSFHRVSQDDLLDLTL*SPCLGLPKCN DYRCEPLLPASYIDVS
3630	17531	A	3653	162	467	NSKQOQFVLLSEITSYVYLHKKRDLSD TIIMGDFTPLSLDARSARQKVNQIQE LN*ALHQADLIDITRYTLHPKSEITYTFFS APHCTYNFLFQSYSSQF

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3631	17532	A	3654	372	1	LMMLSTFSCVHLAFVCFLLWRREMSGVSL CCPDYSGAAAVHRCNHTALQOTPGLK* SSCLCKRHLQLRPQVYITMLGYLFLFLF LRQSCSVAQAGVQVHDHSSLP*TPGLK RSNSPTLV*DL
3632	17533	A	3655	444	341	VGQDGLLDLLTS*SACLGLPRCWDYRRE PPRLAY
3633	17534	A	3656	466	315	VGHGTGLEPTSSSLEPA*ASESAGITGV HCTQQSGCAFCYSTMIPTKPYTC
3634	17535	A	3657	40	276	EFDTAHAFVITFFIVIPITIGGFGN*LV PLIIGAPDMAFPRIINISF*LLPSSL LLASAVEKKIKKKKTGAPLV
3635	17536	A	3658	351	470	FTTLFVTSASLPLKTLAWPGVAHACNF STLGG*GGRT
3636	17537	A	3659	40	182	GIRKENHNLIGRGRLEPGSHHCTPAWA TK*DSVKIKKTRIKTPTLI
3637	17538	A	3660	160	461	INGKDTDTGPMVAHYNTSTLGGGGGI A*GQSFQPSLRN
3638	17539	A	3661	145	437	YFSLSLCCLLELMNSVILFFFLVLRGEFY PPPLVEMQGNPFG*LNPPPGGLKQFFCL TLPKSNWNRPPPRGGNLFDF*KKRGEN YVGRVDLKRTSG
3639	17540	A	3662	255	451	LLSENNFFFFFFFCGGGPPPLPPGGKG GLNFI*TLQPGKRNPPQPGGEP*RG PTPHGLFF
3640	17541	A	3663	185	66	PLEQPLRK*LYLFRDGVLLCHPDWSAMM QSRIMATSAEF
3641	17542	A	3664	42	193	FQLTLRLOENHNLNAGGTSCEFSRSHHC TPA*VTQSQSKQKVKVLGSL
3642	17543	A	3665	216	2	KSKGKCSFLHSRVNRGNSKELLFLRDGV WRYCPAWS*TPGLKQSPHFNIPKCWDYR REEFHHPGLVVYEF
3643	17544	A	3666	43	267	GRILSAMTPGKLKTLCKIDWPALEVGWP LEGSLDRSLVSKVMHKVTYKPRNPQDFP YRDT*LELVLDPPPPTHSG
3644	17545	A	3667	212	2	SQLLGRARAGWLEPRSLRKINKTSSQVW WYTFVLPSQCOYKHTPPRPNFCIFSRD GVSPC*PGWSRTFD
3645	17546	A	3668	104	334	TVLEFPFCFLHIDFCMVLDFSNFFVLN YF*NYRRVQKMYEEFPFFFLFLIFSFS FLFPLSTFNFFFLCPLCDLWYH
3646	17547	A	3669	369	260	DGLDLLTL*STHLSLPKCWDYRHEPPCP ANMPSFKN
3647	17548	A	3670	111	342	NGVSFFPPKKGGIWANGNFRPPKPGG* RNFL*PPQKFGMGPPPPQPVGIAGP PPHAREILLEFFFFFKKGV
3648	17549	A	3671	377	3	FAITGGFIH*FPVFPVYALACTYAKIHF TIIFIGVNLAFPPQHFLGLSGMRRYS YDPAFT*NISSVGSFISLTAVILIIIF MI*EAFPSKRVLIVEAPSNLE*LYGC RPSHLEDPVY
3649	17550	A	3672	39	348	AKTAPLNSLDERMRVSKKKKKHGLTP KPLKKLKLGKFLSLQELQKKNQKPF GFKGLELAPFGKNGENPNTWRNC* MSFFFF*DSHPFIQAGVQWRDLGSLQ RPPRFKRE
3650	17551	A	3673	327	3	SKDPVFVFKVKKNPPTNIGVFFPALPL KRQGFQPLFNPKGFFFFFKPVQLGRGK

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						ISPQFFFFKRFRWG*TKSFFFF*DSHPF IQAGVQWRDLGSLQPRPPFRKRF
3651	17552	A	3674	379	267	EPRLSPCTPAWATE*DSISKQNTKKPK LALNKKKMF
3652	17553	A	3675	2	270	FCRDRVSLVCFVRS*TPGFKGSSCLDLP SSDYRHAPPGLAKIGLHVFCLECCGS LLVCHSHCSLAHQELLENNKHTDVVMG QWNR
3653	17554	A	3676	3	54	PVTKNKNKRPDAVAHTCNSTLGGRGQ ITSGDRDHG*HL
3654	17555	A	3677	291	30	YSLVLLIFFEYCFSTVSFISLMNFCINL YYVLLDLDFGLVCSYFSPILMWNIEYFIG SMFPIFSVIV*IFPCWEMSCNIYKLHQE MF
3655	17556	A	3678	1	298	RDFSASASQVAGTTGMHRAQLFVFRV CVCVCVCVEREREREDGVLLCRPDCC SVAHT*VQGRDLGSLQPPPGFKRFFCL KLPSWSGHRCVDAF
3656	17557	A	3679	20	376	VPPPHLANFLNFILLFVDTGSGYVAVAG FKLILAPCNLSASNS*SVGITGVSHALL LLALKCNQLFQFVIFILLHAVCIYDFIM VRFSLQCFQFDFDFPCFILFVSSKAQF CFLRLPY
3657	17558	A	3680	110	334	NTIDYFKLP*ILSGTR*DMYKQPL*HLN TVREYTSKYGWRPGVVAHACNPSTLGGQ GERITRSRDQDQPCQHGET
3658	17559	A	3681	326	511	LTMMLQMKISVICCLLRNIFWPGALAH CNPSTLGS*GGIARSRLNPSLSLGS QPSS
3659	17560	A	3682	448	248	AKDLNTFFTFKE*TPLANKHMKGSARFT YRNVOIQT*RCLGTPTRVTGV*MRNSA RHR*GCGGLV
3660	17561	A	3683	486	176	PAPINPQRLSLVQRSGIRFC*AGQVGF KLLVSSDPPILASQAGITGVSHQTWP* NYS*NSGMPTHPRQASSWRLREQVYHS LLPCAIIYKNGRQNSLLI
3661	17562	A	3684	238	27	NKHLICVVGQEMGWSHSHGWKPHFK SQCVCPSAVAHACNPSTLGG*GGQITLV QPGKHKKRIALF
3662	17563	A	3685	1	299	LITQTCRVGLKIKCI*TSKKKKKKKK KKKKKARGPLKKGPKLTPEKPPGGPFK APFFWGGPPPRFFFGGGAPPPVFLKKK KQNSPLWGGGFFFR
3663	17564	A	3686	494	91	PLGKRFPFGDIALTKLSRPMWAPGPI PPLGGPGGVP*VTPFKPTTFRPGEPPL PLKNQTFVGVPDPYFPPLGLGPEIP FTPGGPGSILKPLPPSPPGAPKRNFPP KKKKEVMKMLCFHFNLVQNI
3664	17565	A	3687	17	249	YSRFRGHFGHDFGLYFQILRLRLWENHL NPGRGCSKL*SHCTPAWATE*DPVS* KKNVTTIAKRWKQLTCLPLADG
3665	17566	A	3688	296	461	FWLWSSVLKHMNWPVGVTHACNPNILG GGQE*SA*ARV*DAQP*HGETCSAEXK
3666	17567	A	3689	149	422	ASGRQGPDRGCWGGAPRHPARGAKPAA DMGMSGQYTKQAA*GDPSQARGVRLP REPTSRKASGSGSGHSRASGAVPGQRV AQPSPAR
3667	17568	A	3690	1	415	GDPAGGGDPILYGLFL*FPGHPEVYILI

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						LPFGFIISHIVTYYSGKKFPFGYIGMV* AMISIGFLRFIE*AHHIFTVGIDVDTRA YFTSATIIIAIPTGVKVPF*LATLHGSN MK*SAAVL*AL*FIFLFTVSGLTGIV
3668	17569	A	3691	1	393	GTRKYSFLHDSQTS*FCLSNSIPTPSNME ETQQKSNLELLRLISLLIESWLEPVRFL KSMFANNLVYDTSDDDYHLLKDL*EGI QTLMGRLDGTTRTGHLIKQYTSKFDTN SHNHDAVLKNGYGLLYCFRK
3669	17570	A	3692	402	2	FLTQRWGAFLPPIPPWEAPFGFSP*APG FKPPLPPRGNNPFS*KTQIYPALGARPV IPPSLGGGGGESFLPPGGGFP*PRLPFC PPFRGAKNFFFKQKKKKCLFCKAPAAQ HRSACLHCECLPLGNLLKLCPR
3670	17571	A	3693	3	434	IFPIFFGTTLITLAIITR*GNQPERLGN ACTYFLFTLTGSSLTLLALYTHNTLIG SLNILLTLTGQELNS*ANMLY*LAYT IAFIKPIPLVGLHL*LPKAGEADTAGS IVLAVALKLGYGIIIRLTLINPLTKH IAYP
3671	17572	A	3694	452	208	INKSARHGSNNL*SOLLRLREVCLSPG VQCISPEWSSHCTPAWETE*DKTLSQKQ TNKTKCOHLYDRHPSALEAETFLSH
3672	17573	A	3695	464	146	LKQTRATKGNLFL*PKPLTPFGGFRFP FQPFWKPRPLPGPPKSGVLDPGPGQKTP FVLKKPNLLGGVITLFFFLPSGGLGRKI PSRGGGGAKKRPKPRQKKKK
3673	17574	A	3696	2	465	VTRLRERPALVSSTSWTEDEDFSIILA ALEKFEQLTLDGHNLPVLVCVITGKGPL REYYSRLIHQKHFOHIQVCTPWLEAEDY PLLGSAPGVCLHTSSSGLDLPKVVVD MFGCRLPVCANVFKCLHELKVDENGVLV FEDS*ELAAHLEKI
3674	17575	A	3697	173	51	TFISVVGQOVVFGCMERKFSFGDF*DFG APITOG*SFLSI
3675	17576	A	3698	380	26	KQRTNFFLFFFGTGAFFWFFPPFFNKK KKVFLPGGPKIVKKKKKKKKENQNK RKQTKK*KTNKQNKKRETDIPGVEDE TWRQRWGLGGGRVANSSAEMGKGNSTR PSVNS
3676	17577	A	3699	11	414	RLVVPAIIQT*SFAGVILIIAHGLT SSLLFCLANSQCKKKKK
3677	17578	A	3700	1	401	SSSLTLNNNKSFLNGLVTFNEMWILYD NN*DAQNLDOEAPKHIFKFNLDQKVM FAVWWSAAGLIHYCPLTGETTI*SEKXA QQFKEMNRKLQPLQSAMNRRKGPILHDN A*SHITQLKLQKL*LGVEVL
3678	17579	A	3701	395	140	TPDKKKKKIFPPPPKIFPPPKYKKPP PFFFFFFFFFFFPPPPPPPPPPPPPP PFFFFFSIYIDENLICDNL*LQKTLVFL E
3679	17580	A	3702	407	371	SFFFFFFFPPPPPPPPPPPPPPPPPPPP FFFFFFFPLWYKDIIIGKNEQNV*CS
3680	17581	A	3703	36	409	LLKCEGIVKKKGKKKKKKREKGGFFR VLLGGPTFRGAHKKSLLRGVFVNLGG FFFEKGFLLGALLGP PPPPIFTPLGKK KIFGKRGPPPLIFLFF*IRGPPPPSP PSTKPPPPPPPTP

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3681	17582	A	3704	56	415	QAPWGRKKKKKKKKKKKKKKKKKKRG GPLKKNPGGGPTMGGGKKKYPSPWGGEK KNPGNGLKKTPLOGGGNNMAPPKPKKG AGGKKKI*RGGGGKTPLIGGKKKGGPP RTSPR
3682	17583	A	3705	108	1	NLAK*IQ**IQTIMHHDVSPFPIQIGW LNILKSN
3683	17584	A	3706	425	52	PFFH**L*KVDPIPLPFONFLHFSNNI YFSLPSPKFFFSLQPFFFGEIPIFP PPKKNFSS*NPNLVFISSPLKKIIFSP PPNFPAPKXLFKSPPPFFFFFFFF FSGKNTLYVWDK
3684	17585	A	3707	117	421	VLLVTQAEYLLPEVFGTRSVSDGFFRR WNICILSG*ASLI*KSEI*NALKNIS FKKKFIFILEPRSHSVTOAGVQWDHGS LQPTSGKLKLSHLSLP
3685	17586	A	3708	308	3	RSPFWFFFGFFFFLFFFFVFVQLFFS KYNITLYIKKKTETPTETNDNGNATQCN LWDTAKAI PREKFAISTYI*KVGHQI NNLMKHLKEIKQKQTK
3686	17587	A	3709	94	420	KKKKKKKKGGGAKKKPGGAKI*RGKE KKNFPLKGGGKKKVGNGPKKYPFGGKK KREKTPKK*SLGKKKKLKGKGGKTPP KQWA*KWSS
3687	17588	A	3710	413	184	LGECLSLRSKRLWSGAGGVCL*PQOV RRKKWDHLSPTGR*RALSSHSRSPAW TAQDPVSRGLVWGLPGGW
3688	17589	A	3711	3	104	GCSELSRCHCTPAWRQS*TSQRKKKK KKMMY
3689	17590	A	3712	2	393	GLFTSNHDKDIGTLYLLEGA*AGVLGTAL SLIRAEGLQPGSLGNDHIYVIVTAH AFVIIFFIGIPIIIGGCGN*LVPLIIGA PDMAFPRINNISL*LLPFSLLLLASAI VEAGAGTG*TVYPLAGN
3690	17591	A	3713	424	1	FFFFFLLRRSLTVVQAGVQWRNLGSI*A RPRV
3691	17592	A	3714	2	130	GRVGGVGV*NLKLYSQRKKKKKKKKR KKKKKKKKKGGGP
3692	17593	A	3715	3	197	FHHVGDGLNLTL*STRLGFPKC*DYR CEP RPAAFFFFLKKKKTLAPKKFTL DLTTRERS
3693	17594	A	3716	3	497	RSPFSGFAWPGPAGPWEAGAAAGQFLG ARFHSPTCTGGCRSAGTTP*PAGPAGPPP HAPAAAEKPRGAEQSQRRVQETGPPPT RAESNPSGLRGREVPFSAGCVSGSQESD FGAGCPAVT*GTYPYRIAGQVSRAPHP AESRGTAGLSIGPDGRQ
3694	17595	A	3717	40	379	AITSRSPSPAVHSGCLARTHPSNQCLP LSGTLPLSPSSLSLSHPATAAGE*IWDA EKKKKKKKKKKKKKKKKKKKKKKKKK SPGALKKKNPGGPNPPGGGKNISSPPR G
3695	17596	A	3718	445	286	KKK*METRSCVVGSGSLELLASSDPAT LSQSGVQITVSHSGQPVNKLPRVQ GYFLASCLHLLHFWYQNGCHVACLA AKENKFMQAACGLNSPALSLKNGRLS AAYGSDCYVLPFMSKVLGTQ*ALKY TLNPGPAVAHACNPSLTCG*GGRNLRSG

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3697	17598	A	3720	14	472	VGDPGQHGSET RSCARNFGLTHASAOYOTLEFV*SVLIT AVLLLLLSPALAAAGITILLTDRNLNITF FDPAGGGDPILYQHLF*FFGHPEAYILI LPGCALIIHIVTYYSKKKEPFYIGRV* AMISIGYLGFIIVRAHIFTVIGIDRDTRA YFTSATIIAIFT
3698	17599	A	3721	3	298	EAAIKYFLQATASITILLTALFNILS GQ*TIITNTNQYSSLLIIMAIKLGIA PFHP*VPEVTQGTPLTSGLLLT*QKLA PISIIYQISPSLVN
3699	17600	A	3722	86	505	AGAVTYIVTYSL*KKDSFWHWSVC*A MRVNWES*GLSV*AHHIFTVGIDVDTRA YFTSATIIAIFTGVKVS*LATLHGNS MK*SAVL*ALGFIFLFTAGGLTGIVLA NSSLDIVLHDITYVVAHFHYVLIGAVL
3700	17601	A	3723	432	48	FKISLFFLLSPFCPSFSPFSLFFPSFS CFLSCPSLFLFFFLSFHFFFPPTLL ISF*VFLF
3701	17602	A	3724	2	406	HHIFTERIDVDTRAYTTSATIIAIFT VKVS*LATLHGNSMK*SAAL*ALGII FLFTVSGLTGIVLANSGLDGLHDHYV VAHLHYVLISGAFAIIGGFH*FPLFS SYTLDTQYAIHIFTMIFIGVNL
3702	17603	A	3725	174	158	KFFGGGFFHFFFPQKKGFNNPPRGFF TFPLLGNKFFFPVNLGPRGFF*GP
3703	17604	A	3726	2	392	LFSTNHNDMGLTYLLFGA*AGGLGALS LLIRAEGLQPCSLGNDHMYNIVTGHA FGIIFFIPIIIIGGFGNRLGPLIIGAP DMARFRINNISC*VLPPSILLLASAIA EGGAGTG*TAYPFLAGNY
3704	17605	A	3727	48	474	KKKKKKKKKKKKKKKKKKKKTRGPPF KKTPAGPPPPPPREKNPPPEGGQKKPP PAH*KKPPPRGGQPPPPPPQKNPPPE KOKTWGAEGGTPPKPPRKKNGSQIAD PPSNAKNRHPTQEPFPQSQCI PPPPTP PP
3705	17606	A	3728	387	53	PPPKKGVLPSPFNFTYPPK*GVFSLPFP *KFFFSKGLIFWGGGGNFPFKKKFF SKKPRGFFFPF*KKKILISPREKLGFP PRIELKGPPPPFFFPFFFPFF
3706	17607	A	3729	1	397	FIRLQPLSFEKFKFSCTSPDVA*VS LPSPPSGSFFVFL*VSCVWKRRF TMLARLVDS*PSDPPANASQASAGITGA SLRASLIYI*CFSIQGLLFEFLIQV QLLIVYPRHHLYLSVPHLH
3707	17608	A	3730	407	0	TLKHKKKKKKKKKKKKKKKKKKLTKGPK *NGRKKKIFLKGKKKKQGTGELKKKL ILGGEKKGNPPKKKPLGEKNFKGEK GKKNLKMGVIKLGTSSKKIIF
3708	17609	A	3731	3	200	GGCSELRSCRCTLAWTE*DSVSLKKKK KKKGFFKVLKRGKPSGNKREGAKKIKG KPCPFWESF
3709	17610	A	3732	3	380	THHKDIGTLFLLFGA*AGVLGALSLLI RAELGGFQNLGNDHINYNGIVTAHAFVI IFFIPIPIIIIGGFGN*LVPLIIGAPDMA FPRINNISF*LLPPSLLLLLASAIVEAG ACTG*TSYPLLAGN

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3710	17611	A	3733	6	394	AMISIGFLGVIG*AHHIFTV*IDVNARA YCTSATIIIAIPTGGKVFS*LATLHGSN MK*SAAVL*ALRFIFLFTVSGLTGIVLA NSSLDIVLHDTYYVRAHFHYVLSIGAGF AIGGGFIH*FPLFSGYT
3711	17612	A	3734	27	238	GTPSSSHASAHIG*IIAVLPHYLNITIL NLITDIIILTTTAPLLNLNSSTTTLLLS RT*KKKKKKRGPPF
3712	17613	A	3735	402	249	ASHASAPLEVV*SVLITAVLLLSLPVL AGITILLTDRLNLTITP
3713	17614	A	3736	100	430	VTFPKSDSYEEVKIKLEPRQTDLRALGF CLSF*TGKKKK*KKKKKKKKKKKKKK KRG
3714	17615	A	3737	158	306	FLSSVFLSVGVFLSSCLDRNLPDMMQ LWSEIFNK*LYLQELSILGVY
3715	17616	A	3738	279	3	PGHCFYFNENLNFYFQIFQNVLANSGSL LFLYQTLILSFNIFYLYLIQISIVFQ SVIL*FIFNSYSWYGVPLVCLMTFEGK KOTCAHV
3716	17617	A	3739	268	388	HFFFFEMEADSVAKAGV*WYDVLQOPP PPGVKRY*LSL
3717	17618	A	3740	395	153	GWLRFKRCERGLQNIKV*GEAASADAEA AAS*PEDLAKIADEGSYT*QWIFVVGET AFYWKMKPSRTFIAREKSPMGFKL
3718	17619	A	3741	271	386	TCPPPLKLIVYBLGLL*RNMRQGAHAH ACNPSTLKG*GGRI SRSGDR
3719	17620	A	3742	406	190	QLLKRRLQENPWRWG*GCSKPRSPRFP QAWVTERDFVSKSKTKTNQPKNGERKV FFWFFFLRPKPQVEI
3720	17621	A	3743	272	408	MGLQACANSP*YVDIAPICNNRGAHSV GLMWMMLAREVLRMRGT
3721	17622	A	3744	211	407	KGKRNILFGPVKNIFCDTFTSCVNFFR EEVSLDCPGWSOTPAK*SSCLGLPTCW D*RRQPRLL
3722	17623	A	3745	405	189	CVSQDGLDLLTS*STRLGLPKCWDRYK WTNQLFVNGKSLNSFVCSFMVLDTTG FKEIVNLVHLVPLF
3723	17624	A	3746	120	362	LKA*EISWNGTIGTHOEKPEVONQVIL ENIVFLGCPDRIPECOAVTALEPEKK AIVAGCSBHLVPSITLGGQGWIT
3724	17625	A	3747	401	233	NSGRCGCSPEPRLDCTPAWVTRDRPISK NKNKTNQ*QKKCKR*TKGIFPSTRSIL
3725	17626	A	3748	353	109	LGLANFCTESRDGVFPWPGSRSTPDLR *SAHLSLIPKMEYKA*ATMPGLMCLFI KALDFQGCVRGNGGSGWTDIKLQOM
3726	17627	A	3749	412	221	HGLRECLVYPRKQCNNSISLQGHSEV AM*QRAHNHCIIHWPYHDSFPFRKIWINWA RRGSGCL
3727	17628	A	3750	1	355	FHHVSQDGLDLLTS*SPRLGLPKCWDRY REPLRPAENTVYVHFSSWSFTNHSKGIN *TLQDQKEQLPGWL*ILRGVFFNPSIW NS*QKKASIVYVFLCWKRDIFLHFPVS GTFRGF
3728	17629	A	3751	423	125	QVCEKVLISLITENQIKTIVRYHLTPVK MAFRQKTDNDKCRWYGEKGTPEVCWVK CKVQPL*RTAWRFFK*RKIELPYDPAT PLIGI*PKERKSGV
3729	17630	A	3752	3	171	FQPTAFLYANSECSGEESTSYSSVEE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
3730	17631	A	3753	2	247	YLGINLTAKMKDL*KENYKTLMEKIELD FHHVS*DGILNLLTS*SAACGLGPKCWDY RHEPRPAITRFLFVFLYLQRLDHLIRI NSFFIMSVNGMFTFVVLKLFNLIIHA
3731	17632	A	3754	3	197	GLELLTL*SAICGLGPKCWDYRHDPLCPA QYLSFLYAINKLFSSTYLEIHNRLVCCI VTLIIYKP
3732	17633	A	3755	2	103	VSQDGLHLLTL*STLLSLPKCWDVSCPEP PPAW
3733	17634	A	3756	103	2	FRPGMVAHACNLSTLGG*GGGITSRGVQ DWPQG
3734	17635	A	3757	394	244	ASTHPANFFCRNGVLLCCPGWSQMPGLK QSS*LSLPKC*DYRCEPPHSA
3735	17636	A	3758	341	2	AETAPLHSSLGMRDVSXKKELKLNK QKPNPLK*AKDMNRHFAKGIQAGANEH KIKCSTSTNLREMQITTTVRSLLI*VRM AIKKSTNISCW*ARREKILIIYTWNEC K
3736	17637	A	3759	2	322	FPFRTRPLNNTINQMETICIMYTKCYLII AE*TFPFAKGLTKIGHTLGHKASLNK PKRIKIQSAFFKNGKLENDKRRKITG KHNTWKLRIKHTSKPMQSEMF
3737	17638	A	3760	444	422	VRLEHPRPEPFFDPRVRHHVQACGLKLL TSSDPPTSASQAGITVPSLQ*QP*SVR LP
3738	17639	A	3761	266	1	GGGVPLGFVIFPLRPPQGVGFQALAPQ GPQSKIF*IFFGPGKNNRVFFKGRNLVF FPPLFSLLPFFFF*DGVSCHCPGWSLE CSGM
3739	17640	A	3762	70	381	HSITSYI*AFINGFFLFCFVFLIKEME SHYVAQADHELPAWAPPTSASQYAGIS GGSHPTOHYFIFYWIFYFTVFCGGGFLR RSLAPSFQAQAGAQWRDLGS
3740	17641	A	3763	229	390	DIPYSFCFFFFFWKGSFVFPQAGGKGR KL*LKPPPPGLRGFSCITLPGSWEN
3741	17642	A	3764	119	1	QTSRPGAVAHYTNFSTLGG*GVDLHRS GVKNQPDQHG
3742	17643	A	3765	400	200	ITAYCSLDLLOPHLFFSRDVSLLCCPV WSRTPCLK*SPCLSLPECWD*S*ATASG LKHFIKSLPL
3743	17644	A	3766	376	44	TQPIPLPGFQAPPGPMG*PNFLF*EKK LVFFPKPKPTAPAGGGGPKFPLPRKPKQ KKGPHPGSQNFQKPRPKFPFRPTWGKK REFFSQKKKKKRERDVKITDLNTST
3744	17645	A	3767	403	3	DHFFKGPSPQSGEFFPLKLTFFSPPLGG FG*ISLSPPEINFPFPPKRIFFGPPLSF FFKKKKTYAGKGLIFFFPKKPGGGF KRWCPGPKKFFPPPGFWACSPFFFFFF FFGAKVSLVAQAGARSRTS
3745	17646	A	3768	407	177	FHHVSQDGLLLTS*EARLSLPKC*DYR HDPPLRLARCIKMFGRWRCNLRKSPLS LPPSAGELRAPFLDFLEDAQ
3746	17647	A	3769	292	391	RPGVVAHTCNPSTLGG*GGQITRSQVQD CTGOY
3747	17648	A	3770	395	198	LDMGFHHVQAGPELLTSSDLPASASQS AAITGMSHRAQPY*VISMCCQCKHIFIR IPFNHNNV
3748	17649	A	3771	1	241	RTRGRTGRTRGLLSAHTGRYQKHPRIR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TPQIFSTGTTKAEAGELLEPGGGACSEL RSCHCSPARATRVKLHVKKFKKIK*KHP RIRTPQIFSTGTTKAEAGELLEPGGGAC SELRSCCHCSPARATRVKLHVKKFKKIK
3749	17650	A	3772	112	406	FFFFFFFFFFFFFFFFGGGVPII*KPPPP K*FMFFPKKLLPPPPPPALKLFFSPPPP FFFFF
3750	17651	A	3773	24	197	IFSVEWGVCHVQCDBLLLGSSNPASV S*SAGVIGVSHHAWPLVKLFLVKRNKLSY V
3751	17652	A	3774	85	201	VNFHILI*FVNKRILKLEKKKKKKKKKK KKKKINWKKKKK
3752	17653	A	3775	1	382	WENHLSPGSRGSSSEP*SHYCTPA*VTE* DSVSKKKKPNLOAEAKRLTLLLLKKAIF KNRGSPCFKSIKWAQFKKIKQGVFVATR MGDRSRGTPNLGENFLKSFLFSIKIQR FYVLGLKNSPSRNIY
3753	17654	A	3776	1	181	IKMATVTKATYRVCVIFSKLMLLFTKL ETKILKLWNLERA*IPKAILS*KNKMG LSNS
3754	17655	A	3777	70	385	LNKMQTKTFDSDTHTSICFTLHFINTKL QFIPLLAIIYLLFVNFFIFINFFEEPGF CFDDLSSCFLFY*CIPI*FYVFFSAFRL HLFFFYRLSLLTLDLFSFLI
3755	17656	A	3778	2	406	KDDRNTSHOVHFNASQDEADFPDYENF FEDSDSPKSSSTEPSPHIHVPDIQMTI FHCADNFARQYILAKLAKKKKKKKKKK KKKKKSSSPGGGPKKGAFFFFPRGEKN FFFFGPPLIFFSGGGF*NGGGGGP
3756	17657	A	3779	403	176	FLFPIILFFLRQSFVLVTGTGGQQRDLG SMQPPPPRFK*FNEGKGRKKLWGGA
3757	17658	A	3780	3	248	GLNQTLQKRLLAYSTTHIG*ITAVLPY NNYITLNLITVITLITLACKKKKKKKK KKKKKKKKKKKKKKKKKKGGGA
3758	17659	A	3781	3	330	VDRLRTGVDDHFGKHSSESPIFKKKKKR *KILPKRGGVLYNPHFERLRGENNLT GGEGGQRETESPPCLPAGGKNKI*FV*KIQ KKRGGPFKGNKFFPRGGGKIFF
3759	17660	A	3782	399	187	FFFFAKGDLPSHIFGLPFGSPFPVFK PRPRNLILGDP*KKFLVLPFRP*TWFL* NGPPPPPPPPFLDF
3760	17661	A	3783	392	11	KKLVNLFDDHVAPEPLGIFPKKEMKAGI* RAICTLMFIAALLTIEK*WQPNWLLVD K
3761	17662	A	3784	324	80	PGPFFFFFFFFPAKRGFFFFFFFFPLVPFGF PPDLE*TPDPDFFLAELKFFSPDDA LNFFFFKGPPPPPPPPPPPPPPPP
3762	17663	A	3785	354	24	PPNKIFFSPFPQKYPFYKTPPPPTFFFL SSFFFFFFFFFFFFFFFFFLC*VMH FIVKYRCKRGTRILHTPTLRQLVLCC LSDVLLGCCIFIYVTCMLCAPKLG
3763	17664	A	3786	3	369	SCRGLVWVYGELLHLHFCRGNQISRVQK KKKKFGASPPREGAPGPEP*RG*P*Q KEPPPLKK*APPPGPGGGRPPPMGLGGG PAPPPFWKAPFKKQPPSGQEPGFPLK GLFFWKKPF
3764	17665	A	3787	1	125	FRHRFSRDLGLLIF*SRILGLPKCWYD RREPRRAHSIII

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
3765	17666	A	3788	427	251	LTPKGRGCESEPR*CHCTPAWVTEGDSVS KKKQAKNCRSLRMKYERNEFTSSPC
3766	17667	A	3789	250	2	GFPPEVERIKKNPPFFI*KKPGFFFFFND FF*ISGGKGIFFLPGPPFFSFFSFF* DRVLLCHSGRSVAQSQLTATSTFR
3767	17668	A	3790	412	3	GSTPTITTFWVGGLPDPGGGVPPPPAP PGGTPFFFKKKKKKKFQNPFRPCRSRYN GGLGRKNFFLEAKGSINPNFSPPPPG QONKTPFFKKKKSR*MTLQSFPRPGTA PGAAM*PVSPEPCGPPAPALSTK
3768	17669	A	3791	10	187	GCSEL*LIHCTPAWVHSETLSQKKKGRG KGGFKNGIDCFGNKKGGGRFGSKGHF STG
3769	17670	A	3792	1	331	FRVPLGRLSRGEHQQQ*QQQPPPPPPPP GLRPLAGPSRKGSFKIRLSRLFRTKSC NGSGGGDGTGKRRPSGELAASAASLTDM GSGAGRELDAGR*DRPGAGRGTSFSW
3770	17671	A	3793	1	431	FRKGSACKRAFKPAGADGVHGHHRASP QTAQAPVTCASARGSMWDFSHASGQDDR DLHSPSPVCGRWAPSTSPGASGA*G RTPVGGK*VAGVQRIHGLAPC*LV PGIAVHTKKPGSKGTITPGVAHACNP NTLG
3771	17672	A	3794	342	48	KRENNPVGAYNPSTLGGCNPSIVGGFCN RVCNPSALGGCNPSFLGGFCNHVCNPS LGG*GGRISRSAAODHPROHGKMSPOK IQKISQACFARVG
3772	17673	A	3795	2	189	LNFGGRCGCESEPRSCHCTQAMATE*DSVS KKKKKKGSRFQNTPSALPGFPVSGELI LGGPNL
3773	17674	A	3796	1	401	LNFGCGKGCSEPRSCHCTPVVWSE*DFIS QKKKKKKKKK
3774	17675	A	3797	279	3	ILAKVYPMVNSFLEKIHLYLVLVLCCL QHVLYLYLTFTKETGSRSSVAQGVQWHD RSSI*PLPHGLKRSFFLLSPRSWDYMH TPCLATE
3775	17676	A	3798	229	394	VFVKSLLCPGMVAHACNPTLGG*GGR ITMSGD*DHGKGGEVSTYNTKKKKGG AGHM*S*LLRRLRQEDPLSPGVGCESE *S*PCPPAQVTVRISLKKKRLHERDKSS AS
3777	17678	A	3800	450	3	IYLLRGHRLHYSRSPSYFNSYRGACSY MRPPQQATLLGLNLNQITREGPAIAHSP AVRERLSLAHAHVRRLCLPRPGAAPPEP AFELPCLLVAGVQVWRDLGSLQPPPPR FRRSCLSLPSSWDDRRPPLSS*FAEL VEMGFRV
3778	17679	A	3801	301	10	KKQPPKKKKRCFPPLPFPKGGKGSPPF FFLTPPPLKNLPKTLKALPQIFLRTFFP FFFERGSPSVTQAGVLNHLDSLQ*TP GFKHMPSCPVLLC
3779	17680	A	3802	420	51	SASSPPASFFFFFPFKKIFSPHPPFFFF PPFFPPPPFF*PPPPFFFPFKKKKIF PPPPQKIFFFLKPPPPFFFPFFFPFF FFFCGVNQCPSVLI
3780	17681	A	3803	253	73	QTTPSKRYSVYLNCCN*ITTCRIKLD PFLTLDLKIN*KSFADLNVRKATIDTICK KVGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
3781	17682	A	3804	385	55	AGTRPVFAALAAAAAPAPRLPLAPHGSA ATGFPFPPPCPHGEGLRGAPAASSPPPLA HRSTQTPNWDVGESPIPDQFPPL*NGP FALCLPQGLETVNVEISALCFTSHGN
3782	17683	A	3805	191	2	QKHLKALNLFPRCCVCCVCCVCCVCCVNV TF*ACKICTCSDFPGSPRKKYLEFGTKI INIVDFN
3783	17684	A	3806	1	367	KLROVITYLEDLPTIIDEGSYTKQWIFNV N*TAFYWKQMLPKTSVTREEKSMGPFGKA SKRLTVFLGANVVSDFKLKPMPIYNSE NPKAIQNDAKSTLPMLYKRNKACIAAH LFTAWFTEYF
3784	17685	A	3807	3	145	LGPGGGGCSEPRSCHCTPAWATRGKLC OEKKKKR*RLDPEAEVAVSRRGAIALQP GQOEGNSVRKKKKKGRDKVSLCCPAGF
3785	17686	A	3808	362	86	NPFYICSPFFPFWLWQGVVPPWCBG* TPPGPPCEIPLPKKKSKSPGWGPPF FPPWGGGAPKFFPLPKWSPFQTICPL PFGLGEKN
3786	17687	A	3809	245	377	FGYMPSPFETQSRSVTQAGVQWHDLSL QPLPPGFK*FSCIGLP
3787	17688	A	3810	3	268	KRNFLNLIKRRYKPIANFVNSKIVNT FHLRSST*GYPLPLLLNLKVLPLNEI ROQKEIKGRNKGKKTISVYSIMLSANT EKPK
3788	17689	A	3811	2	388	SAENCLNPGGRCGDLRWCHCTPAWTE RDCVSKTNKKETEKYMRN*IGNMLTIID AGRRYMRCHQTITFTFFFWRGSLFLFAP PPSQEGIFLPHPPPEKWKVKRITTEY FCFLRTDGFPCGPGGF
3789	17690	A	3812	292	136	PPTVIARKGKPKPKLSSEPWQFSAEQLG LPSFLICFFVVCRCCLLLELLFCRDEV SICCPGWS*TPGLKQSHSLSPNWCGR CEPLCRATF*FFCLCTLLIFAFVSAVIL
3790	17691	A	3813	359	52	KKGRFFFFEKNPFGLVPKKKKKTPFF PNKKKKRGAPPFFFTFFFRH*VPLCC LGWFRTPGLKGGSCVGLPKPNDYRHKPL PLTKDDYVYVGLPFVSLQ
3791	17692	A	3814	382	1	GGPGMEAPLGYHITPFPFLPKQKNNPGG GAKFVVPVPPPGG*AGKMGLPNPRQPLIT QKGPPPPPLSGKREPPQKKKKKRVITM GDP*NSECR*GCHLRVQKEMRLPLRLNS PPHYIPNRNTDMSCC
3792	17693	A	3815	472	340	TGFHRVSQDGLDLNLS*SAICGLPKCWD YRRGLFIIFNMGWS
3793	17694	A	3816	247	378	PPPPGGGXXNLGLLKLPLPFG*RETPFP PPRGGGPPGAPPFG
3794	17695	A	3817	25	465	TPPLGC*GRRFPRGPGFSPPFPKGNF FF*KFKKKPRPGGAP*FPFPGGRPKN PLPPGPKGSH*PKFPPPPPGGETKRKPF PPKKKKKKKKKKKKI*AYKAYICFDC PLTGPDLKSKDTLAFPSVIGLPRPCTC LSPR
3795	17696	A	3818	475	147	PPKG*RHPPGPFPRFRGFGNPPHRRFF VLRTPGYSFFF*KKRGPPPTFFFTLPGP PGFLGKPPSPGGGQKIPPRGGGGPLK *IPFPPPPGKKKDFFLTKKKKKP
3796	17697	A	3819	461	57	TNQKKAAPPLLLKKKFFFKKTTGGAP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NQEPAVIAGOGGTIALEVLNOVK*LSSYH CRLLVGMHYGCLLVSSVTPFCNIFSGLK VH
3813	17714	A	3836	304	3	RLKATKTNNNQTEINS*YIKDLNARAET IRLLEENIGGKPHDIRFAMI FWI*HLKK TKNIYKLDYTKILDFCISKDTINKVKR* PLEWEKIFANHISDKG
3814	17715	A	3837	475	135	MEGLCFDAEWVHPIFFPPLGG*GGGSPG PGIOTPPGYPGSPGPPFTLKKLPRRGAV FFFFPPLGGLGPKQNVPTPGAGALEPCW APSPPPGGPP*NPFFKKKKRKLKIGWH F
3815	17716	A	3838	415	245	ETGPHHVGQGDGLDLTTS*SACLSPKCN DHRREPPHPDPQVSFTRALFPFMRAPLS
3816	17717	A	3839	460	413	WDYIKLTGFCTAKETRVKROPTENDKTS AKYISDKGLKTRLNKQ*KMNLI*NVW K*LGRYSH
3817	17718	A	3840	2	470	GGDAPHFPDGVAAARRGSSLLRWGCGQA QGLLTSQTGWPGORDAPHLDPGVTAGPRR SPHLRRAWAQQTSSSLPRCDGREGREALL TS*VGWRPGRDAPHFPDWAARQGRSSHP RRWAARQRRSSLPKRKSGRAEAAISNSA SLQRVSKVSVSCRPGG
3818	17719	A	3841	54	332	QFGPHHVDGAPELLTSDHLPSSASQSA GITGVSHRARPSLAHSFTHSLAL*PTPA HSLIHLWTHSLTHSLSFPCSFSPPSHT HSLARPLGV
3819	17720	A	3842	208	468	ENPTFPPLWCALGV*L*EDGFSLYSLSA HVCEIVFLYCPVLESARPLMFLNLAHV CYEWHLFSVSLFHTVS
3820	17721	A	3843	406	2	PSSSSSSSSPPAAFFLGCSPGVFPSPFP LKPAFGFFFWGPKKNFFSPPRGVKFF FGAPPLFFFFFFFFFF*DGVLCHPGW SAHAAS
3821	17722	A	3844	370	253	VGLEPRGQSCSELRSHSTFANATE*D PILKONETOK
3822	17723	A	3845	369	73	LRQDNGNFGGRACSEPRSHHCTPAWAT E*DSISKRRKQNSVPTESYPASEHCYS LTGGGVAIIMEGPTGPDGAIFMCHLRNL CRCSFILPLALQCDH
3823	17724	A	3846	198	388	FRKISINVRVHVRINLNKHTITPIDAQK P*EKQLQHLTMKYSIIMNSRKLSPALR NLF*KPS
3824	17725	A	3847	391	20	GFPFPRVF*HGFANFPLGPKKKFLTLP PR**TWFLKGPPLFFFFF*DGVSILC RPGSAVSKN*QTNKKSIILIRGKLNAL FVHSMILKGPCTDLLIFGNRKVESTKT IDHIFSRQLMA
3825	17726	A	3848	227	2	KRRNPFHKAIAIADSSDGP*SRLKNFV RGFSIADAIKIFRDSWEVKISILTGFWK KWILITLMDDFEGFNTRGR
3826	17727	A	3849	373	2	SSPQKYWGPGGFFFPFGFKTIPPPFFFFW APTKKKIFFGAGRENFFLRGPPPPPIIF FFFFFFLFFFFFFFPPFPK*YNSF I*DIKTHVFLHSGVGRVLYKTRLYET LYHSPKLNELG
3827	17728	A	3850	394	2	EACSVTQAGVQWRNLGSLQAPRRSFCFL RGSLSPQH*EDRT*HGGTQQTSMNE*

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/51,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MNLYQLWLCPALLYOLCSTSYT*EVIQLN IAFCVCLVGFCCFVFLFFETASQSF* AGVQWCHHSLQPLPKL
3828	17729	A	3851	3	164	NHLNLKGRGCSDLRLCHPTLAWATEGDS ISKTKTVQ*RLQNNIPHEHTCKNL
3829	17730	A	3852	35	390	NFVNSFFFFFPFGNGAFRGPGRGGQGP LG*GEPPPPG*KQPSFLTQPRGGNNGG PPPRVNTGFLRKNVFPFGPGGPQPPDL GTGPPPPPEGSPPPGPFQSKTKRTAPGQ PKGGPF
3830	17731	A	3853	6	437	PNK*RTPLGPPPPFFFPFFPPPLSFL KPFSPPPPPPLFFFLPPP
3831	17732	A	3854	1	236	PTPLRLNLQENRNLNPEGQGGCEPRSCY YTPAWATE*DSISKKGGRGLKPTLT SGGGQGLFFLRGPKQSTSGAIF
3832	17733	A	3855	52	351	TVGIMEPQTTDVVYVYKHLKCTDPLLDYI FNQHYPKKKKKKKKKKKKKKKKKKK KKKKKKKRTQKKKKKKKKKKKKGGGAPQ *LTLSPPPPPLYFFF
3833	17734	A	3856	72	420	NTYKKKKKKKKKKKKKKKKKKKKKKKK EAGGGGTIRGL*KENSGGNGMKPRIKKK GGKARGAPLGVSTQLL*RGEGKCLSP GGCGSEHKTTPLAYPLGKKKKETQSG EKK
3834	17735	A	3857	410	107	SSSSPLARYFLGVAAGFPLETLFRTGP RIFFLGP*KTFLPTTGR*TS*SP*KGP PFFFFCDRDRVLLW*PGWSEMGCLKQSSC LCLQCKWRYRYKPPOLA
3835	17736	A	3858	419	239	TTRSQLLLFLVEMGFPHAGQAGLKLTL R*SACLKPCWDYRRESLYLADA*GFYNL EDFL
3836	17737	A	3859	262	1	TAAQEFNFGGPIKKIFRCQPGVEKLDFF KRPPFFFFFLFFFLFF*RRVLPCCP GWS*TFEKF*STCLGLPK*WDYRHEPPN PAS
3837	17738	A	3860	357	133	NTPPFGAGRNKENPLFPKKKPRGVGLF PPPRKAQTEWLYPGPK*FFFFPPPPPG GKNTKKPPQKKKKKKSL
3838	17739	A	3861	253	375	TLSPQG*GGPPPPPPRGGGLEAPPPPPG LFFVFWGKRGVSP
3839	17740	A	3862	3	482	YITDEVNDPSLTIKSIGHOWY*TYEYTD YGLLIFNSYILPLFLFEPGDVRF
3840	17741	A	3863	1	129	LANSNYERTHSRIILSOGLOTLLPLEIA F**LLASLANAKEG
3841	17742	A	3864	289	372	NHLVKKWKADLNHRFS*EDTQIAHRHR
3842	17743	A	3865	266	31	KICIFISPPQKKSVPFPPKVRFPQKRKFP PALLFSAYFFPEAESSTVQAGVQ*CN LGSPQPPPPGPKRPSCLSTLGG
3843	17744	A	3866	1	395	NTSDFCIKPRAYNESEHWDMMVRRL*G KEDNLTLDISKLEQIFETSKAQLNLVS ETAMKVAQDSLTNLMPVTWKTIGNST IANEVLLQCLASLLVYRYIQQLRDS DREGAMMTWAVLSKKGG
3844	17745	A	3867	137	2	APLKKHECLRAVAPKCNFTSLGGRGGE ITR*GV*DDPDGHETP
3845	17746	A	3868	1	108	ENRLNFGRCRSEPRSCYCTPAWATERD SMS*INNKK
3846	17747	A	3869	198	302	LNLNINHYGGV*GCSEL*SHHCTLANAA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ASLHPKKKKKKKKKKSVKSGQAFYSHYA MAILNYIREKKLFLKWK*LLNINHNYYGG VLEKKKP*SYTYLNKKSQLPQLL
3847	17748	A	3870	237	419	KEIQSKQGLRAICIPMFIAASLMIDKG* RQPKCPWREE*INKLWYKHLMAYHSALK RNEIL
3848	17749	A	3871	239	232	KAFLTRVTRKRGIQPGAVAHACNPSALGG RGRITRSGDRDNP*HGFSWGKCLGIE LVGHMFNPLRNCQTVFQSGYI IYLFMP LDS
3849	17750	A	3872	417	219	CHVAQADLKLSSDDPFASASQSTGIAG ISRHWPRGTNP IHHGSTLMT*LPQRP HLTLSPRGF
3850	17751	A	3873	45	414	NILFFFFFHKSNLVPOGGGGQSLG*W NPPPRGLRGF FNLTPPRTGNKGDDPPQ ENFGF*RKGGVTQGGGGSKT PALGGPP GLTPQRGNGNQDPRPPAKKFGKKKKK NRQLPFLGFFR
3851	17752	A	3874	278	2	LTSIYVSIYLYHSGFOLS KISPSPOGOL AYLSIYLSVCHFLYIEIGVITMPASKID K*DLIKIKSFCTAKETIIRANR*PTWE KIFAIYSS
3852	17753	A	3875	233	379	QCDYFNELLRMEILGPGAVAHACNPNTL GGRS*ITRSGV*DPGQHQGE
3853	17754	A	3876	6	247	MLITSASYPEDLAKI IDEGGYNKSQIFN VDETALN*KKTPSKTFTARDKSMGPFKA SKDRLLTLLGANFLKPMNDLILI
3854	17755	A	3877	411	3	AKIPPLTSSQGHRTVCQKKREREREKE KEEGRKERERERKKGRKKERKEERKS* VRMLFLDKVDVFSQKIIITDKEGHYIMIR E*MQ*DIILNMYISNRALKYMKQKLT ELIGRVGRPGRSQTVPGRRNGVQ
3855	17756	A	3878	174	375	SFQQ*TAELKNTTSFTLTPPKLYLGL INLTKYQDLYK
3856	17757	A	3879	1	106	PHRVSRDGLNLLTS* SARLGLPKCWDYR REPPSPA
3857	17758	A	3880	383	24	FALNNFPGGAFSGPLTSPQVGLFFAP GPPPPGGGSCPLAQSFRIIPQKSGGP ALSFSPFLKKNPVVFLRTQPLLPPLFPQ PRVFFPPPPFF*DRVSLCCPG*SAVA QVGSLOP
3858	17759	A	3881	400	71	RIRQENRLNPGGCGYSEPRSRPRTTAMV TG*DSISKNNKNK*NLSEYFYFFFLR WSLTLSPKL
3859	17760	A	3882	282	3	IFNFCGYTVSVYIYEQELF*YGHAMCN NHIVENGVSIPSSYSLCYQSHYILLV ILKYAGWAQWLTPVILPWAEAGGSR QEMETILA
3860	17761	A	3883	1	175	LYKNFFKLAESHGGVYQILRLRGDECL PGG*GCSEFKSCHCTPAMVTDQDPVSKK FF
3861	17762	A	3884	415	233	SQDGLDLTTP* SARLGLPKCWYRHEPP CPAANFELKARYFWMVARYFWMWCNYS ALPS
3862	17763	A	3885	237	367	GPVLGPGMVARTCNPRILGGRGRWIT*G REFETNLNMAKPL
3863	17764	A	3886	359	108	TQGGGGPPPPPLGLKKKINGVNPEGRN SNKPKLAPSPPPGKRKKPPSKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
3864	17765	A	3887	245	377	G*HLPMLPRLGSNSWAHDMLEPPYPPK QFKINISWPGAVAYACNPTTLRG*GGWI KRSRV*DHPDMVKPHL
3865	17766	A	3888	406	2	SLNIFPPFFPPFFPPFFPPFFPKGGRVFP LKNFPPFFPKGCRIPFPFPLMLKVFF GPTPL*NRG*KEGFCPPFFPPFFPPFF *GRVLLCRPGWNAVQSLRTATSAHS
3866	17767	A	3889	3	114	EFHCVSQDGLDLPTS*SAHLGLPKCWDY RRKPPCPA
3867	17768	A	3890	395	1	MVLIG*PCDPPTSASQSAETTGISHRAR QFMLLSQ*LVCHSVTEVLFLLKLFY IYDILLYIYNYILLIYYLFLFLFFFE TGSQSVITQGVSTTIAHYSLSKSHPSGL KRSSHLSLPSSQDYRCAPT
3868	17769	A	3891	2	189	GRVGERGGTLL*SOLLER*ENHNLGGK GCSEPRLHCHT*PSWATEQDISSKKRSF IKALHM
3869	17770	A	3892	410	258	GC*GCSEI*SRPCTPAWATE*EVAQKE KRKKRKKRKKHVLATLAISLCL
3870	17771	A	3893	244	412	GIEACGNFRVTVLKSSALEGEPEPSGR DSS*EASGGRARWLTPVIALWAEAGG
3871	17772	A	3894	208	2	RISPPITPPFPVWTKTKG*PGFFQKJN *KSFFFLRWLSLALVPQAGAQ*LDLGS LPPPGYKPFSC
3872	17773	A	3895	407	18	PLGHPPKKAAGALIFNLPRKPK*KPEF PPPLSPCTCPPPPFPICPAWLPKCV PSSFKG*MGQPP*RDV*GPNPFWAPS LPVWQNPPIPPKKKKWGIHCWVCPLS FNETSFFKMSLRDCK
3873	17774	A	3896	82	401	KGFLKNSPRGEGFLFISFFFLFLATW LWRLKCSGAIARCSL*LLGSNSNDP PTSTFGEAGITAAGHAQFPDPSPPKT RAHHVTPQGLKLP*SSPPASA
3874	17775	A	3897	263	396	VWVFGGLG*Y*TPPLGGCGGRITRSGD QDHPG*RGKPVSTKNT
3875	17776	A	3898	2	386	KIGLELLGLSNPPASASQAGIIGMSHC AWPNFLFYWNHLYPHK*VMPGTVAHA YNPSTLGG*GRIIA*AEFKTSL
3876	17777	A	3899	140	33	IFFFHL*GEIGFTNMMLDIGGGTGTGF QLEEVNPSVNDINKIIAFFVT*GVDV*S RIFTMAKTKFYNISLKLCS*KTF
3877	17778	A	3900	377	2	TPPRENGGLFKIKVYFRGNFKKKFPLC FSKVPIISTMWLNQOPPIPLKKNF FKTPKKGVSHYFPQPKS*GVFFSKK KNFYFFWEEQKQKRGPNAPLFFLKKK RAAARPTRPPTRP
3878	17779	A	3901	2	123	RVSQDGLNLLTS*STCLGLKCMWDRHE PPCPALRCVFG
3879	17780	A	3902	188	3	LRC*TCFGTDGWSHLAHL*FKKGRPGA VAHACSPSILRGQSSWISRGVQNLGQ HVETP
3880	17781	A	3903	422	238	ILHVLQPSWSDSKRPPFFFL*R*GFTM LPKLLNS*GSSDPLASACQRLITGMS HYTW
3881	17782	A	3904	414	1	STHGLPKCWDYRHEPLHPSMSYL*Y FFIYLFTHWSVLTARMQFAEDRLDPL LHCYISSDNGSTSVL*YILVFWSPNL VTITALLGFVVFVFLFFFFETGSRSV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
3882	17783	A	3905	396	236	AQAGVQ*GLSSLQPSIPPGFK*FSC DRVSLSPRLCNGTISAHCNLCLLGSS NSPGL*NRGHQIFSIEGQIFLQAMSLSQ LLCSALVVOQKQPYMTYKGMEMAVCL
3883	17784	A	3906	377	57	RGLVFPFQNPQA*KNLGRGVFFFSGAQ KNQKGGWAFGRPPPRFGRPRGPGAR CPLNLTGGGPKGKALGPPPWGWSKFQK GVPLQWVGGSGLFFSKKKHKL
3884	17785	A	3907	341	3	TRFFFFPLGKKGFFSFGKLGTPRVFP LPFFLNPGGIFYWGPICKKKTFFPPGV KQGSFKRAPFFFLMFIAALFMVVKTW KQRRPSVSE*KNLSYL*TEVFFSIK
3885	17786	A	3908	3	162	MMKAIKRGH*KNPALEKLPHTRGVNG FVTKEDMAPFGKPAIIQHSOYI
3886	17787	A	3909	1	421	PTRFPTRTMGCTMLVRLLL*KHSGAQ AVAHACPNSTLGGGQRIQRTGVQEQPD QHGETPSRTRGRTGG
3887	17788	A	3910	2	424	FRVRSPLGALSGLTGLKFSKNQKKKGK KPQTTKQKKKKSPKKKTTPKKKGGAP LKKKNFNARGENPFFF*GPKKNPGAR FKKGGGKTRGTPKKKAVGKTPPFRGGE KKKESPSQFYKKIKKKVFGGKKIFP
3888	17789	A	3911	3	236	GFCHVGQADLELLATDELPAAPASAGI SGLSHCAWFPV*PHYMSSLSLLATRESL HRVKLQKNGLRKTRELYMKN
3889	17790	A	3912	304	2	VAKKGSKPGGLKKNPPIKGLIGVPGGGP QNQIWEKFFFLTPKNRWGAPL*GGGGP SLEKKRGPPPPGWSNPPPPFFFFFLRQ SCSVTQTGVQWRDLEL
3890	17791	A	3913	91	344	HAAPVCGRRRTLKVHPHAPSWSPPSSWAHP PPTWEPESGTTWAPEGTVTTLGPPQELS LRRGVSYHCP*PLIWRKWPPLPLCL
3891	17792	A	3914	328	402	KSWGWPXAVARVCHPSTLGG*GGR
3892	17793	A	3915	16	179	GGGCSELR*RHCTSAVVTARLQSKKEK KKKGPRKGEVATGTVTRGELKSWAL
3893	17794	A	3916	229	46	AGPELLASDPLTSASQSSRTITGPFLT GLYSKDHIETANISYTNA*AL*ITLRT RGSTR
3894	17795	A	3917	42	383	AFPCFVIGRVISKGKECTLYPFLFLFFF FFFEKKFFFFSQQGKKGGEGSMPEPPS GLKETPLHLLBEGKFWAPPPPVYFVFV F*KRDFTLVARVVSRLPSREGLDYR P
3895	17796	A	3918	402	286	PPPPF*TPPPPKIFGAKKKKNSPPPPG ESFSF*KRPP
3896	17797	A	3919	349	380	KKSPFG*RNFGSLQPPFPGLKPSPLS PSSWVPR*TPPNANLFFPKMRISHV AQ
3897	17798	A	3920	28	327	KTTLNNAITIQAKAGTNGHPPLSPRE NKNQKKKKKKKKKKKKKKKKKKKK KKKKKKKKKNGGGP*KKKNFSGGGGEK FFFFGAKKNFGGGG
3898	17799	A	3921	414	1	NFPKVGSKMLMSPHFFFPKKSFPFP PLFLKKNGRFSPPFPEKKV*F*KKPPF FSPKKKRFPFPKVLKVGKKRVLKNGL PGLLSKKGRTGTPPPLFFFFFF*DGVS LCLPGWSAVVRSQLTVTSASQVQVE
3899	17800	A	3922	1	169	LRSCHCTPSWATE*DSVSKKKKKRTLN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LSPQKLNRAKGIPLRVFPLEKKGQTQLL *NRAGKIFLRVFPLEKKGQTQLL
3900	17801	A	3923	263	74	LLSVWRIPCAQKKERKKRYECEFLIVF VFDLSEENSSYISFKPILCVVCVVCV CVCVW*VKNFKRS**SSDRSKTKTIKKH SHSYLFFPLSFCAQGLQTERSHELLPHL EVS LFKE
3901	17802	A	3924	3	129	TGFHHIGQAGLKLTL* SACILGLPKRWD YRHEPPHPAPFCD
3902	17803	A	3925	281	10	NLPLPGATDYPASGGGCGNEMRSCHCTP AMWTGAKPLRRK* KKRQMLKTIKEM GNFNMVYILDKITK* FLYFKQLILSPLM GELGVK
3903	17804	A	3926	110	1	QLGVAHACNPST* GGGQAEHLRSGIQ DQGGKHGK
3904	17805	A	3927	180	368	EINFITNYIILFFNRRGLALSPL* SG GAIITHTGLHLDSEPPFSDS* VAGTS GTYHHA
3905	17806	A	3928	92	2	VREGVAHACNPST* LGGGEG* ITRSGDR DH
3906	17807	A	3929	2	146	HLNLGGGSCNELRLHCCCTPAWATE* DFA SKKKSKFKITSFTCQIVML
3907	17808	A	3930	221	3	KERATWGTELNVSKTFPT* LKQRKNL* PPNICKYNNLLRP* LGGTVAHACNPST LGSRRGRITRSGDQDH
3908	17809	A	3931	1	102	GGRGCSPESSHNCPTA* VTKRDSISKNI NNKIVK
3909	17810	A	3932	351	69	GCGGGFRFTQPPSSSRGKRRFFFFPPPTW G* RIGPPPRANFFFLFF* KRGFFLGRRE IFFFFPPGPVPPFPWPPQNFQGGAPPP PPFFFFF
3910	17811	A	3933	401	94	RGPPPLNPLPLKKNHAGPPKVG* KFPF PTKPKKPLFS* KTKIFPPGGPPPLIPPPR GGKPKKFLYPPKFRPREPKGFP PPPRG TKKKTTPPKKKKKKVS
3911	17812	A	3934	184	2	LKEFFPSRNSRSLVLTNSF* HLFT* LIY YFFEIESYSVTLAQVQWSDLSLQRP PLGLQ
3912	17813	A	3935	2	393	KILIKVEIGTYRKITNAICEKPTANIV PNRKKLKAPFLNGRTR* GCPVSPVLFINI TLEVLARVIYSEK* IKGTQIKI SIATME NSKKFPQKTEKNTTICSSNSTTGCISKR KEMHISKRHLSPVYCN
3913	17814	A	3936	291	2	FPFFPQTRGPKSSRAHSPGPGPGSST GAR* FPFPLLRASLRPPLGLPTPTGP TGMORPEA* RTPATDKPQNSRRGP* GAG WGRPGCCRCGGA
3914	17815	A	3937	382	1	ONTACTWSQONELLFLCKLPHFPFSLLE PSSCPGPHLGTPTWPAFPSPHTSLTKAH PIGSGPSSPLLTSPRMPPEIQTATG* PASSLTPTVCSQHGNRFPKKGVRAGRS SHLESQHFEFGPEAGG
3915	17816	A	3938	398	2	PPFLLNLKIGAKKAKFPCSPGPKRPI CGQTKKSVFFFRV* DKSTFDCFLCPI VYVKKQIWLAPLHCVFSGRVAQGSKSP LCLSLPFFFFEMESHPTVQAGVQWRDR SPQPPPGPKPFCGLGLPS
3916	17817	A	3939	240	385	KLLFLFLFIYFF* DGVSLCCPGWSAVQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3917	17818	A	3940	230	381	TLTLEPSAIPGAGGTPVSPFI LISSSYREYLAKDLRFSSKQS*WLCSE FRGLGAHAVHCNPSTLGGGGRM
3918	17819	A	3941	1	107	CWVWS*TPDLKQSTCLGLPKCNDYRQA QPHRNLL
3919	17820	A	3942	2	95	DLLTS*SACGLPKCNDYRRKPPRPALF AFS
3920	17821	A	3943	163	404	CRHKAQNLPLPGHLLSEKTLKYSSPK GLRSQH*KLFLFCFG*TESVUTQAGV QWRNLGSLPLAAGSKRFSCLSL
3921	17822	A	3944	3	200	GLDLTS*SAHLGLPKCNDYRRREPRLA YFTFIKKKKKDCOCELLNLPNSCMDTAH VHPAHLTGG
3922	17823	A	3945	423	2	LFFFFSEV*SHSVAQAGVQWNLGSLHS S
3923	17824	A	3946	209	413	TTTCIEQCNKTRRLGAVAYACNPSTLRG* GRWITRSGVDRDPQHQGETTKNTNISTT KKSTKNTKISQA
3924	17825	A	3947	425	3	SPSOGRLDKTPISLGOSTWKGQGMWAQR QQT*TSNPDGSESSRSPTFEQISER SSSAGQNTSSSGSLNSVDPWETPPSR SQQTPTHTGELQASGRCSSGMNLPBEGT DSNLCCSATHAS
3925	17826	A	3948	299	3	ASQTTTFREGCLFFSFFISVCLFVCLFE MEFHSRCRPGWMECNGDRARLHLKTTITT TIEIVKDDTNKWHIH*RLPNIRMSILP KVIDILFNAIPKI
3926	17827	A	3949	331	374	NAPKSERASKAF*ATLEENKEKPLDIN PVVHPHGHIKCVAPPHCLGWLDSAVPA SHALGFPQNSAMHVARSKSASACLTG AVTSAGSGVLGTPNKMPQKVRERARLFW R
3927	17828	A	3950	439	69	TNQKVVWPPKEKGLFKKKQLRPRVGGPA PHSPPLEGQSS*FP*GQRFKPRPPWVK PLFSKNFKNYPGGGAFFPPPSGG*GG KFFPTPKAKVFPFIQISPPPAQAGGTQV PFFKKKKKSH
3928	17829	A	3951	422	3	CFPALGIGPPEHPPKRVG*KGTFPPGLE FGKFLKKNFGKNPGPGQGPPFPKPKQ RGPFPNNGRPGKVKKGAAGPGVVKKKPP RVPPPPGFGPNPGAPPKFFPSRGGED QKRKNFFFFFLRWSFTNEAQAQGVQR
3929	17830	A	3952	223	3	ALFFWNGRTLPRVKGILNPKGGGKFFFF FFF*ETESHVAQAQLQHDLG*LQPPP SRFKPFSCLRLPGSSLS
3930	17831	A	3953	1	388	EKGVSPPGRTCSORNCICTPVWATERD SVSKKKGMSNNFSLILRSWNNKGQGGTY PQKFIYPCFLIKIGHSYINCKIFPK** NLSLHVHVTDVNVRILQLKDCQIHWDV FNFELNLQCGGLGGCK
3931	17832	A	3954	1	396	KLRPKDQDTWPTQSAIVVEFPFVSFYF VKSISEILFFFFLKNFGLPGQLKGRGQ ILVKGNP CGGKKKFPAPPQRGGKKG PPPPQFIFVLKKTGV*KIGPGGV*TPA LGIAPPFPFKGGE*RGGPPP
3932	17833	A	3955	2	199	PGGGCGGEPKTRGCTPAWATERDVSKI NK*KLKLNNSWLYAKSLASSPTGR*EE WGCFITNEHI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, =possible nucleotide insertion)
3933	17834	A	3956	393	2	KEFFLPFGGAPWPLSGPFSVLEKFCG GGVVPGLNTPGGGGFPQGLWAGDFP* PLFSQPIPFKKQKQFFFLPRGGLWAPF PFPFGGLPFSQNF*KTGF*GGFFFFFG DGVSLCYPGWSAVAPHAS
3934	17835	A	3957	278	390	LVYIFKIRCTWPGVAHACNPGTLGG*G GRVTRSGDQ
3935	17836	A	3958	385	311	GPKNPPASASQEGETTEV*HAWLIFFL FFVELNSSHVAQAGLKLPASSDQS*TLY I
3936	17837	A	3959	410	119	SPPPRFKTPFFPIFGAPKKKFFSPPPR PLNILLKGPPLFFFFLEPAFKHIMPV FPQKKKIV*INLYFPFKKENESS*GK HPALHCNPSCKSK
3937	17838	A	3960	77	400	TALPLPKKKKKKKKKKKRGGPLKKKK FKAPGEKKNFKGAPKKKFRGRV*KTG ERKKPGGNKKKTGKXPPFRGEKKKKP QA
3938	17839	A	3961	2	194	CL*SQLGLRLRWEHDHLSGN*GCSEP*S PHCTPAWTE*DPVSRKKKYVNVNQT RGFLSPA
3939	17840	A	3962	52	409	NSKTSQKKRRVRLSLRSRVGDDTKV NTRRWGVFGWHLNLPPTLVLKMEKIL ETYFMTPDLDHPHTTSYFNGQLQAIKV GGTITDLIV*IVSKPNAAGLSNENVN AKFNLDI
3940	17841	A	3963	382	96	LSSQLLREAGERNE*TGWLOOPLQMIIH KNPCIEPRSYCTPAWATEQDPVSKNKQ TNKQTKNSLHL
3941	17842	A	3965	3	169	DAWELRSHRCPPAW*QSETPSQKKKRG KKKIFRFLVLFNKRKKPLNGNLGVIP
3942	17843	A	3966	1	121	AGFHRVSSDGLDLTS* SARLGLPKCWD YWCEPPLAENS
3943	17844	A	3967	200	2	PPFRITYGCVLTPLFLRVKPFKFWGPF PFCLFFFFFEMESRSVAQA*MQRDL SLHPPPPAFK
3944	17845	A	3968	471	440	MELRFYHVGOTGLKLITS*APPVMSQS AGILGVSHST*EAPNSLAITPLSSHLS PROP*THLGC
3945	17846	A	3969	214	2	ESQPECQLQAGDWLSLWNLVCSGLEURA WREAPRLMSFCLFFVSEM*SHSVI*DR VOWHIGSLQPLP
3946	17847	A	3970	53	398	GDLPKKQQCKPLNFCQPLL*YARLEGGP IFLV*HLATYNNKHLLEC/GKVMINCOA DILNKWEISKVGAQKKKKKKKKKRG PLKKKFI PRGGEENFPFLGAPKKKTGG GFK
3947	17848	A	3971	396	160	KRERIKEEDNKEEKDEKKASGKKERK KEKIRDRESKEESSNLLQESLSLCCP SPGHPPNSSL*DPYFATGNSLRC
3948	17849	A	3972	416	3	FPFPRVPEGVFGGEGVFPFGFKGSCVP FPRPRGGGAPI*KPPFPFGGPNFF*K KTGPFPSPPQGAAPAKRAPPPFGGGGG KIFTPKKGGGLFFFGPPKKGVFFGPKKT LFFPKKKKKKKGRPRSHASAHAS
3949	17850	A	3973	232	381	YKTFSLIF*LPFFDRVFSCHPDRSAVV LS*FTVASISWAQGIILAQPLE
3950	17851	A	3974	396	141	CPFFPPFKRGFPPTPIFGCGPFGFFPFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						F*NPPPKLIFPGAPKKKKIFPPPGGKNFF FLKGPPPPPPPPPPPPPPPPPPPPPPPPPP
3951	17852	A	3975	286	422	RKQLISPHSODNSRQKQSWRHATCLQ TILQSYSNQNS*APAIKTILSKKNKG GITLVPKLYKATVKTAWYDQK
3952	17853	A	3976	3	116	GFHRVQNGFDLLTS*SACGLPKCWDY RHEPPRAR
3953	17854	A	3977	223	399	EGPRTQSFFTEVHSVTQDGVRRRLNLS LLPPPPGK*FFYLSLPSNWDYRRLPPR PVN
3954	17855	A	3978	227	422	SFSPSCIFSLVDLGVSLYCLGWSQFLD LKGSSLSFPKCDYRQ*ATTPGLPVVYF FPPVPVTF
3955	17856	A	3979	519	313	KNLLNPGDGGCREIKSSSCAPAVTEK DCLKKKKKTSVCVCVCVCVCVCV*NHL SSLGLFPEPVGLN
3956	17857	A	3980	217	414	IYIFCGDGVSLCCPGWLKQSLFLPKC *DYRHVPFRPTSFHLLTNIGVLQFLKLO ATLSFTLFL
3957	17858	A	3981	2	409	KLTFVAV*DY*EKLLLSASLTSQAALFL PEHPYTVISNPPCSYANIFTLSGTTFH QFYAKS*CVTYE*KKKLLNSPPTGDKPN *GRSQTKKIQT*SEICFFVHLFETGS HHVAQGLLELLSSRDPTASQST
3958	17859	A	3982	234	416	SVLPSTPLNLK*KSCKKKKKKKKKKK KKKKKKKKKKKKKKKSRGGAPKKK GGACSEPRSCPTFAWATERDSV*KNK QPNKQKKNKDLL
3959	17860	A	3983	414	291	TNANKLDNDEMDFLETONLLRLINNEE TEYQNRPVTRREEIE*VIKNLLTEKNKPG PDGTFGEFYQTFKEKLIP
3961	17862	A	3985	403	145	AAAAAFFFFGKGDPSPTVLFGGPPGFS PPPVFKTRPRNFFLGPPKKKYSPPPPGP KNWFF*KGPPPPPPPPPPPPFWLKGIEV IS
3962	17863	A	3986	255	425	GGRFKGNSPTAGLQGFXXXGPPPKFIS RPGV*QRGEWKNPGVNLFLALSTSPFR W
3963	17864	A	3987	247	2	EEAVKVSNNLYTKLDEEQ*VVKKQNLNVE RLKK*ELFLQDLYKVPKLI*IF*VKNL NSFWDAVAHACNPSITLGGRGGIT
3964	17865	A	3988	1	394	HHHTWIIFFKCDKGVSLCLSWARTFG LKRSSCFRLTKCDWYRHEQLCPAFKHF LY*HNFMSTKMQE*HKNS*YPSPTVPK GVTFYIYSICFIIILISAITYKFVHTY IVSLNHVCSNEAPLSLNI
3965	17866	A	3989	208	402	ETDRRLKSGGSLSKTILKMTCPVFFVD GVSLCCPGWIQTGPLK*SSCISLPSWD YRHMPPCPA
3966	17867	A	3990	2	408	THRPYHATPYLFPYTNLLIKGKKKKK KGGKKKKKGGPPFKKHGFSPPGGEKNFF FYGPQKKKSRGRV*KRGEKNPGAPQNK PLGKNPLFPGGEKKKKPRFAS*PPPPPP SFGKKRAPPTKYPGAGLHP
3967	17868	A	3991	81	406	KGGLFLLRPRGRGRKIWKNLGLKNKK NPPA*PSEEGKKGGPHQAGKILKFGGK RGLNKGKGTGQKLLKPGGIPPPGP*KVGE KKEKPPAPGQKLFKKRKGKQKNF

SEQ ID NO. of nucleotide sequence	SEQ ID NO. of peptide sequence	Method	SEQ ID NO. in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
3968	17869	A	3992	396	64	YSSPPPPKKTDDSDASRGPPFFFFPPPEK RGFFPNDFFWVPGFFPPPGF*TPPPVF FFWAP*KKIFPPPPRE*KFFFLKGPPPF FFFFFFFFFFFHLQVLLLC
3969	17870	A	3993	367	193	KLWEKKKTLWKKG*GEIKSCHCSTPAWAT RVKCLTKKKKKKKKKGGEGEIKKKKSF SFLGQKKKKRGPAFF
3970	17871	A	3994	188	2	KRANTLPDFKTYKAIVLKTLWYWRDK HRSMQN*ESNEVELLYHNIRNKLKMD HRLKCQ
3971	17872	A	3995	2	147	QENHLNPGG*GCSELRS*HYTPAWATE* DSVSKNYI*TSHIFSGDF
3972	17873	A	3996	23	329	RNSFRSFAFSNVLNKVVFLTSEKKKKK KKKKKKKKGRKREYLTRRGAGENNKYF YK*KKKINTCG*KKKGQWRKRERKKRL GGKKKPPPEEEGKKKPG
3973	17874	A	3997	164	392	KPLGRAGLVPCLCSSPTGFLM*KTEPCS VVQAGVQRGHLCSLQPSPMFKRPSLLS LPSSWDYRVLNHPSPSAVV
3974	17875	A	3998	396	3	FFFFPPGGKKGISDSQPQFFSGVKNFS PPPPVWGLSRVWPPDKNFFFF*SKV PFSFEGGPNPPFFSLLGGPPPPIF SGEIKTPNPPFFFFFFFEMESCVAQGV R*RHGPLQPPPPWLKQF
3975	17876	A	3999	383	2	VPSPEKVGIKRIQPLDPFF*FLGDCQRK KKSPS*RPDPPEGGKLN*IRLMQPPFN SKEKFF*KF*AFKPPFPKPGEGI*GFF SRAHSFPNQRALFWFFFFEMESHITQA SMQWHDRLSLQPPPL
3976	17877	A	4000	213	1	RGRQNTLFLTKPNQTKPNQTKPNQTKP TTFL*SVIEIRVKKYKTKRKTKNPT SLTRSLGRYKSPTRP
3977	17878	A	4001	412	129	GSLSPLEKCSGTIPAHCSNLNPGSSSP CTSAPRVAGPE*MGQACMPCLPVNFFF WGGGGLVETRSC*VAQADLELLSFSDP PASASVLEL
3978	17879	A	4002	411	293	RDRCLPP*LDNFVFLVMGPHRVGQAG LELTSSEIA
3979	17880	A	4003	46	392	QDFFFFFFFFLKGQAPPPGKKGGTFFPK KTKGGGPRGPPLEPPPLGGPGPPPEGG GDLKKWPPQGTPL*KKPKMGGGGGGG P*TPGTGGGGEKNPLTPGGGPKNGPPPP PPG
3980	17881	A	4004	360	1	KCLGQFFFFRWNICIFISQLSIASQV QNSEIQNAPMSIFFEHSVFKQFILLEH FGFWILGLMSTYKTLILLKLN*RFNA MFINIVVIFMEIDKLIFKFTWKYKEPR RVKAILRN
3981	17882	A	4005	152	408	NKFSVSHYWMGNVLSRYQFT*QFSFCH VRLPSV*VLYTRNKILIFAHKAFKFLD AKYVCVCVCVCVCVCVCVYFGIGENLPS
3982	17883	A	4006	411	67	YLPPSSPTPGVFFFFFFPPPKKEFFPNF LGTPRFFFFPPF*KPPKFFFLGPKKK K*FSPPRGKIFFFKRADDPPFFFFFFF FFFLGLGSLSFMYFHITYK
3983	17884	A	4007	217	2	PLFFFFKHLKAYYSVDVHISFALLRYLL F*DRVSLCHSGWSAVARWLPVAGNTFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USNN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
3984	17885	A	4008	235	406	ITRQEAPLYLATPRV GRHRVSSNFIPI*RRRGLSLLPKLECSG VSIACHSFDLPG*SDPSASASRLLGRLR Q
3985	17886	A	4009	833	237	SLDNRARPCLVSPFIPIKKGSTAEKCGAP GTTSPFFRLSERGHPIIPS*ROWERKS QLCSHLQSSRDPSLGRAGCGGGDLRE SGCTPPGGSSDLPVPTAPIPIEPIC QATCAWKLSEDEYRRANLGECPRS SGKPSSPRTGGSSRAKQTQSSSELG LGIGARRGTDSLESHSTSHENTVLTGLP SP
3986	17887	A	4010	276	2	VEVKGNNFSFEGSSTLTLPNPKQPKETT DQPLMSTYAKIESPGKNPSHDG*LIFDP GAKIIQ*VKNSIFNKWCNDNDPHVXTM NPHFTLI
3987	17888	A	4011	188	27	REKFOIVTINKDKSGITTDTER*KIIR DYVEHLVAHLENLEMHKLGIP
3988	17889	A	4012	1	202	CLHQKVIITN*L*ATTQTTQLSLSPKLD YFSIIIPVALVWTAIKFSL*YINSP PKKKEAEKDLN
3989	17890	A	4013	1	403	CLDQEVITIN*H*ATTQTTQLSLSPKLD YFSIIPVALVWTAIEFSL*YINSP PKKPKKPKKPKKPKKGGAPLNSRGGP NFWGGGKNIFFPFGGGDKKPPRAFWKPK LFLGGGNGLPPPPQPKPTPWGK
3990	17891	A	4014	67	439	TELIIFYIFFETTLIPTLAITR*GNQF ERLNGTYFLPYTLVGSPLPLIALITYH NTLGSNLNILLTLTAQELSNS*ANNLI* LAYTTAFMRKKT*KKKGGGGLKDPWGGQ ILAGREKIKFPF
3991	17892	A	4015	3	260	LIVFTIILLPLT*LSKKHII*IINTTTHS LIISIIPLLPFNQINNLFSCTPFSFD HLSHPIILKKKKKKKKKKKKGGGA F
3992	17893	A	4016	258	3	LKKIPSPPTINLPFPFELKKFFFLSL *FFLCVSPFPFPKGFPIKDPVVF SPPKKKKFFFPFPFAPRPFVFGKP
3993	17894	A	4017	287	2	KKOKNFFFFKNSFFFCRGAFPPFLFPF ILRGKGDFFYPRGLKPALGNO*NPFSR F*IFFFFFFFLRSLAPVTOARVQHNDP GSLQPSPSGFK
3994	17895	A	4018	228	487	SYDVKQEKPNGI*ASKYNAVYVHSPFLS FFFFFPKKKNFFPCPGGGQGNLSLRE PSPPGVKLFLGLNLSKSN*QNCPPPI IF
3995	17896	A	4019	35	228	EELNHLNQGEGECSEQRSHCTPAWATE *DSSQKKNKFWYIHPNCNRIVTTNTPMT ESPKHYAE
3996	17897	A	4020	2	402	ARGNLNTFFDPAGGGDFILYQHLE*FF GHPEVYILILPGFGIISHIGTYCGKKE PFGYIGM*AMISIGFLSFIV*AHHIFT VGIDVDTRAYFTATIIIIAIPGV*VFS *LATLHGSNMK*SAAVL*ALG
3997	17898	A	4021	1	420	TRGATELIIILDIIVETLIFTLAIITR* GGQP*RLNAGTYFLPYTLVGSLSLMLG LYTHKTLG*VNILLTLTAQEL*NS*AN NLI*LAYTTAFIKGIPFYGLQL*LPKRAH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3998	17899	A	4022	409	3	VEAPIAGSIGLAAGLLKLSGYGIRLTL LEMASCLIIICNNNNPPFYQIVTCDEKWI LYENW*LPAQWLH*EEASKHSRPNLHE KKIMVPVW*SADGLIHYSFLNPCETITS E*YAOQINVMH*KLQGLQTLFINRKGPI FLHNNTKLHVAQPMLOKLNELA
3999	17900	A	4023	464	374	HLFPWEDKARRHLPDARTFILAFASLRN VRNKFPSLQATQFLVLYASSTKITKPLK TNQKKRLKKSEQLRNMWTPIKRTNICI VGIIEGKEGEKGAERIFETVPQT*NL VKDIK*KVQ
4000	17901	A	4024	58	323	RHKLLCEHVKKCSAVLITIREMQTKTTLK YHFLLVITARI FNLIHF*RSVGETLICQ WAGRNAKS*PFWRRI SQYLTKLVVCVM YTHS
4001	17902	A	4025	480	150	RNSLLRLRLGEGDMSFGCGGSEL*LHH CTPAWVTEQDPVSKKKKKKAYPDP LK KTDKSNKKGGPDPFRKNFPKNSPPPPQ RSTAFRGAAKSCPTH
4002	17903	A	4026	204	1	KKKFGALFFFFMOGLTLLELEYR*WCD HGS L*P*PGSSDPTSVSQIATMGVH HEFLRSGVLSK
4003	17904	A	4027	116	472	MPPELFKVPSPRPHSCPLGGPQLSTPL TGP RPASLSLPSI EOCICGTALIMAVN YLVQLMGLGLSLFMA*RGAGSSCSAHKKW WLGLASPSC*TFFNRTKGRARMLTPIVI PALWEAE
4004	17905	A	4028	355	444	VSYKKK*SRPGAVAHACNPSLTGG*GGR IT
4005	17906	A	4029	410	181	ASITLLIAVFNNILSGQ*TI TITNTQY SSLIIIMAIKLGIAPFHF*VPEVTQG TPLTSGLLLT*QKLAPCF
4006	17907	A	4030	49	474	PXRXFCCHIVTYYSKGKPEFYIGMV*G MISIGPLGIV*AHIIFTVGDVDRAY FTSATIIIAI PTGVKVFS*LATLHGSNM K*SAAVL*ALGFIFLPTVGLGTIVLXN SSLDIVLHDTYYVXAHFHYVLSIGAVFA II
4007	17908	A	4031	274	427	FFF*EMESHVSQTAGLLGRNHSLLVPQT PGLKRSLLSLLSNQYKSGPHT
4008	17909	A	4032	205	393	TAGGFKNPSPOEG*IKKHHDFNEMFLQN CWKLLFPGGGFTTGQIFFRAPPPINKNI LWGGGK
4009	17910	A	4033	2	386	SEPLSRKKLYLSILSLQSLISLITFTAT ELIIFYPFETTILPTLAIIT*GNQPE RLNAGTYFLFTYLVGSLPLIALIYTHN TLGSLNILLTLTQELKXKKKKKKKKK KNIGGPPLRAPSGAPN
4010	17911	A	4034	3	169	GLFLAMHYSPEASTAFSSIAHITRDVNY G*IRYLANGASIFPCLPLHIGRGL
4011	17912	A	4035	3	317	HASADAWAFIGVLP*GQISFGTATVIT NLLSAIPYIGTDLV*I*GGYSVDSPTL TRFFTFFHILPFIIAALHLLFLHET GNNPLGITSQKKKKGGPF
4012	17913	A	4036	446	194	KKKNQGGGPPPPAFPGVGLIKKRFPPT PGKKFKFR*KFFPKGGFVRDPPPKPG CWEREKKKPLNTDKWVILEGSAGLF GMAKVKARFLQKRGQVRLNPPWKGKF
4013	17914	A	4037	213	1	

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						PNSGKTETPFFFF*DRVLLCQPGWSAVAQS*LTASTFWAQA1
4014	17915	A	4038	307	36	RKGFFFSKCGEFKKLPGLGGWLYKLI FCQKFFHFKPFGPG*IFLPPPKIFFI FSFEMEFCSCCPGWSAMGRPLRTATSAC WQCRMS
4015	17916	A	4039	2	372	NDTSLTVKSGHQWE*TYEYTDYRGLVF NCYILPPLFLERPGDLLLDVNRVILPI EAPIRIINTSQDVVHLS*AVPTLC*KTDA IPGRINQTTFTGTRPEVYVYQCSEICGA HRRSNMLIVLELI
4016	17917	A	4040	107	279	LLLLFFFFFKKSLALAPRNECRGKI*GH CKRLRPSCHSPA*ASPEAGTGTGTYGC F
4017	17918	A	4041	3	351	GSHYIAQAGLKNPSSSHLPASAAHSAGI TGVSHAWLKIPFKEVSVDYSPLHNSRK NAVYVSFFFWKKS FVFVQAGGKGLNL GSLKFSPLRLKQFSCLTLPFS*EYGLAP PPPV
4018	17919	A	4042	1	385	RPRRPDIE*QERRTQEVQLQAVAKVKKE SQLPGTGGPKNVLPQVPRAKAERPKKQA EASGLKKETDVLVKVDAQEAKTEPFTQG KGGGQTTPESEKAPQVTEI*SSELVT TQCAETLAGVKSQEMV
4019	17920	A	4043	3	282	TAILIQT*SFYGAVALILIAHGLTSSLL FCLANSNYERTHSRIILSQGLQTLPL IAF*LLASLANLALPPTINLIGELSVL VTTFVSDDA
4020	17921	A	4044	2	407	GTRLEIMSRNHGIFPFTLEIFKDNEFEE PYREALPTLKLDSLYFGIEPEEHVSG* ESLESCEPATPFSKIDELVKYLLIRDG* VSDDGVQKQTSRDLHAGHFOVPDFKFEF KDHKEVILH*RDVLCGVMDERSR
4021	17922	A	4045	4	380	ENWLTITROARHEDARNLNTFFDPAAGG GDPILYQHLF*FLGHPEGYIILIPGPGI ISHIVTYYSKGKEFPYIGMG*AMISIG FLGFIV*AHHIFTVGIDVDTRAYFTSAT IIIIAIPGVKVS*LATLHGSNMK*SAT IIIIAIPGVKVS
4022	17923	A	4046	2	94	ADRNLTTFYFAGGGDPILYQHLF*FF GHPEGYIILIPGPGI*ISHIATYYSKGKE PFGYIGMV*AMISIGFLGLIV*AHHIFT VGIDVDTRAYFTSATINIAIPGVKVS* LATLHGSNMK*SIPTPILIFRP
4023	17924	A	4047	376	138	LLARQQRQENGVPNGGACGEPSRHRCTP AWATE*DSVFLWREALLTCTAPFNRLQ LLALPSEFFHFRILIVLPQRSQ
4024	17925	A	4048	145	226	EPIQACSSRRVCEPIQACSSRRVCVCV PSRHALPGVCVCV*EPIQACSSRRVCVCV RAHPGMLFPACVCV*EPIQACSSRYVCV RAHPGMLFPACV*AHPGMLFPACVCVCV PIQACSSRLVCVCV*ERAHPRLLF*ACVC VCESPSRHALPGVCVCVRAHPGMLFPVC CESPSRHALPGVCVPSRHALPGVCVCV
4025	17926	A	4049	2	414	ADRNLTTFDDPA*GVDPILYQHL*FF GHPEVYIILPGLGI*ISHIVTYYSKGKE PFGYIGMV*AMISIGFLRVIV*AHHIFT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
						VGIDVDTRAYFTSATIIIAIPTGVKVFVS *LATLHGNSNMK*SAAVL*TLGFIFL
4026	17927	A	4050	472	228	LTRDGGACPFSKLFRVRQKNPLVLGE* SCSEPKLCPCCPAKKT KDYPVSKKKKKF IWIINRTKIPRKRKKKNKAYHKVKYF
4027	17928	A	4051	238	3	RRHGSFAPLPGLPLCISYIWLFTITLC NILYLYFETGSRVYVQVGLKLLCSSEPP PSTS*STEITGMSHGARPHNIP
4028	17929	A	4052	225	172	IARYPFPHQSCSTNMFSPNKSTTSKEEDN GPGAVAHACNPSTLGGGGGQITKSGVRD HPC*HGLV
4029	17930	A	4053	471	30	GGGKIKSGALFPLNVRVVPVVFPRPP LI FPQGVFNQNGDGPQGVFNPGETPGR VFPFPGVFFVKSPFLSLPFPFPPV* KTA VKTGFPYRPGGVPRGLVFPKKKSVLN RPDLMSGPQPE*SLPLPGEPSPVSHAGCL PQAWRG
4030	17931	A	4054	425	41	NWGSGLFCPQLGVFPPPPPGEGGVPGA PPPARLFFFFP*KKQSPVGRGQFKFLP PKNPPPLPFOKVGIPGGGRAGPIFSPP QLFFFTLWSTLTPSPRLCEGSAIHLACT PAWETEQDSISKQTKK
4031	17932	A	4055	312	1	IKNRAHLFQGSPPPLIPVIVITETIS LLIQPIALTVRILANITAGHILMHILGS AALAISTILP*TRIMFTIIERTILEI AVALIQAYVFTLVLSLYLHA
4032	17933	A	4056	648	123	DDPDVPSARGCVFSGAGRGKGAOLKRAWD GALA*LPPLCAQELSPFSLGTGGPAVG LSVNSERDGRGVEVSINAEFTVAFLKG TQRRRINGMPLPQREPSRYCLGLGDE SSAQOTSGLTGRV*QNSDLPELASGDD KGQRSSQGGAVSQSSPRGRQIPPSPPA ALFNFL
4033	17934	A	4057	135	464	QHSRLMQQAKKGVTLVARIDLVDYEDE ISLLHHNGGKEE*AWNTGEPGLCLLVLP CPVINVMGKLQRHNPRTTNGPDTSGMK VWVTPAGTKPQPAEVLAEKGKCEG
4034	17935	A	4058	3	575	LRSRPLHIILSCGLLVTPRSLSPFPFPQ RLRLCRPSRGAAPFFSRLTKLHAFATLP LRIEGSKTL*NCC*LYHGC*IS*IHGG LFDVAANKIIEHEVEKYDRQYRGKELIG PATYKFEIIVHVOIQ*VLEPALSMLQK AMETIQQAFTNVANKHPEEFENLQTVQ STIEDIKVHTAQAEVMIQLOVR
4035	17936	A	4059	389	3	TFKGRKVFYRPTFELCPDPPGFSSKNIW TPPPPPFPFGVPEREKIIFFLKQALPLF SPRVTPFPGLKRGFLSTPTPPFPFPFF WPFPFPFPFPFPFLRRSPALVTQAGVQ WRDLG*LOPLPPGFKR
4036	17937	A	4060	397	1	KRRGNFFFKGSLFT*TPRGPDLWVF F*KAPKGFCAKFPFPFPPLPKENGKTH RQKTPPFHFCQIFKNGFWLHAFSLGDF PARVWGPFPKRFKGIKFKEFPYGSPPP KGPKKKRTAARDLELADAW
4037	17938	A	4061	38	410	AWISIERPFTLVVRFKRLAISGLLES YFRINFLYVQIHITHFTFRKFLVLSYVFR FTDVKFFFYILPFPFPHFLFGWICSVA L*FFIYFCFLPFPFNGTSP*IGLELLI

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4038	17939	A	4062	405	81	FFFKKPTGFGGG GGANVPFQKSPPPGNGKKGGHFFSYKILN NPQHPFLLKKKNAPGGWGNWFSPPWK GAL*PKKNPPKKKKKSPFGKGGKKNP FPKKKKKKKKJA*GDNFDMGTGN
4039	17940	A	4063	415	239	RPSFFFFPPKKKSCESTFFFLSPGFFF PPPPFFTPPPFFFFPPPKKKKFFPPPG KKEFFF*PPPSLFFFFFVFVFFFP FFFFFFFFFFF*GLTSPHKIGLVLA PLLALSKITHASIPVPVSSPKKKKKK KKKKKKKKKK
4040	17941	A	4064	95	241	SPCRSPHRWVNS*ANNLT*LAYTIAPIV KIPLYGLHL*LPKHVRAPAGSIVLAA VLLKLGSGYIIRLTILINPLTKHIAYPF LVLSL
4041	17942	A	4065	28	288	YFDIFVEARSPYVFOVLELLGSSNP SASQSVGITGGSHCAQ*VTILFTTCTL HVNG*I*CIKFLIHNIPILVLSLQYIFG FPL
4042	17943	A	4066	338	134	PGGDCSEPRSGHYSHCTPAWQ*SETPSK KNKKKKITYFSVKNWGRVFIILLNSF TTVRP
4043	17944	A	4067	26	365	WVSLMTSALAMRVDFYFTLLILGLLTS TLTIYQ*WRDVTRESTYQGHHTPPVQKG LRYGILFTISNDCFPAGFF*AFYHSSL APTPTQLGHWPPPTGTTFLNPLEVFLINT S
4044	17945	A	4068	491	174	TQLKTH*GSTTDRNTRVVRPRVNTYK DLLKFL*SKGYDFSESTETETIAKLKVKY MYDNRESQDTSFTTLVERVIOQLVLSHI FKDNANINAEKLSGN
4045	17946	A	4069	210	402	NVSKGLRRVPSTQ*VINISCRPGVVARA CQPSLGG*GG*ITRSQVRDQPGHGET PSLGGPVA
4046	17947	A	4070	202	1	DSATALQPRO*EQNSVSKKKYRTIDLR SEYFARNSFTLAARAGVQWRNLGSLQPL PPGKRFSSHAS
4047	17948	A	4071	412	143	FLGAGV*FRIGPKG*TFLLKNQKLTGH GGGALYSQYPGGWGRNRNSFPGGKGRTR QNPPSLQTGWKKGVSPSKKKKKERKTR KWGGE
4048	17949	A	4072	2	324	RGRNFCMF*SDRVSSCCPSWS*SPGLKR SSCLSLPKCWDYRFEPLYLARLVLMRK STHTYIMYQMQLRFGHRYLSVSTSS ATRPYLDNFFFCCKNKVMPCCQG
4049	17950	A	4073	2	326	RGRNMLPRTPTGRPGNDQOPQKHSLVD* LFILYLFYFLWTGSHSVAQAGGWRNHN LQP*PPSLKSSRSQAGRVKGVSHCAWL LLDFLSPGKPYTYKKVDKVVSPFA
4050	17951	A	4074	422	116	EIKQEKNGPFFFFFPFAKRGFPFTPLI WGPPGFPSPFLKRRQGGFFLGPL*KGN PPVFPKPVFFFWAGPPFFFSFKKFFP LVPGSTFIHFIFHCYLL
4051	17952	A	4075	3	294	VFCHVGAQGLELLDSSNLPVSVAQSAGI TDTSHLT*PDLSFCCKTKFD
4052	17953	A	4076	60	389	PSAQLGSKTHIMAVQP*PPSPPELLHL PKMLCPSAHTPPPPNPPTVCTYSPR SSPAFPQEGPSSGEGGLVLSLSSPPN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4053	17954	A	4077	93	383	HVHFPAPTSPESGRGRVREGAYV KPLFAPGVLPFGGPGEPKREKGGAGGGP KKFSPPPPPFPFPFKTLWAPLFQSTQ GLRLCPFFFP*RGKALF*KRGGGRFKP PPPPPGGLGPPTP
4054	17955	A	4078	2	365	RKVEGRVS*DEDLKLTTELLRYMYLNTIEA AKDLLVRRTKALIDVDSNKKALDKARFK SKDLKSDCAHPRDC*RA*APYFLPAKNE LVVPTGEQRHFLQDVPLIVQRTLTTLRT DHTSLPLSL
4055	17956	A	4079	6	298	PLAINGGFFTLAETNRTPFDLAESESEL VSGFNIEYAGGPPALFPFAEYTNIIII TLTTTIFLGGTYDAPPRP*LSPLSFYE PSPPYPTWSTST
4056	17957	A	4080	414	154	FIPATREGKAGNSLNPEGECCNKRKRSH CTPAWQGGKTPSQNNKKVLLALKV*SI FHLMES*KYLKPGFSLDLITVIPTFYDL FRC
4057	17958	A	4081	347	1	VLKXPRGNIIIFSPKKKKNLFPFGPNRYF PFFFPFPPLPFFFFFFFFFFFFFFFFFFFF PFFFPFPFP*RGGLLLFRKIKLPPTTHP YLSNTRLGWNPGEGSCWRSEGGRGEDCL QDH
4058	17959	A	4082	1	354	STFIISLPFTTIFMCLDQVIVTIN*H*A TTQTTLQSLSKFLDYFSIIKKKKKKKKK KKKKKKKKGGGGLKKKFKNGGGGKKK FFWGGKKKNWGGGVKPGGGKKRGGKKK KGGGEK
4059	17960	A	4083	384	85	FFFFKEFFGCFRFFSPPGFLLTPPLQV LEFPIKKKLSPPPPPLKNFFYTTPPPFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFLLM*AKKFI*SWR
4060	17961	A	4084	1	122	PHRFRGDLGLLTS*SA RLGLPKCDYR REPPRPAFLPQ
4061	17962	A	4085	223	401	NGKLVSVFFGFCFFEM*SRCVAQARV QWRIFSSLHFLPPGFERTISCLSLLSRW D YRC
4062	17963	A	4086	160	408	ALPFRRRGGGAPSNFCLLPFGP*GKKG GYGDAPSCRSGLGQHGETAAPLKAQKSP GHGGGRTQVRRRVGPPGGRRQKLNKG APPPFRLLGGKAP
4063	17964	A	4087	261	81	YIDGRIFCQKLESSHSPGAVAHACNP SLGG*GGQITRSGVQATHSPPEVWG LQA
4064	17965	A	4088	428	140	OPLKNPPLGGRAPPLRGGKLLPFPFG EPPFP*KKKKKRGGGPPPPPPPRGE PKKSL*PKGGGKKKKSPPPPPQKKK NPPPKKKKKKK
4065	17966	A	4089	1	205	FRLOENCLNPGGGGSELRSHYCTPAW VTEQETLSQKNFFN*KTFRKAKSTGNF HMPNTSIIQLEFI
4066	17967	A	4090	154	410	ITGCSITXYFYFAMRREKSEVGYPFSS SINTPLRHLRSDGVLDSTRITSLSTHSA PFIKSKNRPGTVAHACNSTLGG*GGRL TK
4067	17968	A	4091	428	67	LPHPPPPPPPLSSSSSSSSSSSSSPFP PPPLLPQGRTLTRPLPAPAGLGSRES CGAPSSSLGASLHVA*NADRRQ*RAALS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4068	17969	A	4092	431	3	TPHGPLTGSFAAWGRGREQDLLLLCS APTSNKGSTTPIILQIRKLKATPCSSIGP SPSTLPVKLEL*SVLLPGQWLNPSFCHP FRPKCSNRPRYTLPVPKLPSSGLPRP SPSQQVTAFFPLTSRKEDSPSTPASDA PPPPAPVARSAROEVLCEISPSVTME
4069	17970	A	4093	151	1	SINPMWMDVAHACNPTCTLG*GGWLIK SGVRDPDQHGSETSSPKTKL
4070	17971	A	4094	35	363	LQSKYVCTFFPFLRGFFFSRVRGRGA HPGLGAKTTGVKGNPP*PKGKGPGGV PPPPGCFWFPLGKGFPLLPGG*NG KKKPLVWPPKGGELKGGTPGPPY
4071	17972	A	4095	376	1	LKSPFPLGAFPLKGLSLGLLKGKGF TTP*LGPPHPEKGPGLGQWNPQKQVW KRGFPQKGGENPFFFFFRRDGLSLC CPGWQTPGLKQSSNLSLSPSWDYRCLS KSLFKENTETLAS
4072	17973	A	4096	65	446	PPFLPFLNKGPLFTPKRQKGRNFFT* PCPRGKKNPPPPP*GGEKRGPPPPGK FFFFFGFGRFPGGGVFLDLGTPLPLG KGGEKRGPPPGPKKPF*KRKNSPP TGOERGRGKKHCLP
4073	17974	A	4097	34	387	IKADEYVLTALACVFGMEFLSSPHR LHTRIGSSPSTCTCPACFSSW*HGAS VIPSQTAYEDWFTLYNVLTYSLPVLML GLLDQVGASHQGHFWTDENALEKQAN VSMHSSGVYFFLIKPYNSVVRHQSGL CFLFCNCKERG
4074	17975	A	4098	80	422	ILHVLTYCIILCFVLQS*ILWFVLQNYI LHVLTYCIILCHVLTYCIIMCYIHV* FCILALFAGLS*DSPYHESL*SFMEAD DISLCRCVITDQLNFCISLGH*ELRMF QP
4075	17976	A	4099	74	402	IYLLSTHLHYQFSNISTFTDLSFFFFF LKESLFFPQGGGGGGLGLKPPPPGE SPPPPIPRGGGKKGPPPPWVIFFFT* KKGSPPIYGGG*IFGPGDPPPPP
4076	17977	A	4100	3	335	DAWASANVTEYDSVKKKKKRGGGKK KQFPKKIGPRGSLFKPRGGEKPLSLKTP PPPPF*F*KPFFKGGGAEPWEPFLKPP CLKDRGGAPKIYFFPNPPGAPRGAAFIK RGGGK*GPCCGLL
4077	17978	A	4101	406	1	RFPKPPPPPKMSKALFK*KGFFPPRE LLIGPPPPPPKPKKFFPLTFKVLPPR FF*NFNQVSKKRPTFLKVGQ*PPPMLV QKKPTRGFPALFKKKRSLVIREIKRK PTMYHLTPIRMAVPHKSNRC
4078	17979	A	4102	2	183	VNPGGACSEPR*CLCTPAWUTERDSVS KKRADNDKQGALRSFFLGFPFPLPHPT SPAF
4079	17980	A	4103	119	391	DNLQCFFFFWKRGLLFLPRGGGFKSTG PFSFVGTPTPPPPPGEGGLTPKPPPPG *ILFFLEKGFPLLARVV*NRQKKKNPP PSPPKGG
4080	17981	A	4104	413	64	GFKPPPPKPPPPPPQKGGFMGRPPPR PFALFSPPPPRGGGIF*GGGGAKK FHIWGFPG*KKPPGGGNSGGKPPPG GGGNPPQKKKKKQPTTANIFLCLSI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
4081	17982	A	4105	2	196	LSGM RGRVGKVLISLFTDLMLLCLICFHK TQ*LCNG*CHSRMKVCVCVCAVCVCV CVCERERD
4082	17983	A	4106	1	335	FLVET*FHPVGLAGLELLTLGDPFR*ST LGDPKCWDYRCEPLDPASVSFFLCKLKF IFVLLKLIFFFKPPLYSKLTRGRNNYN YFPFNPGLPHWRADKSIIGGNRL
4083	17984	A	4107	1	148	GERGCSLRSCCHTATWAAE*DSIYKKK KKKEPKKFLAGFSGGGKKTP
4084	17985	A	4108	331	41	GLNFLAQKFSGRFSPPPGRVPLGPKPF FFLGKPPILGFPGP*KVFPSPILPPE VLTFSPGGEKIGPPFSGGACSGFPFKG AKKKKKRPSN
4085	17986	A	4109	137	3	TKKERNINRGPGAVATCNFTSLGG*SG RITRSGDRDHPGQHGE
4086	17987	A	4110	3	269	GFRHVSQGLYLLTS*SACLRLPKCWDY RHEP*PHGFLGFFCFFFRDSVQGGQ SENPSHKKKDEGFWKAGAKI FLFKPN SSAL
4087	17988	A	4111	196	330	GALARGSNDCIT*GSVGHVIL*NDPTLN CILDDOTLYGSIMWYERASDAWALL PDEQLPBGDTVIA**A*DNMSGQQRH VSLAEAVYSGADVLLDDP
4088	17989	A	4112	426	241	LLKRVRIEILPTIRGKGSESPSPCTP AWATERISVSHKEKKRKLVRP*VDLSN SSLSVL
4089	17990	A	4113	394	1	GPGVFPFGCLYHARQYFPHHKKKKYF PHPGQKNSVFLKGRPLFGFGLLIFFF LVEMGSCCIAQAGLELPTSNPNLTASQ RAEIKDVSHRSQ*FFVFLFETGCSVTO A*VQCNHSSPRTPLGKQF
4090	17991	A	4114	328	2	KKRAHPITWDTGIEVPSFSPNIRFLGA PESFFFKRNLPQGDLEKPNPCYFFFG VITPPFPLFPDPKPI*FFFF*DGVS LCR PGWSAVARSQTLATHLPGSSDSF
4091	17992	A	4115	220	3	FKKGEGDPFPVWFGJGVVWVWGFFFF ERHSFTLVTOVGVCNFSLQPPRGL KFSHSLSPSS*NYRH
4092	17993	A	4116	342	2	PINFLYLSFNPQV*RSNPSKILHFCF KILSFFYTALFLPSSQLIRQSFFRVYL INTICFLQDLYLYLILNLYLILFLFHL ASRLDLCFLFVVFETVLLCHPGNSTVAQ S
4093	17994	A	4117	124	352	TSGET*TRMKSKIPT*RSPIIDLEAKM KEKFLKAARETQLITYRGTSIQMPVDFS WAKTEAKA*WLMFVLKEKNCESTRSH PATMSFRNEGKTKMFSDEKRLDSVTLPL LKD
4094	17995	A	4118	11	387	KTGKLLATSAPGKIMVMVETPCLVVSF FLSVSKKKKNPLQIKNPLPKPCWVFK RAPTPNH*KAPGPKPTP*KQPKQIP CRPPKGPFCI*PNGINPSPLFPEKKN KGAFFPKNSKQK
4095	17996	A	4119	2	407	NTFODSGSSSNREPLRCRDARDLEL AIGGVLRAEQIKDNLREVKAQIHCSIS RHLECLRSREVMVLYEQVDLIYQLEETL QQQAQQLYSLGQFN*LTHQLECTQNKD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
4096	17997	A	4120	157	2	LANQVSVCLERGLSLTLKPEDST LTGSHSVT*AGVQWCKHGSLLPRFLGSK RSSSLNFLYSWDHRCGPPHSANF
4097	17998	A	4121	3	168	TALKSGRQVDIRELGHVVCPCWS*TPLE NQSTCLGLPRCWDYRREPPWLANLNMF
4098	17999	A	4122	2	376	ETGFHCVSQDGLCLLTS*STRGLPKCN DYMKREPPRPADGFNIRDFNPLLRST CCCHVKKDI PASPFTMIVSFLRPPQPCR TDPIQNTLPLVIMSPVALLGCDSESAFP VLANLFPSSDCTK
4099	18000	A	4123	11	221	GTOLLRLRGEIDLNLGRGGCTEPRLHH CAFFWETEDPV*EKKQAKAKNSLLTA ALLKTQVKKDSVAN
4100	18001	A	4124	2	125	AIYIKTKSNRW*GCR*RGMLVHCFWKC KLVPQ*KAAMRL
4101	18002	A	4125	425	152	TFVILALWEAKAGRSLEPRS*RSAAW QNPISITKKYK*GGRITSWGG*CGNGL *WCRSTPASATETPSQRKKK*ENLFT LILKVIK
4102	18003	A	4126	3	99	CQAGLELLTL*SDSLRLPKCWDYRCEPP RPA
4103	18004	A	4127	396	58	ENCNPLSWSGGIISGLLLVSGYNKFP FLVCLLPVIGPPENTAGPSLVPGTKWHD HSTL*TSQTPGPSLVPGTKWHDHSL* T SQTPGPKLSRLSLPSSWDYRHKTPYPA H
4104	18005	A	4128	51	549	LGQSYLLLLKCFSPFNQVQGLDISYIN IEGITATTSPESRGCTLWQSSKHTLPT ETSPSVYPLSENVEGTAPP*AHQSFMSP PSWGGSPNLNFFGGGGFEKQSPKLKKK FTLYPLGPPSEGEHGF*PSPLCFFPGFQ SPPKGTGIPSGDELGF*TPPGPKKK
4105	18006	A	4129	97	362	RR*SACLSPLKRWYRHEPPRPACSC
4106	18007	A	4130	376	279	DQDDLDTLTS*STHLGISKWDYRHEPP HRAS
4107	18008	A	4131	133	344	IIFFFF*NFVLQAGGQGNLGLSKPPPP GLKQFLGITFGRSWDHQPSTFRANFCI FRKKVLLCCPGWS
4108	18009	A	4132	164	3	MNSESSESLDHLKKQ*QCCCLGSSSE PSPRLKQPSHLSLPSMWNKTSK
4109	18010	A	4133	355	2	GKKQNRKTGNFTKTHSAPPPPKERSSS RATBOSMNENDFDMREGEFRSNYP REDIQTKGEVANEFEKNLEECITRIEPT EKCLKELMELKTKAREECRLRS* C DQLEE
4110	18011	A	4134	193	357	HHCNPSLCQNDLFHVLVLSPTGVQWYN HGSLOP*PPGLE*SSCLLPQS*EYRH
4111	18012	A	4135	357	104	LRRL*YENHLNPEGGGCEPNLLRCTPA WATEQDSISKIIII*CNFLH*QNMOKI KONPKTNSSKILTEIKISLKNLRELE
4112	18013	A	4136	179	381	DTSLHIQNRLSISKKGL*TLFYI*DR VPLCCPGSAVVQS*PTAALTSLKSSC LSLLSNWDCRC
4113	18014	A	4137	89	318	CLEISCTKIGQDLTYTENYKTLGKVKC PNK*NTTFMDQAEVSLKISFLRLIYR LRIIPVRI PAGIFVEILKFG
4114	18015	A	4138	315	60	KKLPAETHAPLAEATD*AEKLPAGETH AEVQAPTEQTFAAAT*IAEASVKVQF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion.
4115	18016	A	4139	377	51	PPAEASLAKFFAEITQPPADQGRGSEDI GFTSPFFPD*RIPLGFLSCIGWTLQSPHF RNIGSVSPFPFPGFFFPQEMRVLCCPG WSQTLGLKPSCLSLSNWVYRCAPLVP GMPIF*LSCLFLAIGLFLEVIYIGY
4116	18017	A	4140	413	175	NFGIFCRDGVLLCCPGWS*TPRLKPFSSC LPKCWDYRREPRTVPGLPFLFLNLRKDG NSVLEIYLEYKITQIIIVORLLVL
4117	18018	A	4141	1	394	ETPVTKRWSGLGVVAHASNPSTLGG*GG QITRSV*EQPDQHGSPERRGLKERRGL MVMKATFLGRHLEHIVGHRELRLHN NSKKKISSHPLSTPHVPGTVLKPCLRLIL CFKHQKQPVRRKPPNSPSYR
4118	18019	A	4142	22	376	LVNKGKTIFFFLKRGVLPFKPKGKRGIN TVNGSLNFRGQGNPLA*PPKKPGTKGGG HNPGET*PFKGKEA*QCGGSGPLPGP RRPSGLTLQKGGTYGREGSPPLPGPTKEN PRLTK
4119	18020	A	4143	161	1	FIPAKYEHFCFFVSLF*DRVSLCHPG*S AVV*SQLTASTFOGSSDPLTSATP
4120	18021	A	4144	18	159	KHLDPGGGCREPRSCCTPAWVTAKL HLKK*K*VELKSPSVIHT
4121	18022	A	4145	383	109	LFFYKTYNTGHCGLCTLTFEFLQVKQK NCFNPGGCGCR*PKLVFCPTWCKKQGF VFQKRLKPKPKPKPKPNWRGLFLPPFS KRPKPKI
4122	18023	A	4146	374	164	QCQLRLSLRWEDCLSWGS*GCSEP*SCP CIPAWVTARSCQLINKSLPAEIVIPSLY NQIARG
4123	18024	A	4147	25	375	RKKRALFFCQGGSQPPPSNLMDDPPFPG KKISWNLNLFKKKKKF*KKKKF*KVK KNPFLPKPGRPPPGKKKKGKGGKTPQ KGKGLFAPPPKKPKIKSPHFKIPKKOK NFWOR
4124	18025	A	4148	376	202	HYNSKVFPGGPKRSFLFLKALSFFFP APIPFWLHSKIFFFFF*DRVSLCHPGWK LR
4125	18026	A	4149	3	144	LFPCDWTTFGLKQSSHLGLPCQNDYRH *VTVPGLPISFVFFFP
4126	18027	A	4150	3	188	QLQQLSLSLRPEDHMLNGVEGCKLSL HRCTLA*MT*DSIS*KKILKKCF*KK HSFLY
4127	18028	A	4151	83	358	GWAKWLTGIPALWEAKAISLEDLNA* A*QTYAPS*EESLHPIMNTLIRDVPVVT SRVTDTSTIARHNLFCWDLQASIGH LILIGPO
4128	18029	A	4152	162	1	TVVWHHKNLSNWNKI*FLELDITTYK HLVUDKTIISNHVWDALVNTQCRAG
4129	18030	A	4153	369	20	POLLARQRCENGUNPGRGAP*PKSREPC PRAWKT*DSVSKKKRKKSCFVHRIL KLEEAHYSLGNTAQRLEVSCHKKILC LSISIDPYLQFKMNPVPPSKPLYQIDW VGLL
4130	18031	A	4154	117	2	QIFFFFFFFKMESHSIAQAGVQWHRHLS L*PLPPRFKR
4131	18032	A	4155	369	217	FFSPFFPKFPFPFKKTFPP*KKKNPDP PKKKKIFFFFFFFFFFFQTP
4132	18033	A	4156	214	283	ASPSGEQGLSSGP*GLIN*SDKFSVTHS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PKPHCETA*GGTSLSSSSGSPQAPKSP HHGPDSPSLSDSIPMVISPPPEPPLRAKG CPQGGPGGASWGGTT
4133	18034	A	4157	319	712	QDFVSKQHSYLCNKLKSSLIQVAMNRA QVCLISSSSKSGERHLYLIKVSRDKISDS NDQESANCDAKMNFICIMLYKIWLN*K RLNK*HNTAI*LKIYFSNKKKFSNLNLS SVINSFDVKKERLANNTLN
4134	18035	A	4158	183	369	LKKKQSGRGVEVFLKVTPECGKAGILF IYVFFEMESHSGVGQTGVQVCNGL*LOPL PPESSD
4135	18036	A	4159	190	336	DPISIKNFVFGTVVFLFLETGFLHV*AG LELPTSGDLSTLASQAGITG
4136	18037	A	4160	10	390	QGILLPCFSNSSSEERGRISNTFSFFF FWKGSPIPOGGSGQAKKPR*REPSPSGL TPQRPGNGGPPPPGGQNF*FKKKKG*PG GPGR*TPGPRGTPLPGPKAGNKRGGP RGRAKNFLKNQNGPT
4137	18038	A	4161	53	376	YLFAPFFFSKREANQGGQPGMEGAKKKF MAP*PSKGGGGVSGGLTPFNQWNPRAQP PPRGELIILEKKRPAPNAQPGPENLGP REPSFLAPQKGNKSENWPPPP
4138	18039	A	4162	1	356	GVFLVFSNFWAFPLSFFFLKGLQILVLM PQPESQGNLAPQNP*PPG*RGFPALTP PRTGNKGMAPQAPQPPGFLKKGGSFHHG QGGFKTPTLGNLPLAPQGLNNGLGPW PPPPFF
4139	18040	A	4163	345	26	APGFKFALPGPPGGFFFSKKSKNLPGLR GSTLQAVGPTFLGG*GKRSCLKPPGG*AS RGPGWGPSPPPGGPN*IPVSEKKEREGK KKKGREKKKETFSNNLLIFLSF
4140	18041	A	4164	18	284	TQQGTSGIFEGNFFFLGTGLISLYCPGW RAWGGDHGSLQL*PFGSSSPASTPLGRS WDYRHVPFGWASFFFKTLFNGVTQAGL ELWG
4141	18042	A	4165	377	30	FSGKKKFFQGLWGGCGPPLIPPLWGV*E GQPPRUVGGNPPPLPPKKNPVFTFKPKQP GVGGASVSPFLGKFRPRI*PFTLGPEGS G*PNFPPPPPPWAPKQNSPKKKKFPYN CLW
4142	18043	A	4166	305	1	ESROVLTSRLTLLSIEFNYLLNNSTYK HITSLPINIRYQGDQLKTLKKTDLNKK *GNIPCLGIGRINIVKMSLLSKLIYKPK AMPVKIPGELFLRNOQA
4143	18044	A	4167	394	78	EGKKQGRKKGRREGS*EGRRERERKTR*K AEKEGMKEGREGKKEGRKEGRKGRKE GRKEEGQXGGRTDGGWVWVLSLDTSQLI SFASGPKWREASSLVWASLCL
4144	18045	A	4168	1	431	CNTCVR*CAVWCV*MGGERLCVCSN RVCCV*VERVCVLCVMSVCCVCCARQ CVSVCHSRIESSRPSGGVPASKCQTHL YLPKLSAPPAGLWDLPSATASLSGSL CQPSCPRTSFATLVSSMYHRPVTGELQ SIT
4145	18046	A	4169	3	423	YNAREIEAAQRDHATALQPGYRVRFCL KKVKLKGQAWWLA*P*PFFETGSHSV PRLECSGVISACCSNLNPGIV
4146	18047	A	4170	118	402	QICCTPTPKKMKVKITLHLSNNMYLYI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HLTQDI*DLIDL*NTADMLKDLNK*R EIHCLRI*RLNI IKTSI FLKLPYRVHAI PFKISARSFVE
4147	18048	A	4171	404	285	RGCGEPW*HECTPAWTE*DLVSKNMKX QNDNLSHLSLA
4148	18049	A	4172	274	431	ESLVGQRNWKARYFYRITAPGQAQLMP AIPAPWEAEVGGSGGLEIETLL*NNSSR PGAEAHACPNSTLGGRGGRITRSRD*DP PGQH
4149	18050	A	4173	24	366	FLCLFHTCVLAFVQQQLCSVWGCKVEN ADREEKQPCDSQAREBPLCRGFPNRP NINTRIEKLFFVCLF*TGSHSVTQAGVQ GCHSSPQQLPGPKRSSHLSLRSSWD TGM
4150	18051	A	4174	397	1	TEPVLANETNGPWDRGFLGLGGLGPENT DNSHAGVADGOLLKEPPEPLSTRSIMEPM SLNANWDSPHREWAGTPTLSLGDYET QVM*SWGIRGILPQQPWKMGSLSLTAS LSLSFAHTLKHKHTHTHTLY
4151	18052	A	4175	90	387	KGRWLFFPQCGGERHNG*TAAPPQTGGKE NPFPFPKPKDRKKANAPPPGGIWKLNK GFPPIGQGGPEPPPPRGGPPAPPKGGG KRGGPPIRPGKKLLK
4152	18053	A	4176	398	280	RLKWEDEPLNPRV*GSKP*SHRCTPAW VTE*DPVSNFF
4153	18054	A	4177	253	395	LFNFFFLVKMGSRVYQAQGLKPLA*GNP PASASPRAGITGGSHHTQ
4154	18055	A	4178	366	48	PWASPGISLSFSFIRTKPTVKVR*YRVG PQRQPCPSRWAPACPFSPMPPAWVSP GSAASRPPIRHAGSQVATASPPAAGLG APAWTAGLGEKQLAARMGT
4155	18056	A	4179	44	413	GDGVNSAFFFFFLEKKVWFIPPPGGGPK PEFGFRAPPPPGVKIKFGFTPLRTGE*R PLPFPFGKGWFFKKNGGSPMPPGGV*P DPKGAPPDPPGPKGGE*RGEPWPVGMNFA LLKERKPLFKE
4156	18057	A	4180	396	235	HEVSLCCPDWS*TPGLKYSSCLGLPNCW DHRCKNHGPGKQTQLESGHQRVAGLSR
4157	18058	A	4181	85	408	YTCSLRITQDHHFFFFFLGKKTFFFPF GWGAGGQI LITSPKTPPGVKIPLWLNPR GGGPGGPPPTLPLGF*KKRGFPGGGQ KPRFKGDPPLPPKGGGLKGGPTP
4158	18059	A	4182	1	149	NHLNL*GRGCSSEPLRHCTPAWTE*DS VLKKSYIHLGQNTYRKVL
4159	18060	A	4183	310	3	ATAPESQITRT*RNHNYIEVQSEAAASA NLETAVNNPENLGIIMDEG*MKKQIKW EMTSRITFIVEKSNMPGKTSKAQALLIGA NIAVNFELKPMLIYHLEN
4160	18061	A	4184	1	359	PTRLVLDRDRPFFFFFLGSGKKKNPGV FLYPGGGWTPPKKKNSLWGGGGLKKG GGGVFFKPLDPLGGGPFLLKNSGGVDKKK RAPPFTTKTPL*KKPPPPFPKIFKARG FW*KMGEPPFFCPCPPSFLKKGPPPKKE GV*KKPPPPFPLTPPPNQGNTFFFWGG STPPQNIKKPLGFFSSQTPKKKKRAADR DLELADAW
4161	18062	A	4185	1	362	HFTKYLFTSC*K*LLCWMODCKRKGIP MNTNVIQEKATSLYGSGLGHKEGEGKAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EFNASKGWLDFRKSFGKFNVAITGEAA SANQKAADKFPDAIKKIIIEKGYLEQI FNAGESAL
4162	18063	A	4186	366	47	AALFLVDPDPGRGGVKGPPPPPPGFFVFF QRGRVPLPSFGGFFFRPPNSPPGFPKG GGSGGGPRGPA*THGVFLKKNPFCNGAG KKGGFFLKKKKKPVTVESVK
4163	18064	A	4187	394	112	KNTENLKIISNAWHVSVASAPNEAETGG STEGTQCSKL*SCHCTAWTVRETLSPR KFFKKRANLYLTFRI*KVCSLYHRRTKNS PKKHTQGRKF
4164	18065	A	4188	230	372	KPMFLFPNPAILLGIYLYEYKSF*HKD TCMRMEITALFTITKTWNQ
4165	18066	A	4189	149	2	NRSLSRFMRFKEGSHLPPI*VGKKAASAD VEAASVPEGLGKTTINKGGT
4166	18067	A	4190	2	159	MHQPLLRRPQKQENCLNPGGGGSCSPRS HHCIPAI*AIERDSLSSKKKGGAF
4167	18068	A	4191	180	415	LGFLLQLLVGSRMFI*FALELSHGWLGS SLSF*PVCVKQSSHLSLSSSDWDHGMSP YPANFCIFCRDKTLPCCLGWAQ
4168	18069	A	4192	424	41	PFLLRAPPKGLL*PKNSFPFGAPP*IPF PPKKIKIFKTPGGGGAPLFLPRQVKA EGSLPRRVFGPPPPFFPLPSPLGAKPN PPFFFKKKKKKEWLHKSLSLFSYSAHFVLC LKYSLSFFYQSVKTK
4169	18070	A	4193	105	424	ELKRLVLKIRIGIPEKGKAQCKEIQKLA QEVKGEIFMEIGSLKKKQ*KIQETLDTL LKMQNALESLSNRIEQUEVNRNSELKDV FKLTQSNKDFPSQIKKILYNV
4170	18071	A	4194	3	240	LCLQSQLGLRLQENPLNLR*GCNEP* LHCTPAQVTERDPVSKENKGSFIPMKI GKLVSLTLNRMCMCNCKNSEKENV
4171	18072	A	4195	385	1	KMILTKKMEIKHDEKELQKTEVDLKI ENNTTRARLTNNI KKKFPPESEKTNKNH TKKSL*DOTKKKTRPKKKNPFSR*V RHRWRINLLESNRGKKNPSGVQKRRDS VPTLITQETWICE
4172	18073	A	4196	3	272	LFVLIWALKHKSVDVGNSTYAKEKLES ASFKERI*KSYYEVAKIYGVKNFYCIYEI VKKEK*IMHSIYRVQYYLQFQTSLEVLE RIPHG
4173	18074	A	4197	236	379	GGRFKGSNFTSPGLQNSFFMGPPKINS RAGV*QRREGKNPQVQFNRR
4174	18075	A	4198	375	1	NFKIPAPPPONKGPLRVGTFFPFLTSPF GSPPKSPKAKWARRDRPF*NPGETLQE G*VFSGRFFFFFFFRDRVLLCHPGWSA VAQSRLTTSDDSRVITILLVGRGCSEPR SHHCNPANVTRVK
4175	18076	A	4199	1	270	PSRTGPGIIPRRPRTSRNCNQLGF*GCG EPRSRLCTPAWATEQDSISKKEHGLLV FLKGFTHYIRLLINLFAARGKRVLFFAL GGREMW
4176	18077	A	4200	388	1	PPGIINLFDPL*PPPPVVMGPPPS*KL ISPQKKKNKVPVPPVPPINIFSGPPPTL VFVWLFFVSLKQJLIL*KSQVSAASLV RHDGAPRLTSSAGRGHAEPFTQPRPTH RNACSFVLIHQSYKVF
4177	18078	A	4201	298	158	FKIVINQFPLTPIFAPSGGGRG*GRGE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LRSCHTPAWVTE*EPT*KKIKGKKRT EQESRRQNLA
4178	18079	A	4202	128	358	KLMIPFSPGQPPFPGGRWGGHPFARFAA PSGR*GAPLPGRPY*EKRIPSARTPPRL GGWPSMLRTGHDNDGGVWE
4179	18080	A	4203	406	1	FFFFFLRQSFLLVAQAGVQ*RNLSGQCP LLGPF
4180	18081	A	4204	322	2	KPRPRKTPGGPPPI*GGGAPPPRGGAP KGGSPPPPPPPPGGKGGKKNNPPGG *KPWGGFFFFPPPF*TPPKRGLFLKKK KTQNPKKKKGGRSRVTSRV
4181	18082	A	4205	3	127	GHRVSRQNLGLYLL*STRHLHFKC*DY RSEPLCLACFLFL
4182	18083	A	4206	1	216	GFRVRGRLGLDLT*SACGLGPKWCDC GR*PPRPAHLGGNSNAEPLGACPLLS GHMHRVVRWATATL
4183	18084	A	4207	427	0	LEFTTNFFFWARVFLPPPF*NPDPGFF FLPHKKKNPPPPPGFFFFFYAPPPF FFFFFFFFFFFFFFFFFFFFFFFF FVILKTVSC
4184	18085	A	4208	2	404	PRVLGIGWCKERFLCYFFFLERQFCF LAQGGPCGNFG*RAPDPGEKKIPGPP PRGGGEGPREPRGRKIFGLKKGGGFF GGGVGPGPKGPPPPKPKWGYGSKPP AQKRGGFFPGKKRAPFTMWNG
4185	18086	A	4209	40	412	PLFCLSEKPRYFYAIYIMLSLKFLESC IMSNSSAVSASVY*W*KIREFLTSW TLEKLDPEVHQFAFT*RAKAILRKN KFEGTLTSGFKTHYKTTITTVY*HKD TQIDOWNRISS
4186	18087	A	4210	219	392	HFFFIANYNFGKGVSTFCQAEQGRNLG *LHPPPPGLKQFFCLTLRLRNHRLVPP PP
4187	18088	A	4211	409	2	LERKTVFSPPPFIFFAVFFLSPPFFY PPPLYIFCPKPKKKIFPPPGKIFFFFK GPPDIFFFFFFFFFFFFFFS*FPIMYQ IVFNISYNLIKVDSHLYLFDKKILLCT ISSDAW
4188	18089	A	4212	24	399	ADAFSTTNLHGLGPDLPPTTQIYINLG MAILL*AGAVNIGYRSKKNALAHFLPQ GTPTPLIPILVIETINLLILATALVWH LTATITAGHLLMHLGASLAGSTISLP SLTVFTILILLT
4189	18090	A	4213	411	197	SWLTAPSFKFSCSLSS*DYRLPVPH PDNFCIGSRDGRMVSI*HDDPPASAS QSVGFTAPKVLGLQT
4190	18091	A	4214	218	126	KECEPLLFRSSNSVGAIDLKNNMRRVLI KSCTFGVVAHTCNPSTLGGRGQGITRSG DRDHFG*HKSALGSCASCIFYLWDLHLH IVFE
4191	18092	A	4215	1	332	MAPSLCLSNKKRGFTGPGFAGAPKPRR QOGHPREKLAFFKKGPKGLKSFLVLK TDPKPFPLSPKGGALKTEEP*TKKK GGAEEKPPGGEKRLPLGPFCKPKPNWG
4192	18093	A	4216	1	185	KLYLSILSLQISLITITFTATLIIFYI FFETTLIPTLAIIT*GNQANFYLILLV SFHEN
4193	18094	A	4217	1	388	LRFCWETLFLPLPNPFFSFLFFSFS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/51,5,1 26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFLGGKFCFCQPGGGPNLNRDPP PRG*KEF*APFPFRGGENQSGPPPPNG GGF*KKGGLNHGGGGGFKPPPKKPPPL ASQGRNRKGGAPPLK?
4194	18095	A	4218	3	195	VIYSTIFAGTLITALSSH*FFT*VGLIEI NMLAFIPVLTKKINPRSTEAALIKYFLTQ ATASHPA
4195	18096	A	4219	261	1	EFFRRERKERKEKKGATPSRTCKMRER EERFS*ERERGERGEORGEKEERERGER ERERSEERERERERERPKN*MLNGRTRR TRG
4196	18097	A	4220	5	375	DEMLHLKFTYILN*TLKDTIIPKVNENL YN*DFLNSKVQGTPTPPRPSRPPSPSP DPPPGPPAGAGRRARRPGRGSPGPGP PAPPAPPFRAGRAAGRRPAPRPGGR GPAARPAGGG
4197	18098	A	4221	258	267	GGGALKKKIYCGGGGNFF*SPSPFF FFFFFFFFFFFFFFFFFFFFFFFFFL IYFIFILIF
4198	18099	A	4222	127	330	KKKKKKKKKKKKKKGGGPFKKKKFLPR GGGNFF*GGQKKLGGGKKGKKGGK PGAKKKKRGKEK
4199	18100	A	4223	1	377	RRFHLRRENQLQEKQTMWGIFFFGVAGP PGGGKSFSPSPFF*GKNTFTTTPPGG GGQNLVGNSNSNPPPRDPSPSPGSEK I*KTTPPPLVGPNTKKNKGFGGGSPK KKTLLPPPLDFF
4200	18101	A	4224	223	431	IRKTGPLGFGGQNNPLPKV*PPGLTFF QKGPPPPPPPPQKPRFLKYPKREGPP PPKVLGTTPPGLL
4201	18102	A	4225	173	2	RCKLHCLPFTLAIITR*GNQPERLNAGT YFLFYTLVGLSPLLLIAIYTHNTLGPTR P
4202	18103	A	4226	11	377	FLTVVFICISLFGRLMGI*FFVNFPCFL FHFHFFSLFKDII*FSDILLEIIYAH VCHICCNLIFSLYVFPVFGSLKYKC* NLPAIILDPADVSLIFMFRTGKQRDN QFSLKILIGF
4203	18104	A	4227	1	412	KNSKVQNTATDLKNAESPHSRIDEAE RISELEDRLFENTKSEETK*KRKK*SM PTOLENSLKRLANLVIGLKEKVGEL*V GSFFKDI*QNVNPLEKNQICQAEAYIT LSRFNPKTTSRHLAIKLSKVKDER
4204	18105	A	4228	373	163	IGVFLGGAPFFFFFFFFFFPGGPKRGG KGGASGKTG*GGGGLKGGGQGWPPFF FLRTWPTTTRAPGL
4205	18106	A	4229	392	3	PPC*NRAQFNFGGPFKKIYSSPPFRGK FGSLKGPFPFFFSAPGGPKFSKGGGL FFGAPDF*GGFGGKNYFWGQGF*PHSP PPPSWGPKRRAFPKSKKKKRRRRWGE GEGQGSNHLKHGYFQI
4206	18107	A	4230	211	400	YALITWLYCILNNYALSVFFWCCFCFLY FKFIYVFLNLLFLFAP*LVLCCLKVQNH SGSLISVSYFPLLEACRIFPLPFL*NL *MIFCNMNVLYFKQLCSALSVFLVLF FNF*IYLCIFKFIYVFCFLRRNPTLAQA GVQWHDLAG
4207	18108	A	4231	69	386	KRIFFLGRGGGKRMVNGNPPPKGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GNFSA*PPORGPGKPGPKNVIQGFKK KRGFYGGQPPNLGKELAGPPKGGKRG KTHPGGKFYAFGLGGFLSKKRN
4208	18109	A	4232	394	287	PFEKKKPPPPFLFSPFF*KRGGDDLFP SPRGEKK
4209	18110	A	4233	442	112	LLGLRLWEDGLSPQGRSCSEP*SCHCTP AMATQ*DPVSNNTNKNPNPNQACSSLN SLPWTAAVWRTLGEHCNGREALPARAKN ATKAPVLVTHHICQTVRTISCALLPH
4210	18111	A	4234	415	58	SLQKGHPFFPQELQDPQNGRSGWSVP TTGLFFSLDFIRF*FMAGVLVGHKHCW EWTAALVLLFLDRDRVSLCFPLHTLGL LKRSSCLSLSSWSYRHTPHPAST*FF G
4211	18112	A	4235	406	168	HGETPSFLKIQKLAGRGGLL*SOLGR WRQGNHNLNWGRSSVYIYTEKHTVHTQ SVTTTFMSSMQTLAYSPLSLKSS
4212	18113	A	4236	247	397	TVCFSVIYITELLPPQVK*FPCLTLPS WYRVSPPPLPAYFCISFRDGV
4213	18114	A	4237	36	405	RLYCFIKGLNVKNKTRIFVFFPLETNE PFGPGGGEGGANSFGPEPLALGVKGGPR PPPPGGGE*GAGPPGPNGLLLKKGVP RGGGGGPKPTQRFPGRPPQKKKNFPG DALGKKKVVFF
4214	18115	A	4238	407	3	KKKKKLTFRPGGGGPPSPLPKRVQRKGG NPGGGFSGKKKSPPPPPRGGKKKPF KKRFLSGNNTGKRLXGDPQS*PAGNA RKKPGWGERALARGPMTDRKQPHSG DGSQSGTGQEPGNSGPPVKVH
4215	18116	A	4239	144	405	PTVRLVLLVLLKVAVSKNLR*GG LV*QORQLWKRLISNTEFLYLRQSKMMH LVL*PTVNTLSLSKGQARWLTVPVIAL WEA
4216	18117	A	4240	369	40	PLLQGTASWFRWGRAGDRPRKEG*LHP RETRVPPALHHQAPAGVSLTSPGPPFW LSLQRLRHSSSDSLPAVCQYSGSWREE KAAAEAPALTPAICTCTICISVLTJVL
4217	18118	A	4241	397	1	ISKSLFFPPIFWKKKKKGFSPPLNPLGG VFFFFFLKIEIFLAKRFFFIELGAPG FKLIFKKYFFPRGGFKTPKKKIFLNPFF KKKGGGGGALFFFFFEOSTSSVTQAGV KNHDHGSLOP*PRLK*SSDP
4218	18119	A	4242	230	393	ADRFSGPLPSAFETGSGHSIAQTGVO*HN VGS*PLTPGLKLSCLLPLNCWDYR
4219	18120	A	4243	434	104	KQFTFQSTTGGSPSAGRPFFPRAKKKK PFF*KKKKSGNIGGLPFPFPFGGEKK NLFPKRGEGSHKTDSSPH*RGGKKNL SPKKKKKKKAWCWDYRRKPLCPATYF
4220	18121	A	4244	2	425	FVFKIILKNLSEIQENLQFSKIKKTHD LNKKFNKETGNITKNQTEILELNSMSE IKNTVTSFNNRLNQAEERISELEDRSFE MTQADKKRKGESLQDVLVTMK*TNIL NSFQKEKKEKGLQNLINIEVAENFSSL
4221	18122	A	4245	12	424	IYYKTLNCT*IF*FGGALACFHSGVFFY IHYVGFVPSVYLVSHVIVSVWTSGYLL YSLGCPNLSLFIPLKLFHFHGVLTIOV GYVWILFVCLFLSNSFINI*PTYHAIP IPIYILPKVYNSMFSIFTK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4222	18123	A	4246	215	425	LSIQISQIRNLIVLFINIMGKILRAKRK *GTS DAVNQTPLRPRTVAHSCNPSTL GGRGRTTKSGDRE
4223	18124	A	4247	413	2	WEVESFSLGKAFHWGCATENPGPPHPKFL LLFIMKAFPPHVRVGFQDCFNPKDGRFT* PRTTPCPRARGAKKNSVSKKKIKITWR NPPPTLPPPGNGGTRKRPSSPPPPPPPT TPKLTTPGGEROL*PORAEGAGDTK
4224	18125	A	4248	61	281	ITWKDFDSFSLVRSKAFHLALFAFTGN CIKCHIKMGIYPEEKFNHKKVLYLEID VCGH*TWKKIFLFFFLRQRFTLFAQAG GQWLDSLLOPPPPGKRFSGLSFLSK* DFDSFSLVRSKAFHLALPAFIGNCIK HIKMGIIYPEEKFNHKKVLYLEIDVCGH IRLGKFFFCFF
4225	18126	A	4249	23	13	RVRFPASPGGREVTVCGLGREGOERRL RWRHKPFLPLAATS CAVVPRSVTSVTS GSADGGQSLAVGASTLATVGGLELLNS NDPPASASQAGAGIAGVSHRAWP*T
4226	18127	A	4250	182	342	KGFFFLPGGGGGGFE*FNEPPPPRVKG IFPPPPPGKGEKPPPPPPPGYIFVF
4227	18128	A	4251	2	219	PSLRKMQKLARHGGLTLLSQLFGRLLRE DCLSSGGSGSTHGSSEL*SYHCIPAWAT DGDPSVSKNTKFFFFF
4228	18129	A	4252	223	324	LGAVAHCNPSTLGGRRRITR*GVRDQ PGQHGE
4229	18130	A	4253	165	336	ESDAQGHQVAARVSHVLEKDALLVFSL CKIAMKPLGEGPPDPK*ADSSSWPPSVQ
4230	18131	A	4254	3	233	ETAFCHVGQAGLELLTSSDPPASGLQHA GITGPATKSAP*WS*VSGPHLGAFLSLA MLLAQDWRALESARFFPLL
4231	18132	A	4255	394	44	AKIFPPGVKFFASTFPGGGKKRGPPPP PVNFFPFKGGGFPFWPCGV*NPAPINP RWPFPKRWGKGEADPPPKLNLNLFPPQG GGGKFPFGKKGAFTGPPFFPFEMEFL CRFD
4232	18133	A	4256	152	2	YWSFFYCRSCCTROGTVAHNCNPSTLVG QGARFTRSGVRN*HGQGESPR
4233	18134	A	4257	404	190	AQLIRGWRQ*DHLSLGGGGCNEPSSCHG TPAWITEPNQSLSQKTKQKMLIPN*Y *TVSPKSHPELQFS
4234	18135	A	4258	288	407	ENCRPRAVAHACNPS*ENCRPRAVAHAC NPSAFGGGCEQIPRSGEQEQVOHG
4235	18136	A	4259	406	163	GWGVQTHPGHHGETLFFLKKK*VGGGG PTRYSPIFGVGPQNGLNPOGGGSKNPK LNFLPLPWQKGVPFSSKKKKKRD
4236	18137	A	4260	101	276	LTSIVPSLWEARGAKRLGLRPAACRESS LCHCTLPWVTG*NLVSKKKKRGALGF FF
4237	18138	A	4261	2	414	WVAATPNLVFVGRGNCQDWFQPFPLTRG GWGGVLFPVVKRVIKGLVAPFSGPIPIR KNHQKVGGFLEPNKTNFKE*NFVENKNT RRGIKNVPEKKKPKQKGPLPQPIFNEN QTGWDFFDFFAKKKKIINSPLGWA
4238	18139	A	4262	337	382	RDAREFLHCLSV*LIT*LOKEFFVPGQAG VQWHYFGFLQPLPSGFNQFFCLLSLSRW HYRGPPPSLGKFLVGNLVGWLVFETKFW FCWPGWRAITGFVWPATTVRVQAIPL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
4239	18140	A	4263	406	184	OLLGLRLQENCHLGGEGCS*LRSPPCIS AWATKLDVPSEKPKTKNKKPTGLGGLNQ GPASLLKKIRKLGKKRPG
4240	18141	A	4264	233	440	LPVHHGWSLRKLTLGKGGEANPSFTW GQQGKAKQKGQKPGAGAHACNSSPLGG QGR*ITRSVQDQ
4241	18142	A	4265	2	230	GARL*SHLLVRLRKENHNLKGNKREL KNPCHTFAWGTKKDASAANKNQPLPPPK GVKSPQREHGLVTCMFVQ
4242	18143	A	4266	1	349	HKTNIHFKLVMSNVETFFFGKGFSC APGGRAGPLFGLVETPPGREKAFPGPNP PRRGE*RAMAPCPGKILVF*KKTGFPGR LFWFGGPPPPGLQRRGGNGGNPWGPE FWWF
4243	18144	A	4267	2	375	RSQDPAQSSAGNEGLSTRASGCGCTG SPNSASPPALCSIRRALAAPFGNARD LQPAPEPPTHVSQSCAAKPPR*ADPA PRRPVPSSTQGLRSAGAQRGTGRHLHQ PQCRHVVKPG
4244	18145	A	4268	377	3	TPAWMTERDCTWRRRTSAPGGSWPSGPV PSPGAQ*RPSPQGLGLWMAAAAPRC* TAPGPRFPFHGPGSPQASFPTRPPRCR HPRAGSAGPTGATPPGSTQQRRRHSQ LPGHPGHRVALG
4245	18146	A	4269	1	294	LEDWGGRGARAHYDGFSLFESDHYRLR LGQYHGDAAGDSLSWHNDKPFSTVDRDRD SYSGNHALYQRRGCWTHACAQ*ILDVY ATGPKYQVHCEALH
4246	18147	A	4270	2	218	TGRITILSQGLQTLLELIAF**LLASLA NLALPPTINLLGELSVLVTTFPS*SNITL LQKKKKKKKKKKIFF
4247	18148	A	4271	32	443	LHSDVDQLAGLVFPGCPWPLASPARRAP AGPWPRRAAAPPS*DAAPRALVASAGSP AWPPST*GLPAPAIVVASPASASPTSA RSRS*ASPTARRCRPGGTAAPTASRSQ COWRP*PCORSPPSGTCSSAAAAAPT
4248	18149	A	4272	434	57	HLSPFPASAAPKPLQAASLWSSPFLV LAQVPMMNTDPCQPSPA*PASELSPMP PARPAAPFENWSHP*GGAGTVALPLVFG ATFAHRAASPSPTLPLVLTAGGHCFLY TYQIFLKPHYTKR
4249	18150	A	4273	288	424	GLSLVAQAVQVQNCOLVSL*PFFPRVKQ PSCLSPPRIWDX*HPPP /
4250	18151	A	4274	1	429	NTRGAAGPQMPHPPRASAFPENPCGRK N*GGVSGP*ASGSSPVKAGPAGTWKRG GLGWGTRVRRGRPPRRPGASSGVARQQ GPGHPGFPSPRRRLSVACALCPGQTS GTRAGLAVNPGIQLCLKAQARSCPRDH SSD
4251	18152	A	4275	253	3	PHQFNAVITYFSPVSRGCPNNALYSPFV IVVLFCFVKTVGVSVTQAGV*WHDHSSLQ P*TAGLKRFSSTLTLSSWDYKSTPPCI
4252	18153	A	4276	406	3	PMWSQGGVCAK*CARAFIREGIFRRSAD TQVVREVOQKYNMGLPVDVDQYNELHLP AVILKTLFLRELREPLTLFDLYPHVVGFL NIDESQRVPATLQVLQTLPEESYQVLR QTAFLVQISAHSQDNKMTNTCI
4253	18154	A	4277	373	3	DGVSLCPPGWSAVAQSNLTAFL*ALGFI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FLFVGGTLGTIVLANSLLDVLHDTYYV VAPFYVLISGAVFAILGGPIH*FPLFS QVTLGQTVAKIHFFPIIFGVNLSFFQH NLGLSGMRCCI
4254	18155	A	4278	71	176	AGGRGCNERSHHCTPAWATE*DSVKEK KGLGFFW
4255	18156	A	4279	2	379	SPFVLOSSLGKNSETPSHGKRRKR KRTDENQ*KHPLRARPGGAPRAQGA QSGGGRRAGCRKLVRHGTGNPKREP GLIPQEGRSGLIHPSNGCHKPCPSRGR PPFRFKQGRGRMQN
4256	18157	A	4280	2	338	CDMPRRKLDPLSGRNTLGFVVCVAAQTS GLK*SSCLCLPKCWDYRHEPLRPVWVYF KLWHPSPWPKPGFYFSVFFFYLPLCTTA SLFCSCLPPCCSRVTLVGESSCLWVAG
4257	18158	A	4281	407	1	EEGVTATGHTAERGADNEEERGEVANK RGRREVQPEARRMTTATGTTAATRGAR T*TAATATAPVTRTAAPATTASSTRTL RTPRRARTASVLWARCRSWATWRASR TCDCRTASHSRPTATRSRTARMA
4258	18159	A	4282	367	225	PCDSACLGLFKCWDYRREPRPAGVLFL *ASFS*QSKVEVVCCKLTHA
4259	18160	A	4283	452	1	NTCGLSQVCRGTORGGRPKRCPCHPFRWR DLGDEQESSKEGRPGREGVQGGLLGAT PGAQSH*GL*AEAAMSSGHALPGQGV LTPLSPSPPNHRRPRAGRASRQSRST EAQRAVPSQGAAPGWETDWGSSHQWQPC QAQQEGRTGR
4260	18161	A	4284	436	22	CHVTGTQPIKVSMAKDSREIRSGGKYQI SYLENSAHLTVLKYVDKGDGGQYTCYAVN EYVKDSCTAQLNIEKRLIFPSFTKRLSE TVEETQGNFSKLEORVPSQITVAVMYK NNIEIOPTYN*EITFKNNCIAAARI
4261	18162	A	4285	301	403	LSIS*PCDLLPALVSQSAGITGMSHARF RVKSLI
4262	18163	A	4286	380	2	AQVLYSSREQRRQDLPEQVIAQAE*V KASACQLTPEDEAMESGPAALDKDFQC TRKHHPAEVQGSPPRCMSRYLVGDGCKT FAEQNVCS*CCENLVLSIHAFITFILRI QWCTSTVNOAQVCI
4263	18164	A	4287	453	3	YLYEGSIMEEPKEPVKGPLGLHCPGKF QG*RNYSNHAVRVGTRCAPEGVKDLTS SLQSVITKPEQNIQELMKHFKKEKSEAE NHIRTAKESLEENMAKIHKGQLEKLEK SQCDRLTEELTONENENKLLKYQCLK DQLEEREDV
4264	18165	A	4288	52	400	LDLYFFYRQCLASFLRQSRSAIHLACN LKLGLSGDPTPASQSKETSMRYHI*P NL*NSMC*NCVFDTHTRIGENIWESI* *EINIQAACRIPKTQOQKTHFQNKQGLH SNLN
4265	18166	A	4289	2	263	IHGHLWSQLPGRLLKWDRRSPGSRGCS EL*SHHCTPVWVTEGDPVSKKRINICKQ NLNEKNTLVDTFRHSFTHIKISLHNFQ MFL
4266	18167	A	4290	3	142	YLGVRHLSIDGLDLTL**SARLGLPKCW DYWRDPPRANFYILFK
4267	18168	A	4291	324	19	ENSKRHEQKPHRREIQMANKHVKTSLA

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						IREMKIETIMKYVHTPIQMA*VRNNDTS VQVQWHTLQVASPLVAEVGWGEARNLRL QIVKMVPMNSHCTPAWVT
4268	18169	A	4292	2	204	IHFCDRDRSLCCPGWPRTAELKQSALLG LPKCWDYR*ATKPGQLQSVFLGLKIFL ILLVRGVDRYL
4269	18170	A	4293	427	3	RRKTIVPTPTGGERGISNEDNGLKAVG NIPGSPICNVSKINIMKHAPGGHARFC IWTESAFRKLDELTYGTRRAASLKSSYN LPMHKMINPDLIRILKSPETQALRAPR KKIHRNVLKKNFVLRPL*RIKLTSRHRK R
4270	18171	A	4294	24	372	FICPLQDYVICSDTSCVVKILATTOR RLRDDSVQSFPPFFCKGQGLLAPRVKEQ CGDLG*WNERPPRLREFPGLALPCWNN GLAPPPLILVLEKRGFFLAGKMGMLNL LHSP
4271	18172	A	4295	1	332	IHSYVFPQS*FFGTINTSDKPLRLIK EKKREGTN*HIMHPMKFGIDPEDIKV KKKYYKQLCTHKFONLEENVHFLKKKTI HLI*NR*FE*LYKYRN
4272	18173	A	4296	407	30	WSVIYGEN*ESLGWGAHPSHVANIIVTG LRYLFSYGRHALDMLESSQDNMRSWWS QMSSEIDVDNLGHISLCAVQ*IRNLNP GLKTSKIELKFELHKSCKDAGSEVTKK EFIEVYHELAVG
4273	18174	A	4297	350	1	YKTVVMNKEK*YVGYNIEQOKLALKT TVLDEWYTLPDGRIIKVGERFEAPAL FQPLRINVEGVGVDELLYSTIQAAVGT RSEFYKHIVLGGSTMYPGLSRMEREL KQHV
4274	18175	A	4298	623	1	SRRGCAATCDGSITAWFORQAAGKPSV HSKLEAEAKPTPGDHAASESTGFSCLP GGVHRTAHAAHARNMPGDSNTGSGQSPAG RWRKAGSAPRHHPTOPDWTHPDALROA WARNFASSE*SF*RCCTAASPVPPTPPS PYLMRGVPVGGCGQKIRPLQEEAPP SSPVLVSR*PQAGTPSSPAVSSLYHGL SPTGRODRWR
4275	18176	A	4299	469	3	PVRNCLGARFVSGRAAHAL*QSASTL QGDPRTKRQAISA*SSAFDVQDVSHVLT PFYKPKRAQSKDLIKAILDNDFMKNLNL SQIQEIVDCMYPVEYGKDSRIVKEVDVG SCVYVMDGKGVGVTKGVKLCFVGDGKV YEELAILYICRRPCI
4276	18177	A	4300	506	321	KPLSLLLKIQKLAGHGGSC*LOLLBRVR QENCLNLGGEGCGSLPKFWDYRCEPPCP DCWPS
4277	18178	A	4301	454	1	NGEKPTYSGKKYVFL*NTRRPTLPTWG KTN*GERPRSSVYSCSWRLSSSSLGRS *NSVGSNLIIATLTAQELSNS*ANNLI *LAYTIAFIVKIPLYGLHL*LHKHVEV PIAGSIVLAPVLLKGGYGIIRLTILIN PLTKHIAPLY
4278	18179	A	4302	3	463	AVSLPLPLPRFGRPLPLRVGVVCPLRCH ILRTQRLGAPSR*QTGAKQAGVWEELR SRLSLGPGLGRIRPYSGDPGQVTDSSGA LASSLERGCYPAALLVGBGEGMYLGPY

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						HPT*DGKRLSLAKPFGGGETRLTRSGHT FRGEGIPPSAVCL
4279	18180	A	4303	469	2	FFFFFETESCSVTQAGV*WHDLSGLY
4280	18181	A	4304	194	3	FFFFFETESCSVTQAGV*WHDLSGLY
4281	18182	A	4306	517	254	VVEETAFRLIGKTGIGLVTSGLDAASAS QRGGMATGVSHCNKKEFVLNII VMSSGL TFLPFSDFEV*GS*GLSFLPSPALNLTG LRN
4282	18183	A	4307	276	3	KIRMEGTPLHINPVLNMLGLLEYLAT SSLAVYSIL*SG*ASNSNVALIGALRAV AQTI SYEVT LAIILLSTLISGSFNLSV LITTLV
4283	18184	A	4308	234	398	KKFFFFPPLGGGGPITTIWSPFLPG*RE SPAPP*PRGGIKGLAPPNNFLFLDKR
4284	18185	A	4309	403	100	SGGQKAVGPPFWAAPPGYKONTNKLGLPLP QPSTEGGAFWPTQGPKEPTGLPPLPG*LN PRNTPP*WPPPPPPENTRSKGPHTPSP TPLCGPPPKNPLRFFFF
4285	18186	A	4310	399	85	WKPIPLAPEWRGVIRFRALPPCRPLHCP TLKLTAPSVIHQRT*VHMGFLVGVSLSV FLERESCSFTQVECSGTLALRSLELLG VSDPSISAFQORAGTAGVSHHA
4286	18187	A	4311	230	2	WTEEDTRRCLVLFSFFLFFLFCFVLRLQ RPACCPGWSAVTQSLTAVASTLAQAKR SSHLSPPQRS*DYRHTFQCI
4287	18188	A	4312	1	420	NTSMGVGELSLTIVINMLLPYVWLPKG KFPPFPQNSRPPSAPPHSSPPGLRSDPFS SGGLFFHLEVLWGLPLPPPPPPASTHVR RPLGTQGCP*LAWYIHLISASYQKANA POLSCILQDCIRSGKDILIFTFTLCLS
4288	18189	A	4313	403	207	ESSEG*LNPLAHLAMRYKGCFFKDVRK SEFILKSIQVRKSLIATRMSLLQLDFTC RYSRCVCFY
4289	18190	A	4314	469	328	TSEGGGNEELRLCHCTPVWLTK*DSVSI SGRLKKKLLKQSLVVRCP
4290	18191	A	4315	1	212	NILPGVELKRLNEDSLNP*GGGCREP *SCHCTTANATEKIDPVKKKKKKKPPG FRPHLSQDPGPPK
4291	18192	A	4316	63	559	SNLTFWQCAVPAVETTPSSLCGPVPSPT SSATPKPIPS*ACPPPPDCALAAEVRAL PAAGRPRFSEACLTPQPNPCVLPCLWD HSPTSCPTGSS*APHSCAFLPVRLGGG MTTVHPTVHLPIHSSLTFAWE*PSPPPAC LTAPRPTGHCLLSVPPSYSSSSPS
4292	18193	A	4317	135	405	PAPPSPHPKPDSVSCVIFPS*PAPPSPH PKPDSVSCVIFPSHVAGPSGLPEMTLLE PRGPCPPEVPPTSPFVG*AWHPFPARR ASGRMDGRTDGRGRHLDRSTHSLTTP
4293	18194	A	4318	413	1	LYLVGRA*SFHRSFPQERHHPGSKPYD CKECGETFISLVSGIRHMLTHRGVVPYK CKVCGKAFDYRSLFRHERSHPGKEKPYE CKQCGKAFSCSSYIRIHERHTGDEPYE CKQCGKAFSCCKYIRINERTHTGGV
4294	18195	A	4319	479	342	GVGVNDGILVLGATNIPWULDSAIRRR *DNTVINLFLTADVTSR
4295	18196	A	4320	400	26	HSEAVTTRVSHSPVGHISLHNPAPTVA LTP*YNNPLNIPV*ARAQKIQGGLTHHT IPHILLVITRDTSRACVVCVVCVVC

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						CVYAYIVVCMCVIYVVCVYIYCNVTFI PTLVHLPINKMY
4296	18197	A	4321	370	1	SDRGQKAGAGATRLGSRQTGDDEKGT KSIPIWDKGPVNNFPGKSVNVSSNLVTQ EPSPEETSTKRSIQNSNPVKKKCKC NECGAFSYCSALIRHQRHTGKFPY* C NECEKAFSRNV
4297	18198	A	4322	342	82	GLGLTTNWLTLGKSAGRGCAPSSGGLWL AVGDSVYYHRETEGGKPSGRPC* PS* AGLAPSPSPPPGCEAPGSCCLHYRCLL TAH
4298	18199	A	4323	284	3	ITKKPRVIVGGGCFSPFFMGLSKKNGLF PEGALSIILIFGPAIPGGAQVISSAKE KKVILSRGCVVAHACNFTLGG*GGRIK RSRVPDQPV
4299	18200	A	4324	365	3	QVEVVVVNHPFRLEESTIYQ*CRLEGAT SVAGEQISEYVNISMRAEDGSPPLSTET HITLHVINDINPPTPHLSYSAYIFEN NPRGASIFSVAQDPDSNNARITYALT EDTLGVY
4300	18201	A	4325	253	3	PSFLSRD*SHIKKRLCESGMISADYNLH LPGSSYPTTSPSQVAGTAGPSMSLQGR ASHDITSSRSIGAKELLRPADHPQCI
4301	18202	A	4326	307	95	FLFLLEDKILLSPRLCSTGTI\AHCSLK LLDSSYPAPVAS*VAGTSGMCHYTLRW KNHLSPIGQCSEI
4302	18203	A	4327	371	2	WAPNHSIPTPSGSETTRINAPTPPSNSP RPCQDPGHRTDPWYPEEEFLTNPDP APASWSFPQEKRLHFPALPCP*HLDSS LGPTTLTSPSPFPPTSIRPSQTNHSGKTP PPLSYAQHDCI
4303	18204	A	4328	409	1	RLLEARQPELEMAALIFPTLKYKHVERE QKYHQLDEYFTSAVVLTLLAALFGLV YLLIFPQS VVVLLLVLCICFVLVACVLY LHITRVQCFPGCLTIQIRTVLCIFIVLV IYSVAQCGVVG*LPWAWSSKNFLY
4304	18205	A	4329	262	2	LHGAYLVLDIAGQNRKPRYSFKWRVGQ FFFLVSPRDLTLRLPRLCSTGTVMAC HDDLGGDPPTSAS*I*GTTGAYHTQ RV
4305	18206	A	4330	1	399	NTP*FLKGMGLVNVHVFTEDLNKLKYVSN LGIGHTRYATTONV
4306	18207	A	4331	408	3	SSVGILHVRHTTGKPEYCKCHGKAFSCH SSLREHVRHTSGKPEYCNQCGKAFSHA QYFQKHVRSHSGVKPECTCGKAYSCS SSLRVHVRHTGERPEYCKCGKTPFRYL ASLQAHVRTHAGA*IKYKSGHV
4307	18208	A	4332	110	426	GLSPGTWSDMTGGPVAVTAFFPCTLTGTHA GHIIIDGIDIAKLPLHTLSRLSIILOD PVLFSGTIR*APPLRPTPOAGSVPSD LEHKEEGVGDDPRGVSCSC
4308	18209	A	4333	133	1	EPCCPSALAAPEVLGPEKYDKSCDWNSL GVFMYIL*VSPSPPLY
4309	18210	A	4334	165	1	IYLTFFKIKERKVVKAVQYW*KNR*VDO WNRASPEIDPHE*SQLISDKAKECI
4310	18211	A	4335	42	440	SARRAGDPARGAPSRNNASLPDPRELTG RPAGGLQ*GNCPAPPTPOLPSPSVRPV SGRGPPPPSPFGDPRANRPNKPKAKV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LTVMGEGFGIIRRAACPOLSWMTFFPGS LPEKRTGPGIQAQSPSPSRGG
4311	18212	A	4336	1	160	NTCGGGAQL*SQLLRIRRMHEDLNGSQG CSELRSHHCTAA*ETKGDPLSINEY
4312	18213	A	4337	236	1	QRELLCYIMEIRTVAVRIUAKGVSEV YLAMEEGTQYAKKCEYKGI*ELVLE SHYVYTAADVLRPVCCIESKVS
4313	18214	A	4338	408	3	CQSSVS KKEKTNGAQNFGAAQGNNELR DSTEQFQEYVRQLRYHQHLEQEQQRH I*QOMLLEGGVQNEQDGRDQONRNEQFL NRSIQKLGLNIGMDGLGNEVSALIQQC NGSKNGSNGL*VMSFDTFPHV
4314	18215	A	4339	363	1	RSQSSLPKSFKRKTSVVSATKGVFAGTS DT*GVQPGWQ*RWGASTATTQKKPSISI ATESLKSLLIPDKPLAQGAQVVDLHADD SRISEDTERNGDDKTHDKGLKICRTVV RARYSINEV
4315	18216	A	4340	1	353	DVFLDTLARFLHSCNFFLCYLL*DFFK FIPQFFYWMFYFDYIFISRRNFYVLLLT HFFTLPLFLFVIRIQCLHLFFSFFFFF FGKGNPFLPPGWRARAQFVWNGSPPLRV NALLP
4316	18217	A	4341	376	3	LELREGGFLPHIADEVREERSPALDDR AGRCQGGPRIQVCLTPKSMFLAFHM*T CEHLEQCFSTSL*PIEIRTLH*D*GCV CMCAVYVICVCHVMCMCAVICVARM KRPLESIHTSCT
4317	18218	A	4342	158	2	LAFFFFCETQSCCQWHDLSLQPLPQRF R*FSCLSLSPSSWDKKHTSPHPTCI
4318	18219	A	4343	145	2	IFGEQVVFDMKNKFFSGDF*DFGASLTQ AVHTVPNV*SVI*PCHPPRV
4319	18220	A	4344	1	434	RSLLIFRATAYEYRYIDQDLKLPASKRS SCLGLPKGWDYRHPDCLARFIWQIFI AYKLR*KHYKSRQSLPSRSGSC*CACT FVSDPSHWGTMAQILGSGWITLGQVQRSC LADQPLLELLPPTLAPCLP*NDVLLFFF TQSQ
4320	18221	A	4345	4	475	KHSCRSLEHLDRPLPAIQETCPVRAEP LLLVIRINASGGLILRMGAINRCLKHPLA RDTFVCLLAVLGEHSGSKSFLNLHLQG LPGLVIRAGRGRREAGSKDGGSCIGSAGS GIPVCGDKPTN*CSFPSPLOQSEGGGR PRGGEASLGQCRWRANG
4321	18222	A	4346	313	442	DSTLNFFFFF*TESYFVAQAGVQGHNL SLKPPPPGFKRFSCL
4322	18223	A	4347	437	338	AEOVEFYGDYIAPNPHLSNLNGCOQG RNWDPAQLSRTTQGLTALLSLKKCPMI RYQLSSAAKRLAECVKQVITKEVELFE FRRTVEPPLLLILDRCDADITPLLNQWT YQAMVHELLGINNRIDLSRVPGCMRPL *RIHPGTLERSTRLLFMPSSSWTMA
4323	18224	A	4348	409	118	GLHDASFVAAPSTQVVFYFETASEF DFFERLHTRSVARVCNDVGGKLLQKK WTFLLKAQLLCTQPGQLFPNVIRHAVLL PADSPAPHIYAVFTSQ*AAQPSGRMS TSSAAAFRRPHSCRL
4324	18225	A	4349	2	418	YTLPDFPHHPRHLSHCRLLQSRSTAYQ SPGACTPISQGHGQQRSSPCSSSSNPAC

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						*SSSSCGSTGFRCPGSAHPGCCSYVL*M GR*RSSQAPRASPIAQGRSAPAGRAGH PALPSFLP*GAPPPPSAASSPGL*SPA
4325	18226	A	4350	401	276	DPLNVGGGGYS*FRLCHCSPTWVTEGDL VSKNTNTHNKKHL
4326	18227	A	4351	446	277	ACDFVLKDGVEVIGSICFRMFPSQGFTE IVFCVAVT*NEQVKVSAAAPRQPOSTAHS
4327	18228	A	4352	408	3	PKSSLFTSRPNKGKSWSTRKPAISLAYSN ENAGQSWNGQDAGPLLVENPRDYSTEL SVTIAGVASLLFLNVLAFAALYSRKDRTR RQ*PLCOLSPHRGIGASELGHAPO*ELP ALLLGPINHECEAGPHDITLV
4328	18229	A	4353	62	280	VRIGCLTSVPEASSCGLPITPGGCC*PLG TLPCRSSRSTRFSRSTRSQSRSPKITY SPGRRRRSRSRSTPTT
4329	18230	A	4354	364	3	PVGEKGSLVPKSPVEEKGKSPVQSFPV EEKAQYRVKPSVVEEAKSKAEVVGKGDQK EE*EKEVKQAPKEDKVEKKEKPKHVPE KKKAEPSVKEEAVBEVVTAKSVKVGLE KEINSECI
4330	18231	A	4355	3	558	LGTPLNRRGKVPFRKNSPLFTSLRFTLP RASPGPSRGLPMWQAGSTPMTLPRSTP SMSPLM*VWNPPTAVPV*KLPMWAPPA PLVLLVTILTEIQEPATPAPITQF*KPT SLMVSRLPVCVPVQGPRTTRTLCATTIA PSHATLRLPGLSTTSPRLWTLGLLLEGO ASLPGK*NTSITLPSVS
4331	18232	A	4357	258	1	LGFHDGPGAGWSPQHGGKSAQAQ*FPQP PTVPTSLADVSDAPLPFCGHSRPPQHHP FRLPHTSFTSPGLSAVCLIVHPAARVSR CI
4332	18233	A	4358	97	343	DRDLGDEYGWKQVHGVDVFRPSSHPLIFS SLIGSGCQIFAVSLIVIVAMIEHLYTE *VFTLNCIMSLFLNFSFNHWNLLSQS
4333	18234	A	4359	182	2	KDYFGSSVENGGEELKQEDGLGGYSVI *ARDDDEDDDDDDDEDEDEDEDEDD DDCI
4334	18235	A	4360	88	2	RGSRTDTG*RGSDRGTG*RGSHGTGR*R GSRTDTG*RGSRDTGTGGGRSTGTGGRG SRITGGV
4335	18236	A	4361	2	250	ELRDEGKASSAKQRLKACAGLQKFRERAF KAWAVARLSQRFPKAEFAEVSILVTLDTL KVHTECCHGDLFGDEESAGLAKYIM
4336	18237	A	4362	169	456	EQLLCAGQGQLSCEPLHLFSPCPVGPOTP AHRPGRMAPGPPSFLSPGSPCGLGLAIP CSCQPPWAGVDPHLLFPSPMGRAGLSPS ERSAGEGVIPWF
4337	18238	A	4363	1	419	PEFKLQKLRKSONSAFLDIDGENEIQLS KSDVLSFLEIVMEVQCLKVAENRI VYCTMEVBEKLTQDQASRPQWGTG DFTTTHPRPVVKVLFTESTGVLALEDK ELGRVILYPTSNSSKSAELHRMVVKN
4338	18239	A	4364	375	448	PGAVAHACNPSTLGGRSGRINRAG
4339	18240	A	4365	1	444	DPLTNHLYHFLRTAGSQTLGLTAVQVLY SAYEENNRFTLLAAVRNNHNOYVNPSCV ATTFESIKEILLRQSGVKVESVDHDSHV HGFCQNGRSLCKLAVSVLKSRESLPV IIVANEPLQPLCKCLPGYSDSWCEIDI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4340	18241	A	4366	52	402	DEWLPPFW CPQEVWFHSFCCHCTSAFMKDYFLCLVR FGDLKEDKVTTRHDGASSDGHIAHFRHA AKELFNEDVEEVTRYALRCGAIVTACLC LWLARVHGVEVWICACGGSMGCVYTSQN QKQFF
4341	18242	A	4367	119	247	WVLLSFOLHGVAVLGTALIAMGEETGA MALRTFGHLLRYGEP
4342	18243	A	4368	2	430	GSTVVDGQGFHGBDLSKAPGMNSLEQG MVGLNIGDVSSAVKTVGVSVSSVALTG VLSGNGGTVNNMPPVSKPTSWAAIASKPA KPQPMKTKSGLPSPSKPMNDIGTWN KGPVPKAPVPQAPSTQACPKPSQVQGT LP
4343	18244	A	4369	1	406	ETSTPEGEAGPTQRLDIPVENFVESKNI FLGAPLIICHVIDKRSPLYDISATDLAN QDLEVIVILEGLGRTTGISTARTFYIA EETQWGHFRFVSETSEQRPDSDVYSKFG KTDLVTTSCRNARELDEKPSILI
4344	18245	A	4370	2	284	GTGTLCDLTALLSARYDGVRTCILPCWK TISTIPVALLIHYHQNASCGKRAILE TRQHRLFCADPKQWVKDAKPHLDRCQA ALTRNGGTFE
4345	18246	A	4371	3	184	EDYNILLSIMKGTTRPINKETIEALNDTV DQLELTDLCRTLTPPTIAEYSFSSAPKV LIQP
4346	18247	A	4372	44	304	GLFRSIGCQGLPRLPEWPTVWVGCHRG LIMPVPTQVSEPLMFLDTPGVLA PRIESVETGLKLALCGEPGLGLGPGPLPP HL
4347	18248	A	4373	1	422	LHLFNPAAAFSFRSLFSGFILDPLSRAL GVQPGICGLASSPGISEGWDQIRSWTHP PDDHLSGFCRSQVWPPSLPSTMTL SGGTALKPPYSAFPQMOPLEWVKQSG PYQPMGNGQALVYEGQLSCAAGLSAQW
4348	18249	A	4374	2	423	NSGTHTPGLEDLSKNGRIFETKLVPNG CSDLEDSTFTLLQSKDLKQPLDPTCID TSETLSNQKLFSDINLNDQWQELID ELANTVPEDDIDQLFNEDEPEEKKEPEFS QPATETPLSQESASVKSDDPSHSPPFAHVS
4349	18250	A	4375	292	429	LKTSVFPSSSTEISLQORLEYTARAILTA KSTGTIASISADGESLRE
4350	18251	A	4376	544	32	ALHACACGLGLSEACFLHLLLTGTSTPG PVDGQGLDNGGFRLLKAILGVS PAPERV HGASEHNADTVGSVARACVLPTSTPLAR TAAAKDESPFLAGLTMGPSREPGGSCLP LPSSGLLSSPTRLALPRPPSVSVWQDVG SSGSMPTPLVQCQGHFRFYGLTVSWAVMV LK
4351	18252	A	4377	378	232	PAKRAEEELLJHDTRCWLNGGAMPPEARH PRTGASALHVAAGYIEVMR
4352	18253	A	4378	291	1	QMLSDVVASRYRAPSTTYVINSLSKEGMDG LHGECSSFLGPSVAMNQTAGLEMG ICDGHFRQNVGCGYVLKPDFLRLDQSSHL PEKPISPFKGQSL
4353	18254	A	4379	171	458	RGPLFLTLHIVNSLQGNFRREYIVTQGS PLPGTKDDFWKMWVEQNVHNIWMTQCV EKGRVSKQLSNHQSFAFCHLDRILPHHQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4354	18255	A	4380	214	410	SETPQNNVGM LDHLPTHPSFTGEIEVKWFVAVQTGLPM CILGAPFPPIRLGAQSIQVLDSSELIPWA VQNGRIAPC IGDSGVGKSNLLSRLTRNEFNGLG
4355	18256	A	4381	2	74	IATVSLNIVKMPRLPKAIYRFNAIPKIR PMTFFTEIDKTLKCMWNHKKII PGNSPA H
4357	18258	A	4383	2	423	LERVCWIKDII VAVTGENMEVMSKSTIQK YQHKRISLVEAGVTRHRSIFNGLKALAE DQNSKLKSKPEVVI IHDVVRPFVEEGLV LKVVTAKEHGAAGAIRPLVSTVVSESA DGLDYSLEKARHRASEMPOAFEDVTY
4358	18259	A	4384	356	1	WYFCELASLT CVFGRGLFSLCLVLRV PVPCLIQPGSLLGSLLSLLRQGLAL WPRLCCSAIRAHCSLELGSNDSPASAS QSAGITGMSQCAWPLSLLSVSPRVPGLS SVPLIF SGSKKTLRSSLEETITLDEKPHRESFF YTHLINFSGKRYC WQLYWTTWCOKTSRNQGLAHVPRMECS MITAHCNLKLGLSSDPPASASQIDPS
4359	18260	A	4385	1	125	PSLAARVLARGYGNFVFLWLRNDRM HGECAPNVSVAVSTSHTTI IGGIRGGG GGYSGSGSSYSGSGGSYSGGGDGGGR GSYSGSGGNYSGGCAGSHGYS CSGSSS GGYRRGGGFGSCNSGG
4360	18261	A	4386	53	215	IKTRISVTHKEEFLTFIEGATEDMKNK TLQLAFAINQEPSDAKMLQVLKSGEGA TVNQGLEVAQVFLAEIPADPKLYRHHN KLRLCFNEFIMRCGEAVEKNKRLITVDQ MEYQQLKKNYNKLKENLRPMIERKIP LVKPIF
4361	18262	A	4387	2	390	KLGNFLGGCVKRESFPVFCGGQWPDFGS LQHPPSRPKQFSCPTLPGNWNFRNAPLR SGKFFFSVPVFLVETGY
4362	18263	A	4388	2	441	VQGMQNLQFTTGAHHLQGANIQPRIDI ARTEYLSNADRLRWQASSLPADDLCTE DAIMLKRFTRYELQCGEAWEEGCGW LDLSQFCRAVYVFAKKNETFFELRIVD LIKGRSSLGFGPEKPSQEDGR GAASEHPTKEGSHGTSKASSLCAADAGP AGHFASVYNPLAFTVTTIVTLTVGFPGV RVTDEAGHPVPSQVSGIQRCLQGMKAPP VTVTVSGEKG
4363	18264	A	4390	242	24	LSIDGFPQSRSTIFASWSAGDPPGSGVATE WLEVPFI IPSHIGHELVGLGCCPEVMFL WLELLKFFYTLDCALAEYVICVIRQDILT RENNNWPKRRIAEIGEMICCSIFVEYFI CATHYLIOC
4364	18265	A	4391	1	244	TVDFPFPQYKCCQYEMTKVLECLQKQVN GILESPTGTGKTLCLCTTLAWREHLRD GISARKIAERAGQELPPDRALSSWGNAA AAAGDPGIPS
4365	18266	A	4392	2	146	TSNFCSCLVLEEASDYLEDITIKNLVK KYSQ
4366	18267	A	4393	204	489	DVLRRNFARSAYLYLFDIRVTLWNAAPRL ECSGAIIAHCSLLKLGSDNDPPTS
4367	18268	A	4394	2	171	
4368	18269	A	4395	2	197	
4369	18270	A	4396	2	285	
4370	18271	A	4397	366	461	
4371	18272	A	4399	157	3	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
4372	18273	A	4400	2	343	DIDFKTHDFDFSVNFNEELVALYGGSLQ KQTKFVHECIKTLKLYKGQEPAPKPSVA TIGHSMGGGLVARALLTKNFKHDLINLL TTQATPHVAPVMPDLDRFITGSTGWLKDH G
4373	18274	A	4401	214	430	ELGNLNNVVVWEAEELSNRNWNGQAV HGELSPVTDFFRESCROYEMGECTRGGF CNFMHLRPISONLQRO
4374	18275	A	4402	3	227	LTQVSFQMTGHAGLNTAQAGMAKVSSEL KHFOYFLNRLGSLRLVRMKMGPRGPLLP FLLGSPRATHANKRQISF
4375	18276	A	4403	158	313	NRDEFCHVAQAGLELLGSSSPPAATSQS ACITGVSYHVRLPTLSNPKFCSSLL
4376	18277	A	4404	3	628	HCIREGGQDVFSNKDVITSLDWNSSEGFL ATGSYDGFARINTDGNLSTLQKHQGP IFALKWNKNGNFIISAGVDKTTIWDIAH TGEAKQQPPFHSAPALDWDQSNNTFAS CSTDMCIHVCKLGGQDRFIKTFQGHNTNEV NAIKWDPTGNLLASCDDMTLKIWSMKQ DNCVHDLQAHNKEIYTIKWSPTGPGINN PNANMLLASL
4377	18278	A	4405	35	180	MCVDVHYFFCLLGPNNNNNPTSVAURTP QTNGSNVPPKPRGREPFSQK
4378	18279	A	4406	1	438	DFQRPDDHGDVDNEKLVELLTDCSNLQ DQTYILYLYLVIKGPSWDTNLSGQNGVT VQNLGLGYGKTGLNQEWGLIPYISSLF RKKVDVLAEAETDLSDQKQLTVGLSDE PREKIIYAPLPPELTKLIEASGQDI IGVLTO
4379	18280	A	4407	1	428	TESVNAYFGKADPTKCIKVTIGDMTMSF PSGIIKVFSTNTPAVLCFRVKNISRLE OILFNAQVFSDFQSCDNTDFWNKMG AVTVYLLKLEQNFPAASYNVVLYKQV SLNGIQSTPLNATYWKCSASTTDLRVD YK
4380	18281	A	4408	174	383	KNSWFGVAHAHCNPSFTLGGKGRGITRSL YRDHPVQNGEIPLYLKLTAIVTFLGLL TGLHDLVLTNTLT
4381	18282	A	4409	1	288	LMAEKDSLDPFSTHAMQLLTAGKASRV PLGRPAIPGMSGGPFVPLASRPLGTEAV GSSGLILIFGSLDSTFPQPGVGRGIR LQWRPEGDFAIP
4382	18283	A	4410	292	422	LVSSECFQVSSKILELARKQRMNTDIRR NIFCTIMTSEDFLDA
4383	18284	A	4411	412	238	FFSRHRVSWQDQAGLELLTSLDLSALAS HSAEITGLNHHQAQLTTFNNKYCWLISQ VH
4384	18285	A	4412	1	405	VTSSDKSLKVLLDAEDKVFNEIRNEHFS NVFGFLSQKARNLQAGYDRRRGMDLKQM KNFVSQELKGLKQEHRLLSLHIGACESI MKKTKQDFQELIKTEHALLEGFNIRE TSYTEEHIDROVSPIESRLMCL
4385	18286	A	4414	2	149	GFHHVQAGLEVLTSNLPVFSASQSA TGVSHCQALRSDFGFKRSSPA
4386	18287	A	4415	1	366	DICHRKLGVECPSHASINRLVQVQVSSI TASLRFEGLPLVDLIEFQTNLVPYPRTH FPMTAFAPIVSADKAYHEQFVSVDITTA CFESSNLVKCDPRLGKYMACCLLVRGD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,511,26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
4387	18288	A	4416	1	164	VVPKEVNAAT RRRCESMTMFADTLLIVFISVCTALLAE GITWVLVYRTDPFGTLAGEGPGGRY
4388	18289	A	4417	2	141	DIAIPCNNRGASHVGLMMWMLAREVLRM RGITISREHPDLTSSVMG
4389	18290	A	4418	136	1	ECTKAFGLHKLVLGMDFLPFSKMPKPKPN ENPVDYTVQIPPRDPMQ
4390	18291	A	4419	1	280	GNKYCYGYRGFSGCEDGRRLVLKPEWFR GRDVLVLYGCVNHLTSLACKRGPSRMV GLDIDSLIHSARQNTIRHYLSEELRLLP QTLEGGPGA
4391	18292	A	4420	3	446	TVTSQVRQNYHRDSQAARQISLELY ASYVYVLSMPYFDRDDVALKNFAKYFLH QSHEDRDHADKMLKLNQNGRSLLDQM RKPDCDDWESALNAMEWALHLDKNVNOA LHLEHLKLTDKNDPDLSDYIETHYLENQ VTAINELG
4392	18293	A	4421	6	182	DPSCFSEPRSCHCTPTWRTEQDSISEKK KKRNILKNWAKNYITLSEKERKSKQRS RR
4393	18294	A	4422	1	456	GTISYVVWPKKQALVEFEDVLGACNA VNYAADNQIYIAGHPAFVNYSTQKISR LGSDSDRSVNSVLETTILNPIYSITTD VLYTICNPQGPVQRIVIFRNGVQAMVE FDSVQSAORAKASLNGADIYSGCCTLKI EYAKPTRLNGSK
4394	18295	A	4423	2	257	FHEVGOAGLKLISVDFFALDSQSAEIT GVSHCAQPVLCILNQLCAKAVLSPDHP YPPKSGRHEGQVREQKMSPCSYIYFKRT V
4395	18296	A	4424	106	259	CCCFKYFFSNVKICFYRDLKPENILLNE DMHIQITDFTGAKVLSPEKQGV
4396	18297	A	4425	3	364	MDETERTQSEVEDQDPSCPRLSRELLDE KEPEVLQSDLRDCYSTPSGYLEPLDQ PYSSAVYSLEEYGLGLALVDSEYLVK VISLHLVFIQVIFLFPVPLTDPREVIA AGRTYGR
4397	18298	A	4426	2	241	HHVNLICFVFVFCVETGFCHVAQVGLER LGSSDLFTSVLSAGITDNNHWAQSKPS PSKGTGMNRPGLRVGKGVMWSRL
4398	18299	A	4427	2	438	TLRIGNPCGPMVMPGCKMGIMPGHYHK KGRIGIVSRSGTLTYEAVHQTQVGLGQ SLCVGGDPFNGTDFIDCLEIFLWDSA TEGILLAEIGGNAENAEFLKHNSS PNSKPVESFIAALTSTGRKMGHAGQLL AEEKV
4399	18300	A	4428	34	427	AGMLPAVGSADDEEDPAEDCEFLVPMPE TTHSEEEKSGLGAKIPVTITGVLSAG KTLLNLYLITQHSKRVAVILNEFGES ALEKSLAVSPGGELYERLELINALCLCC SVKNGSLAIENLMRQKE
4400	18301	A	4429	330	8	YSDRISHNIDMCPSKYIFRGPVHPPHIS TFLHTAHLVARGNENYNSPHDEKAGY QRKEKCCDDPMAGAARIHLCFFEMGFR SVSQAGVPWPHITSMPQPPRIK
4401	18302	A	4430	446	222	VTSDDPPASAPGSAGITGVSHRPPQPIWG VSIQLYFSGCPDTPQGRLTREHCDGQD GEQGGPCSESAQFCHDWS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
4402	18303	A	4431	3	243	AREDSADVFVSFFPDFVWTLRDFSLDLEA DGOPLTPGTSQKDNFIFLRLCIRKFTS LIRTSRSYQSDDTVSVASSGARG
4403	18304	A	4432	433	0	PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP
4404	18305	A	4433	25	185	ARWACSELRLRCCTPAWATEPEPVFKK KKKVQOQQGWPGGLTPVSVRGRILT
4405	18306	A	4434	2	329	VRDIKEKLCYUAVDFEKENATVEFSSSL EKSVELPDGQVITIGNERFRCPREALTP SFLGMESCGMHETTILNSIMKCDVDIRKD LYANTVLGTGTTMYPGIADRMHNEI
4406	18307	A	4435	2	374	WVTFISILLFLSSADSRGGFRDAHTSE VAHRLKDLPEENFKALLLAFAYHLHC PFEDHVELLNEVTEFAKTCVADESAENC DQSLHTLFGDTLCTVATLRTYGDMAEC CAQQEPERNECF
4407	18308	A	4436	2	352	KVRRIDSRLEAELDREIRNPQISCOLIYS PSLFLGAFPLFFFGFFPPPPYLLAPKN QFNPPPLCTGGVPVRKPPIPWEPVPRP APPLFSQNDLGFQIAPFLWVINGGSPS GGSGRA
4408	18309	A	4437	2	369	QSCETLFHSWKDVEVCSSALSCLSQVSV HLQGLSESLFPLPGMEVQORDSQMALVES LEYVRGEISKAMADPTTWKTHLLTSDSQ GGNQMLDEGDFEDFSQMEIAIRAILCA IQNLSEERKNE
4409	18310	A	4438	2	231	SDTSRFQLPCFAARERFPDGLSLRLPLF PFLSQVYNEQIHDLLSPKGLAIREDDPD KGVVVQGLSFHQVNDWARVG
4410	18311	A	4439	1	365	MAHAMEVKKCLGPDMDIDICHEQFLEL SYLNGVPEPSRGRGVVGRRAAPPPPP VPRGRGVGPPRWALVRGTFVRGAITRGA TVTRGVPPPTVRGAPAPRALTAVMQRI PLSPPPATK
4411	18312	A	4440	92	510	LAALPDGQGLHIPSRSRAGFAGLSWAV VGTGALSSSLILPQMARCRPPWPLRPN PLQGWIFNVVPLVLAIPASLFSGFLSDH LINOGRYRAITVRKLMOGMLGLSSVFAL CLHTSSFCESVVFASISIGLOTFMHR
4412	18313	A	4441	2	266	FPFHLPELGKNECPWHQDCESSAAVSF CEFSPHSFCKDHEKGLVPSALEGRGCC SEHDPMAFVSPPEYNSKIKCWESQDHGE EVKE
4413	18314	A	4442	2	279	XGAELVFLPSNTRSLMYPDQGVVTRTFK AHYAGYSMERIVSMEENPREKIMKKL LKLSSPKEIPAGEKLCPNDAHDFTELD RVIHENHE
4414	18315	A	4443	2	371	KWVTFISILLFLFSATDSRGVSRDLAHTS EVAHRFKDLGEENFKALEIAFAQYQLP WPFEHHVELGNDVTESAKTGADESADN CDKSLHTLFGDTLCTVATLRETYGEMAD CCSQPEPCEKG
4415	18316	A	4444	2	372	WVTFISILLFLSSGYSRGVFRDRDAHKE VAHRFKDLGQENFKALVLIAFAQYQLQQ SFEDHVKLMNEVTEFAETCVADESSDDC DKSLHTLFGDTLCTVATLRETYGEMAD CAQQEPERNEC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4416	18317	A	4445	1	283	FRKNAEDILTMELGRATMKHELEAAQKK HSLWELLRIPIKRIWILSFVRSAGVC WRSTPDPVCLGITSGGCRTAQIPACSFL WKLHLSIGAPA
4417	18318	A	4446	173	2	KKKKCVLPYEGHGVFHALVCVVCVCVC VCVCIQVNRNFCFISWINLSVQVSLLD Y
4418	18319	A	4447	104	221	SCHLHYSLGDKSETLSKNHHYHHHHNH HHHPAGYFKMK
4419	18320	A	4448	241	1	WVSWDKAPSWVRGLGSGSRGGVWGGGSP PBRVTDVSCSLPDPGRHVMEMEAKTDRD LCKPVSAFAGAGATVGPQGLGRC
4420	18321	A	4449	229	349	WKRSHSFGLEVAHACNPSTFTGGGGRI MRSGVDDQPGQY
4421	18322	A	4450	76	189	TSKPAATIRSSGGGGGGGKROGKKDD SHWSRFQKV
4422	18323	A	4451	40	359	SGEPLPFFFFSLARLIPGVCFVEMITRY RLLIQLKIWEKKVPQVSTPTLVESRNL RKVGSKCKKHPEAKRMPACSHYLSVVLN QLCVLHEKTPVSDRVTKCTTES
4423	18324	A	4452	2	371	KFONALIVRYTKVFGSGSTPTTVKYSRN LGKVGIKCKCKHSEAKGMPCAEDYLSVVL NQCVLHEKTPASDRVTKCTESUNRR PCFSALEDYETVVPKECNAETFTFHADI CTLYENERLFO
4424	18325	A	4453	118	369	GRYLLLLKTKRQTANNIKTPQYLSNMS KKFRHSEFFFFYLKWSLALQCNLSLQ PTPRPNQLSCLSLPNSWDYRCVPPNLV
4425	18326	A	4454	364	3	GHLSLQRLLPFVWLCPAPRGGAYRGRO ASLSCGGLHPVRASRLCLLPNQACTMAG APPPASLLPCLSLSDCCASNQSDSVGVG PSEPACAGYLLVCRFLSPSEKRSPSAGV MRFSRCL
4426	18327	A	4455	1	379	AAFTCCQAADRAACLLPKLDELDRDEK ASSARQLKCSLQKFGERAFAKAWAVR LSQRFPAEFAEAVKLVTLTKVHTECC HGDLLCADRSLAKYICENQDSISSK LKECCCKPCKLEKSH
4427	18328	A	4456	1	362	LKPARSLVFPWFAPGGSGSLRGLKLEAK CQGDGVSVEETIIPFSAHYNLFGLPLI SRRADEVLTSLRELSALINQSTGLPFL TLPRGTCLPALLPYLEQFRIIVFWLG DDLRSWEA
4428	18329	A	4457	250	330	ENWTHLWLNCEGFASWIEVCVVDHCFPE
4429	18330	A	4459	96	319	YLTIPTFSQAMENCKDARLTITSGAYNEN HRLLEMLNKPGI.TYKVPQVQSALSLL SPLFEMFLPYLSYQCVS.IH
4430	18331	A	4460	50	339	NSQTLKLSNVQCLKTRALFFFPKGIYFO IKTLPPCPTSGDPVYVRVNLPLPKKGKGC LKKISGNRKTLPFDKTLKFLVPMKRV PKSPLNVVKN
4431	18332	A	4461	2	357	GVDGVRWRTRDGDIFNKEILLIPHLLEV HNSLISVDVRRRTITYFDSQRTLNRRCP KHIAKYLQAEAVKDRDLDFHQGWGYFK MYCHLALSQPFSTQDDMPKLRQIYK ELCHCKF
4432	18333	A	4462	182	325	IRLSSWLDCASCQVYEFVRKESSTIAP APAEVDVTPPRKKKKHRL

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4433	18334	A	4463	1	338	SRHSFGPTPQPPDCSLRTGQRVSQVSDTS SCSQLSSSSSSSSSSVAPAGTWVLQAS QCSLTAKACRQPEIVFLFKLVDMVESTD SSQLPKASLLSPSPVWMASSPFLLSK
4434	18335	A	4464	2	343	ITDFPLGAYLKDEVLKINEVQKQTRAGQ RTRFKAFVAIGDYNHGVGLGVKCSKEVA TAIRGAII LAKLSIVPVRGVYGNKIKG PHTVPCKVTGRCGSVLVRLIPAPRGTVGI VS
4435	18336	A	4465	1	371	INSTLKMSFVGENSGVKMGSEDEKDEP QCCLLEIFPALASSLSASAEEKSPILL GVSKGEFCLYCDKDKGQSPSLQKKK LMKLAQKESARRPFI FYRAQVGSWNML ESAAHPGWPI C
4436	18337	A	4466	246	12	LCFTPLPSYILFFFEFTKSHSASPKLECS GVITATSEVILLGGGGSELRSYCPTPT WVTKLDSITKRRRRKKRDL
4437	18338	A	4467	2	355	WVTFISLLPLFSSAYSRGVFRDHAHTE VAHRFKDLGEEFNFKALALIFAQYLQCC PFEDHVKLANEVTEFAKT CVADESAENC DKSLHTLFGDKLCTVATLRETYGEMADC CAKQEP
4438	18339	A	4468	2	361	EDHVKLNVETVEFGKTCVADESAENCDK SLHTLFGDKLCSVATIRETYGEMADCA KHEPERNECF LQHKDDNPNLRLVRPEV DEMCTAFHDTDETF LKKLYEIRARRHY FYAPELLL
4439	18340	A	4469	1	373	SSQFSSPSESVSQVTSVSPSSLPSPCL SLSVCLLVCVLSMFFSLPVCLSVPLCV SPRPHPSVSHAHPHRASALVNCWPWPAP TSAPSVFYKQSPALKTQASPHPHPH FPTSPMQSQK
4440	18341	A	4470	236	371	KVLGAVLKKGGLFCFVFGDRVSLCHPG WSAVVQSQ LTAAVTSA
4441	18342	A	4471	345	201	AMMTAHLFWAFTEYEFKSTAGKKFVFK TLILLIDNDFPLWDSKEGKL
4442	18343	A	4472	1	144	AGFHHVGEAGLGLLTSRDPASPCKRAG ITGLNHHTWPF SVILTYTY
4443	18344	A	4473	3	333	KNHLEASIGEHFPFDPHSPSCPHLLSS NYHLSLSCFLGGFFSETGSAPSRLCEGS VIAAHCSLKLLGSTSP LTSASWAGITG MCWLSPAVSPRPSDPLTCTSQLENI
4444	18345	A	4474	288	1	TSAVNRISIKSQADQEAETQKLRDYSHQ GIQILAWQKFEYKPGKVTMDPEDCI LQL AKKKEEEEEEEEEEEEEEEEEEEEEED QEEEEEEEEEEEE
4445	18346	A	4475	3	124	PRLECSGIMAHCSLDLLDSSDPPTLAS QVAGTTKKISLH
4446	18347	A	4476	196	2	SCYEHPGRIVYGFLFLRQDLAVTQAGVP WHDHGLQLPPELKRFGSTSHLLSSQG YRRAQPRR
4447	18348	A	4477	3	162	LERNKELEGSLOQMSTNEEQVQSETEV RALHVLATHTPRGLGLCVPLCNLE
4448	18349	A	4478	167	2	ACGISPFLSSSCFGHVRHASLP LAFHH DCGFPEASPA MLVPVQSGLNLF IKYVP
4449	18350	A	4479	195	26	WVSMLDIHNDGHPHEAVICVCFLSQSLL ALLPRLECSGVISAHCNLPGRQSGTSPS
4450	18351	A	4480	175	1	NRSATKCDWGEKRTSQEINLFWFFVCL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FEMESHSAVQAGVQWRNPGSLKPLPPRFKR
4451	18352	A	4481	122	357	YHAFLYQWYNLKKREHKPRCSLLIIFLGGERKLQSIQLWNISHYIQRVLEIPSGLGAVAHACNPSTLGGQGEWIT
4452	18353	A	4482	137	2	FYSYLKILEEMGPHYVFOAGLELGLSRDPDSAYQSTEIIGSMH
4453	18354	A	4483	347	208	GQAGLELITSSLPASASQAGITGAGHHTRPRIYFLKKYLAFLVLS
4454	18355	A	4484	411	268	RLNRRGGGSCSPRSCRCTPAWATEQNSISKNNQKTKTLPLCCRLILL
4455	18356	A	4485	2	102	PCLLRMQLAGHGMHLCSSQLLRRLRCFLHSLYP
4456	18357	A	4486	1	113	HSXSTHAGHAGHTSLPKWCYRSEPPRLAKFLNTRY
4457	18358	A	4487	163	353	QVAATLNNLAVLYGKRGKYKEABFLCKRALEREKVQKGAUVVFIFVLVCVCGPFFFKRDP
4458	18359	A	4488	408	307	RGCSSEPRSHDCSAANLTERDSVSKNNKNKSPKKQ
4459	18360	A	4489	337	179	YSINFAILLIFLYGLVWAAIINHYRLHGLNKKHLLIMWNGVSPRLSCQ
4460	18361	A	4490	229	345	LENETLGRARWLTVPITPAWAEASRSRGQETITLANM
4461	18362	A	4491	180	365	RNNLKTVALDMSFYFLFLFYFLFYFLFYFLFYFLRNSFALVAQAGVQWRYLQSLQPLPPRFK
4462	18363	A	4492	269	385	GNLQNLKRVFYKIQHFFMIKTLNKLVIDRTVLNIIKAIY
4463	18364	A	4493	103	336	QLLVSLINLFLQAFKLQIDCGHTCMHFQRNCLCLPPTLPTPRNLTLSPLSCSGTIWAHRKLRLPGSHNSPASATR
4464	18365	A	4494	305	379	YIKIENFCGLVVATCNSTLGGRG
4465	18366	A	4495	47	224	ETATKTRRWETALVPOHPRPLAPVTVKTTGNSTIANFLLILVYLSFLFLVYSCIQQ
4466	18367	A	4496	3	129	ITLNPGGRCSELRSCHCTPAWATERDSVSKKKKKPPPPPF
4467	18368	A	4497	396	112	LPELEFAAVSHDCASELQGLHQSKTLFQKKINRIINNNSHIAISLLGIYPKEFKAGTQDICTPMITASLFTIVKQKQPKCLATNELVYRM
4468	18369	A	4498	1	152	LSLPGSQTWRRALIVPATWEAEVGGSPERPRSLQVAMITPLHSSCGRRG
4469	18370	A	4499	92	2	KRPGVVTACNPSLGGRGGPITKSVVRDQ
4470	18371	A	4500	116	1	AGIAGMCLHAQLIFLYFLVETRFCHLQAGLELLTLNS
4471	18372	A	4501	99	1	QGTVPVRWKKCLVQPLWRVTNSFLRKVKIDNS
4472	18373	A	4502	140	288	RQPHYVAQAGLELIGFSNLPALTSQSAGITGASHNNQPTSRFLKEKKIG
4473	18374	A	4503	330	181	IFFFLFFFFFFFFFFFXXFFFFFFFFFFF FFFFFFFFFFF
4474	18375	A	4504	171	2	VETVSKESLRICLDIRYFFFTETKPHSIAQAVQWYQGLQPLRLKQSSRLS
4475	18376	A	4505	345	74	SVERTCHSPKFLNLFLLVLFQARDQILN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						GSHPVSEKACETGGFQAQIQFPHVEH KHKPGFLEACHPYQTAEFASALTLDFA SRTVQK
4476	18377	A	4506	268	102	KNIRELWPGAVAHACNPSTPGGRGRWIT RSGDWLNLRTCEHVILQQKGRFRLIS
4477	18378	A	4507	1	67	GLPKCWYRREPPHARCKYF
4478	18379	A	4508	339	180	ANFFVFEEFGFHRVAGTGLEVLGSSDL PILASKSAGITGISVVRPQTNTE
4479	18380	A	4509	174	3	NPKVKVYIITPGDPLFLLLLFETESH YVYQAGVQWHDGLGSLQLPRLQRFSVCV
4480	18381	A	4510	84	3	AHHITTVGLDVTAVFTSATIIAI
4481	18382	A	4511	127	2	LLIKIHCWRSVVAHACNPSTGLVGRHWI TRSGVQDQPGYG
4482	18383	A	4512	109	345	ETFLIQSHGEGCLCFELGSMFCVATGTF PHVTWLIILTLNLTSSYSRAGITGVSH HARANNLFCFGSNPSHGITOLNF
4483	18384	A	4513	290	13	RDLRFTPKQKGFKNITAPNPLQKQTHVK KGRGTPPTPTPSKDPGPHPLKPKPW GRVWGEKKKKNKNGPKDKKKKKKKKKKE RKIQHSRF
4484	18385	A	4514	234	362	DGDVLSPKVNFFSPKVEGTFLDGRRL KYRLNGDFLFLRLKL
4485	18386	A	4515	190	330	CLALQSECFRRKSLALAQAGVQWRDL SPQPLPPVFKRSSLHFFE
4486	18387	A	4516	2	199	CVCCVCCVCCVCCVFFFLSKKNGPPPL CPGGPKTLGPKESPPLAPKNRNGNSGLT PPPPPTFFF
4487	18388	A	4517	94	339	SAYLGLKFFLFFFFFFFFFVGVPDPFF FPNKKLKPQIIFPPQKRPPIFFFPFP PGGKNFFFFGKFFFNPREKGPKNLGL
4488	18389	A	4518	95	3	LYLPGAVAHACNPSTLGGRGQITRSR VQ
4489	18390	A	4519	14	121	LIFFGNRNRLCCPVNSOTGLKPFSSWL SLPKCSD
4490	18391	A	4520	207	2	ISREKLCVTRIPDNHVIDESILFYFLFY SLALPPRELCNGTMAHCSLHLPGSSNP PASASQVAGTTS
4491	18392	A	4521	169	1	ANLTQVGSYYSLSLHTLIQVTFKFNIRA VRPGTVAHACNPRTLGGPDGWITRSGRD
4492	18393	A	4522	2	82	GFILCVCCVCCVCCVCCVCLYIFFF
4493	18394	A	4523	300	3	LFPLPSPSPSQIPGGQKFLPIFPPRPV KKFIPPNFWAPPLISPRPFVWRLGPPT QGFNYPLGPGPPPPPPPSLGFKKSNNP FTKKKFSPPKKQK
4494	18395	A	4524	348	94	KPGEGGKGPONPPGGLKPGNPLNPGGG GSPENPFPWPPPRGAKKTRFQKKKKK KKGRKESRLNYGMEKKKKEKVFLSAL N
4495	18396	A	4525	313	161	RQHPKNLKSKEVNIIRSEAPGHPRRNKKK TPNLKKKKKKKKENKQKQKP
4496	18397	A	4526	118	3	FFFFLKGSLVLAQAVQWRYLSSQLAL DPGKRFSCP
4497	18398	A	4527	153	2	KDAINKMKKMWPGVVAHACNPSTLGGQGG WITRSQAQDQPSHYGETPSLPK
4498	18399	A	4528	258	2	GGQKRLPGFIKKPPFRKIFLNKLGEGP GKNSLSKFFFFFFETESHCLTQAEVQW LNLSSQNKPPRFKQFLCLNHSPSWDXR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleo- tide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H-Histidine, I-Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
4499	18400	A	4529	296	39	R SRIIRNIQILLGGFFETGSCHVAQAHLKL LGSNDPPASASESTEITEMQHCTRLSIQ IFVAPFYSNIKLSSTKEPILIKLLLYNC K
4500	18401	A	4530	292	37	SRIIRNIQILLGCFTCSCHVAQAHLKL LGSNDPPASASESTEITEMOQCOTRLSIQ IFVAPFYSNNKLSTKKESILIKLLLNXR K
4501	18402	A	4531	3	138	LGNWSGCLCVVCIFIMGSGACLVICTIC LYCCVPVNTCLCMDGR
4502	18403	A	4532	380	2	GGPFKKRESAKAPGRRNPGGGREKTFF PKKRPQPQKGKKTPPGSGGGPPRGGG KKKPPPKREKCHRGGRGSGGPVVTKP EGPFFFFFFFFFFFSLPFFFFFFCFFI FILFPPIVINGFY
4503	18404	A	4533	3	191	LSKITHASIPVVSFKKKKKKKKKKKH KKKKKKKKKKKKGGGGPKTKLGGHN FSRGLE
4504	18405	A	4534	370	48	GPAPEVSSNGGGGGCGPLGLKPLGSQF NGVGYPSPKSPLP/QAPLGOGFPKPR NGOCPTFFFPPKKKKKCALGDGTPTSGC PRRSNHDETDODCGGWSRVPR
4505	18406	A	4535	147	1	KGEPLFFFFFFFFFFFFFFFFFFFFFFF FFFSYFYIYLFLSLRL
4506	18407	A	4536	198	1	NPPYFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLSFIFIIFYFNFI SNSIVIGFY
4507	18408	A	4537	2	356	ONRTIGNSKTSASPPPKECSASPATEQ SWMENDFDELREGFTSRNSYSELREDIQ TKGKEVENTERKHLHCITITNTEKLCLO ELTELKTTARELRDECRSLTSRRDQLAE RVSALe
4508	18409	A	4538	347	220	KCSGTIIAOCNLIKLGSSNPPVASQSQA GITGMSHHVQPKYC
4509	18410	A	4539	308	2	FISCSCHPDTPAAASQSAGITGVSHCARP IFSPICFIFICIMCIKYLLRTGDSVMYF HGLCGFCGLCCYLESYIRKLISHMKKLSIL ITSREKCKILQINIGDR
4510	18411	A	4540	2	194	IKQVVSTALSPrLCSGTITAHCSLKLP GSASAVVARTTGTHHAQLIYFSSETGS HVVDVDA
4511	18412	A	4541	101	2	MEENLGNITQIDIRGKDFTSKTPKAMAT KAKID
4512	18413	A	4542	1	84	AEEAEAEAEAESEEEEEEEEEEEIEKV KSEILLFVSSKTRLRSANHFVEFCFL KNSIALAQAGVQWHILLSLQLPLLGGF VDA
4514	18415	A	4544	1	335	RKKKKKKKKKKKKKKQGRKKRKREKKE EBAKKTKNKDK
4515	18416	A	4545	104	2	OKKKKKKKKKKKKKKIYDFFLQIN CMCHK
4516	18417	A	4546	5	108	FKRLSCRFSSPSWDYRRPRPANFCIL SRDGIS
4517	18418	A	4547	131	1	RRPRPQVLQDATSPIIELITHDHAI IIFLICFLVLVALF
4518	18419	A	4548	156	3	GGGGMSCLSRSPALLKFECRVISSY AWNRAPVVPATRGAEAGESLEP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4519	18420	A	4549	2	340	LNFGSAGCRELSHCHCTPAWTTTGRGSVS KKKKKKKKKKKKKKKKKKKKKKKKKKKKKK RRFLLGNFWKKGGGQANFFPLENPNP QLKTGKKAFFPRKGGGGLNPPQGGYQG A
4520	18421	A	4550	165	335	PHVLPERSIHRFPKSHSPFGVAHAAC NPSTLGGRGWITSQGEFETSLINMEKS L
4521	18422	A	4551	123	3	GRVDRLSCLSLNSWDYGHLPHLANFC IFSRDGVLSWW
4522	18423	A	4552	3	131	HPEVDPIPLPGLGISDYGAYSGISEP FGYVGMDSYDVPRL
4523	18424	A	4553	87	364	ILASQSVFVRYAASAAGGLLETESQPS AAGTASAAVPSLEAGTAAFRPTFPGLA PSSPPAPGPPAPTGVCGRHFLRSESSA SGPLRAL
4524	18425	A	4554	114	0	LTWAPSHLIETIRNQITQALLTYTLGL YFTLLQRSE
4525	18426	A	4555	91	3	TTTTYIAIATACVCCVCAVCPCVCCVC M
4526	18427	A	4556	239	364	CIKITFSRPGAVVHACNPSTLGGQGGRI AMSRDRDHPPQGGK
4527	18428	A	4557	250	1	STEHVQLRNEFMKTSVILIFLEILLYI KVHLKCLTITDHLGLIKSLILFRPG AVAHACNPSTLGGGGRI PRSGDRDHS
4528	18429	A	4558	2	90	QDGLDLTWGSACLSLPKCWDRSEPSL F
4529	18430	A	4559	65	394	DPVSKKKKKKKIRKNEKKKKFGKKKKPL KKKLRLADLILPKKKNFLKREWKREK GGDPFWKNKPVQKGTNNNLGQNGLGK GPSDLKNTPETKLNVLQKKQIFF
4530	18431	A	4560	93	2	GIISAHCNCLPGSEDSFASASQVAGIT GQ
4531	18432	A	4561	125	4	GAYILYLNKSKSIRPGVHAHACNLSTL GRCGRITRSG
4532	18433	A	4562	3	84	RSCHCTPAMATERETLSPPKKKKKNF
4533	18434	A	4563	145	3	GFYHVVPQGVGQSPCLSLPKTNWYHCEP PLIASIGFFPFFPTQSR
4534	18435	A	4564	125	388	IRKPGIYSPQSSBMQHLHISVLMGV TKRKPFMDLDTBRCRFLKKCTGQIE DLNKWEGIPCLWIRLNTVMHVPFKLI CRFS
4535	18436	A	4565	59	325	VARKGNLVSPVIFYPLDIEEVIETPLN VLSSFDGEKVELEFFFFFPPFKKSPF VTQARFQWPNLSSLKPQPPRLKQFFCLG LLIT
4536	18437	A	4566	326	3	PEKEFRRLVIKLIREAPEKGEAQCKEIQ KSIOEVKEIFEKIDRIKKQLKHQETL DILLVMQNALESLSNRLEQVEENSELE DKVFDLTQSNKDKAKIRKRYEQS
4537	18438	A	4567	333	209	EQAFDPYGTLSGGTFSFKHFFPHKLMA RPAVALPQVNLK
4538	18439	A	4568	125	2	HNQMSRSIDCSDPILGHNCNLCPGSSD SPASASQVAGTTG
4539	18440	A	4569	212	2	PICLSGKKCYGQNVRIKCHMWKHNHRL GVVVHACNPNSLVQGGGRMRSGVLEQH EQHAETPSLLKTLK
4540	18441	A	4570	142	14	GRVDRSNPGRFLSTSNSSLYRPREIRP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4541	18442	A	4571	2	419	TSQAPSPVNHIIIST ARDSFLHDSQTSFCFSDSIPTPSNMBEET QQKSNLELLRISLLLESLEPVRYLRS MFANNLVHDTSDSDYHLLKDLEGIQT LMGRLEDGSRRTGQILKQTYSKCDTNH NHDALLTNYGLLYCFRKMDKVETFLR
4542	18443	A	4572	3	194	HEGRQLSQLRLRLQRNCLNTGGGGCSE PRSHSPFPAWVTEHGFIQISLKLFIIS HPEPFL
4543	18444	A	4573	2	286	CRDGLTYNDLFLIPGYIDFTADHVLDT ALTKRITLKTPLVYSMDTVEAVMAIA MALTGGIGFIHHCNCTPEPHANEVRKVK YEGGFIIDPVV
4544	18445	A	4574	44	325	RQWLGAEAYITKEQKYSFLHDSQTSLCF SDSIPTPSNMBEETQQKSNLELLHISLL IESRLPEVRFLRSTFFNNLVDTSSDD YHLLQDLEEG
4545	18446	A	4575	374	33	LRLARRSGASLCGRSGGPPPTCANICPR YAPLIPPCRTSLLEAGLVVMVGPDFRV RLVTSERRFRYQPPFPGENRFPCLSLP SNWDIRHAPRLANFNLSLFFFFFLVETG Y
4546	18447	A	4576	400	225	PIFFVVFVFLFVLFLVETRLCHVVQGLE LLGSSNLPISASQSAKITGMSHPAWPRA EF
4547	18448	A	4577	2	372	ARETIFCFNSNIPAPNMDETROKSNLQ LLRISLLILLYRTRLTLCTQLHLIQT YKVNARCSHFSSSTCGPLYSCTLVSL TGLDMKLCHSTLLKQNSALMSLLKIQVN LNQVSPVFNAH
4548	18449	A	4578	349	174	GCGEPRSHICTFAWATRAKRLCKKKLKL QLKNVVKESKHQPLQNFSLTSTINTQ EN
4549	18450	A	4579	3	124	HELLNPEGECCSEPRSCHTLAWTRAR LRLKKKKKKKK
4550	18451	A	4580	181	1	MSSYYPSPCSRLLMATVYNLHLPSSNS PASASQVAGNAGARHYAWLIFVLVETG LCSC
4551	18452	A	4581	227	3	HRKRNRCVSRRTALLFLSLGDGVSPCLKII IIIKVLFWLGEVAHACSPSLGSRGGRI TRSGVRDQPGQGGETPSC
4552	18453	A	4582	257	2	RVRQLGAFSLSPGSGSPSKITGALKING PFRAGFVGSPPYRSLPLGGGROIPRSGD PGPGPLPRGNEVPLKKNPKRSLILPAR A
4553	18454	A	4583	3	94	HEIAMAFLILTERKILGYIQLRKGPNV GP
4554	18455	A	4584	345	50	IYIYICIFLNNRNVSLHCPGWSKTEGLK QSSHLGLPKWDYSHPELCPAKTSHEKA QDRIPKNDPSCPTSPAQMSTNLIGWASS YLOYSAPAYNNKN
4555	18456	A	4585	338	19	PQLSRFRFPKNGNPGSGACSEPLRGLPC PSAVVTKRDSVSKKKKYHTLSGLSTTG IYFSQFWMGLVQASRFGVWGVAWSMI DGAVLLRPHMAEAGARLSGLGF
4556	18457	A	4586	2	224	ARGVGRAGLEIOTSGDPPASASRGAGIT GVSHRVQLLGDRAKFSLLKKKRGIIILPG EFYSPCLKKRPTLNTPDNF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
4557	18458	A	4587	344	168	PPGTVVHTYNPSTLGGQACRIGSLGVQD KPGQHRQGLSLGVEDKPGQHSETSPVQS NP
4558	18459	A	4588	212	328	GLAVAQAGLELLSSNPPFASQSAGIT GVSHHTQPYF
4559	18460	A	4589	110	323	LSNQKNQLYNPNTLLYCVVRRLKSSYDK QAEVQSGKLSGLAQPHGFTPLSGLNLP SSNEYTRPPRPNTNF
4560	18461	A	4590	2	127	ARGCSEPRSRHCTPAWATEQVSKKKKG REKTFGQFFFWVI
4561	18462	A	4591	211	2	ARGSLEAGSSTPAWATINQSTNKKTKDKT ALYWKMPSPRTYKARQKSMFGKSSKDR LTLFLGAKVSLV
4562	18463	A	4592	3	120	HEKTRTNPIKRWKVDNRLSKEDNDN KINGWPGAVF
4563	18464	A	4593	388	227	GHVGQDGLLELLTSDAPPASLSQSGITG VSHRAQPKWLLFQHRSPCLPEAAGK
4564	18465	A	4594	1	348	PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PLPPPPPPPPSSSSPPNPATTSSVA C
4565	18466	A	4595	2	138	ARAARGFRHVQAGLELLTSGDPPASAS RSAGITGVSHHTQPTNF
4566	18467	A	4596	315	2	ALKPNYSSTSMNFKARLPQYNINNLNLA PLYSSTSNQINII VI ILINKENHTLFP CLVNSRLKQSSHLGLPKCWYRRELLC LACDKFFIYSAPAIQLLSC
4567	18468	A	4597	1	146	GTSVDQSGLELLTSGDPPASASAEIT GVSHRTQPLITIIQLYLYC
4568	18469	A	4598	293	3	GGTFWPRKKLGRKQFPHRPPGSGNDPF SLLFFFLRQS FALVAQGVQWCDLGLSL QPPPPVNPFLRLKQFGPSTSCFPILPAS GSGFFGREAASAC
4569	18470	A	4599	174	2	RSVAPFLKSARPTQYRKEPTDGTGSPQ PPFRFRFSLCLTRLSSWDYRIAPHPAS C
4570	18471	A	4600	59	252	LAPFGHELGTSESAHOTDNRIHLEGYOK RLDASGLERASYPLAAEFKVGGRGSSQ PLTLCGYP
4571	18472	A	4601	233	366	IHYFLDAVAHACNPSTLRQGGRIITRSR DRDYPGGHGETPFLLK
4572	18473	A	4602	182	325	LFVFCFLRQCKSVACAGVQWHDHCSLY PQPPSLKQSSRLGLPSWDY
4573	18474	A	4603	202	2	GGSSSGLLRCPAVLGLKQSSYLSLVRWR DHNSWLKRSTHLGLPKGWYRREPPHLA CILKPSINLV
4574	18475	A	4604	317	2	FRLGPOVFFSPPGAGFFFCGPVWGPGPF SRSLQLLTFGAKFFFLCLSLPESFGAPLR GPPSGFMAHCFFFLVLVLEFFFRDVSIL LCCPGWSAVAIHRDPTTARA
4575	18476	A	4605	233	71	FFVLLVEIEDQLNEKKQEGKIRKKRMK RNKQSLQKIWDYVERPNLAGHSGLR
4576	18477	A	4606	114	1	HFRPARVSSCCPNWSAMVSRLLAATSAS RVQAILQSR
4577	18478	A	4607	348	3	LKFNQFQGVVHGARCPSFFGGLGRGIFP TPEVEVLVNLGPAPALPFWPPSQTLFSQ NQKKNQKKQERKERKERKKKKKKER KKKEKERERKEGRKKQEQEKRTAKSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LG
4578	18479	A	4608	174	3	TVVVVVQCCVFCVCLLKQGLASPRLECT GIIIAHCNKLKLGPSDPPTVEKTKLV
4579	18480	A	4609	171	334	DPHSSLNIRFSRVAQAGVQCNLSLQ PPPPGFQRFCLFSLPSSWDYRCAPP
4580	18481	A	4610	2	164	ARGSRGHIWSAFCHVQAGLELLTSRPA LASQSAGITGISHRAQPLNTLYSMS
4581	18482	A	4611	2	164	AREPRGHIWSFCHVQAGLELLTSRPA LASQSAGITGISHRAQPLNTLYSMS
4582	18483	A	4612	180	334	CCLMGSSVLLPRKFNLTLAGFGLQQRKS LIRPGMVVHACNPS TLGGGGWGI
4583	18484	A	4613	189	1	SGFSRVVENGKCKGKGQSLVLLPIR VFFFFFPEMKSHSFAQARVQGNLGLS LQPLPLGFK
4584	18485	A	4614	216	358	KSTPRILGTVAHCTNPSTLGGQGRITRS GDRDHSGLHKGTPRLSKNI
4585	18486	A	4615	179	393	EKQEEGSGWAKTEDGVMLMLSEAGIS CWIKAFILDAETFTFHADICTLSEKERQ IKKQQTALVELVHKHP
4586	18487	A	4616	2	126	ARVQRYLFFFLDGLPDPMSIRGSVP NQMMERITPQSGK
4587	18488	A	4617	338	181	RVGEAGLELLALSPLASDSQSAGITDI SHHTPQSPFLEHLLVPRYRISGK
4588	18489	A	4618	3	197	HEKREPVONSTVEETIASSDYMLRPLPL PFCFFLFFPKIKMGVSPCCPGSCQTPSL KQSSCLNV
4589	18490	A	4619	1	339	GTRTFGSGNGPTKPDLLQLRLVATERGL VIVNCTHCLQAVVTTDYAAGMAMAGAGV ISGDFMTSEAAALAKLSYVLQPGLSLDV RKELLTKDLRGEMTPPSVEERRPSLQGN T
4590	18491	A	4620	3	306	LEPGDGGSCSELKSCHTPAWVTERDTS KKKKKKKKGGPLKGTILGSPKFNQGNQK IPSGQGGQKKPNLGLGRNLNFGGKKNW NKFLTKIKVLRKKNF
4591	18492	A	4621	397	29	NTKEKILSARKNNQVFPHTQKKNFFPK KRKNFREGIPNFPFPKSPQKNHPPQ KKKPPKPKKTIARPPKRAPPGAFKKK PPPPFLSSLCISYSFIYFFSLINLFF FFFFHDSVY
4592	18493	A	4622	2	235	VSLCHPGGTISTHYNFCLPGSRDPPTSA SAYALLIFVFFVETGFPLVAQAGPKLOG TNSIPASASQSAGITGMNHCT
4593	18494	A	4623	209	324	ILRVLSGTVAHACNPS TLGARGRQIMR SGVRDQPGQY
4594	18495	A	4624	52	287	NFFSFLFFSFLSFFLFFFLFKGPRRGA RAQKGKPHPKKKKKKKGGGKNKTQKP PSFLKPGRPGPRGKGQTTKPGP
4595	18496	A	4625	102	1	THSFFVSISLSLHSHTHTHTHTHTEIY RVREIR
4596	18497	A	4626	125	1	DRHVPQHTANFVVLIEMGLFHVQAGL KLLTSNGLVPLV
4597	18498	A	4627	3	167	ERLRQGNCTNRESEGCSEPSPHCTPAA WATQDSVSKKEKKKKKKKKIV
4598	18499	A	4628	135	3	AASTLSKGTITAGGNLCLPVSSNSPASA SRVAGITCARHDWIL
4599	18500	A	4629	320	210	WFLGTFRRVENAESVNIDLTYDQSTT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4600	18501	A	4630	98	326	DTGKTPSS SSPTLAFQFYFFSCATKEAVKLSFPKSL LLGTGSRSSVAQPGQWNNHGSLOQPQPAQ LRLSSCLTLVSGWDHRCAPP
4601	18502	A	4631	275	2	RVKLLLVFMRQSCSVIQVSSSTVNGSL QPQPGFPROSSHVSLLSRWDRHKMPCL ANFFLFWRAGLAILFVHSLVNTESP LISIKSN
4602	18503	A	4632	180	1	KGLTLFYVFFVFKMRGLAMLADSSQTP ELNQPSCLGLPKCWDFRHEPHPPVKEFK PFFH
4603	18504	A	4633	234	5	KPLRDKPLRSFSNLEPKNNLFFPPFPQ KINGFFPPFFFTESHCVTQAGVQWDLDS SLOQPSGLRQFLCLSLSS
4604	18505	A	4634	171	2	GRVDILTFWQHFTLFSFFSFWQGLSV TRLECSGVIMAYCSLDLSSGNPPPTSAS
4605	18506	A	4635	324	211	LRLNIIFMPTVMNPGMYTGSCMCVCVCVC VCVCLCVCVC
4606	18507	A	4636	95	1	MROSNLSPRLCSGTTIPAHCNLCPGSS SNS
4607	18508	A	4637	234	1	KKGHDITLTKAMPVTLSSRMSINVCCK IYKVKNSPNYSSLTHHINNIKPSFTRE NTLMFIHLSPILLSLNPDIT
4608	18509	A	4638	2	243	WGKVNVDVGGGALGRLLVVPWTHMYF EFFGAFYISFCFLFLIFPHLFFVSSIHI VSSFYLLFYNFPIIFPTLCHFFFL
4609	18510	A	4639	118	2	GRVDLQCSGATSAHCKHLQRSRHSFAS ASQVGAHATT
4610	18511	A	4640	50	168	NRINKMHLITFLKXKKKKKKKKKKKKKK KKKKKKKKKK
4611	18512	A	4641	315	87	GIFLDRNLALLPRLECSGTTIAQCNDL LLSPKDSPASPSVPARTTGVPQRPDRLT LFELIYIRYKGMIFSQDC
4612	18513	A	4642	383	2	KFKKKKFAAGKAPARLSPPFLWGPKGGF PRAGVLSPPGPPGETPFLKNPKFPGHG GGPRSSPFFGGLKGENSLTREKGGPINP NLAPAFPFPKQGNPFPFPKKKKKKQRS SPAWNWDVGTGNAGK
4613	18514	A	4643	3	205	LKRFCSLGGQCSSEPRSCQCIPAWET QDSSIKKKKKKTRPGGLTLEPPFPFG VKPKGPIAGAI
4614	18515	A	4644	149	1	FFPIKADLVFFFLRLRLADSGAGVQW HDLGSLQAPPQGFPLPCLSL
4615	18516	A	4645	474	344	AITHENYLPSSASGDCDEDLQAACITLV NALMDHFQRLAAHTV
4616	18517	A	4646	165	357	LCNALSHLLPOCTFTPLISILCIIDTIS LLIQPITHAVRLSANITACHLLMLHILL STLSICTL
4617	18518	A	4647	2	339	ARGENDLSPGGGCCSLRLHCTPTNAT RVNCVSQKKKKQPKPKNQTKPNQTRK GSPGFLLNLKVISPEKSLNPNILKTAP KVTRFNWLTPEIPFPWMEEKSGPDPRIR
4618	18519	A	4648	313	187	LTSGDPFASASQAGITGVSHALPPIV QPPSHSLTPTPLFC
4619	18520	A	4649	236	324	GQVMVFGMMAHACNPSITLGRSRWIVRS R
4620	18521	A	4650	225	313	GQVMVFGMMAHACNPSITLGRGRWIVRS R

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4621	18522	A	4651	240	76	FCVHAHNTHTSPSQASGSSEHMHYTH PSGSPETHHTYTHITFLASRAEPOLP
4622	18523	A	4652	273	379	KQLAAQCVRLSPSQAIASPVTCYMPR WPEVTEE
4623	18524	A	4653	369	189	GTVKQAGACRNLGSLQTPPPGQFQFS CKSLYSIMCYSKDCTMTLGIIRANNR LHL
4624	18525	A	4654	168	346	DRICRASSYTIHMLYFVFLIFLFYWI YFLFFVLHFHTIFILFYSFIILLLL FYN
4625	18526	A	4655	56	354	WKRTFFFFFLETGSGFASRPCTLLFL YSLGPNRVLIRVFLFGSSRCYLYFL LGSLFLFFIYMLFLIRLFFVFLSGL LLLLSSYYRFIFFF
4626	18527	A	4656	50	186	SACLLCPKCWDYRHEALRPAMYLLTGS YVAQAGLLGASDPPE
4627	18528	A	4657	131	366	DHFVASSSVKEGLFFVFFVFFIFIF FFILVICFFYKFIPIILLIIFIFIF FYFPLYLYLLIFLFFIFIFIG
4628	18529	A	4658	290	155	LEYIVEKGFHQDDKASPELLTSRYLSDS ASQSAGITGHRAPTKG
4629	18530	A	4659	163	372	LRLPALFALEWFFVFLFLVVFQFVL FLFFFTFFLYFLVFLVFLVFLVFL FFICIFIFWFFVFF
4630	18531	A	4660	227	378	FIFFSNCSTALVHPLFVLSRVLKSNR NKFIGRARWLPVFPALWAEAA
4631	18532	A	4661	3	141	RSRHCTPAWQSETLSQERKERRKKK ERKKEKERRKKKKKKK
4632	18533	A	4662	346	3	TFKFLGGVCPFFSPPKRVFSKNSPGGF FLPFFLGENFFFAFPVNGPPGFFKGG PPFFFFFFFFFFFPPPPPPPPPPFQ DSFDNLGIFVIPYKIQDDFSSMSNATS ILIKIAL
4633	18534	A	4663	302	3	GDINRRSHSPFVWSKFPAPCFMSSLDVF YKSSDFFYFFFEFTEPHSCCGGISAYCN LCLPGSSNSPASASQVAGITGVRHHTQL IFASVVETFKITYKN
4634	18535	A	4664	2	76	RLAFTPOLGGHWPPTGIIPLNPLEV
4635	18536	A	4665	1	210	SPTRS PKPTPPYQTTLAEFFFKKKKK KKKKKKKKKKKKGGGAPLKKSPGPKI NRGKKKKFFLKG
4636	18537	A	4666	2	356	GSRPGGKRTARRWTRPWLRLGACLTG MAFAFHQVYIKI KSLRKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKPRG GGFKKLMOGKFFMGOGKIFFFIRGGK KKHGG
4637	18538	A	4667	1	323	RTGTYCYDVCESGCAIQLLLCLKK KKKKKKKKKKKKKKKKKKKKKPPGA NPGKKKNFSKPKRPKTPPGNFEKKPF PGGGPNGAPPKPKNTPEKKKFF
4638	18539	A	4668	167	446	ELNKLCLPKKKKKKKGGGSRQKTRPK KKKKKKKKKKKKKKKKKKKKKKKK KS
4639	18540	A	4669	321	52	GVFSFSPKFFSPKGLNFWGGAPIF SPPKKRFSSKXPPGGFKYPPRLGKILW GPRENWPGPGFLKAPLFFFFFFFF FFFWG
4640	18541	A	4670	82	359	NAYGIILKGNEDTKTVKWKSSCOLANT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WEFHIRALLGPNCFLLFKRRGLTLLPR LDCNGVII IHNNLESGLSNPPMLASQV ARTTGLCY
4641	18542	A	4671	249	60	LLIFITYFYFFLFFFLFFFFFFFFFF LFQVQHLVPVHLCYDLSPLYKCVGLVK CPFKYT
4642	18543	A	4672	2	319	AAASTLVFVSFFVVLGFFFFFFFFFWG PPKKILKKKGGGGGGGGGPRGGPRGG KRNPGGQKKGGGGGGGGKKERNFGGG PPRGKRRGGGGGPNPKGGGLK
4643	18544	A	4673	3	451	HESFNPIVISOLERGEDFVLDLRKAKK SQGLWSDYDNLKYDHTTACTQDLSLSC PWCETKGESQNTDLSFKPLISEQTVIL GKTPGLRIDQENNETKQSFCLSPNSVDH REVQVLSQSMPLTPHQAVFSGERPYMCV ECGKCFGRS
4644	18545	A	4674	446	189	SISLSTLVNVCQLISLSDPASGFVDHVC CIFTFYSINFALLILFLFYGLVWAAAI INHYRLHGLNTKHLIMIMWVGSPRLSC G
4645	18546	A	4675	26	170	HLVVFLVIVAHWASSROIISHWKNCTR DCPVCLPLKNASDRKNQSQK
4646	18547	A	4676	3	378	HEDEFDKMGNQHALLAEAMEQOSISLAK AGVVCILPARTSI IAVAHFSAGLYLIFN TVSVVFFFSNFI FLILSLFNYFCISYI ILFLIFIFIFISSLIVFFCLISFRFL FFFSALSRIFY
4647	18548	A	4677	18	242	PIGLALSPLKESGVII LAHLGSSNPPPT SGSRVACTTGHHAQPHCFNCFPMSS EVECLFTCLLIHILSRA
4648	18549	A	4678	288	2	PKYRWVFEKPTTASENAETPSERQKEGI KLTIIRISSRKKKDPSPKVLPEPETQEK PEKEEETNVGRTILRRSPRISRPAPKVA QIRDPKAHKKK
4649	18550	A	4679	340	208	SVGQAGLELLTSGDPATASQSAIGITGL SOCYPDPSVPETFLPI
4650	18551	A	4680	4	379	EENTGINLHDLGPGNGFLDMAPKAQATT AKKKKKKKKIKISPLFLGGLPKKGKK TPPGKGNFGNFKFGGDLTPKIFGDPG ASTKKKKFPLKGGRLKKTFFKKKKKRG PHPLESPSPFSVF
4651	18552	A	4681	1	350	SRFSGAKEAKMKKRTGYTTVDISQWHR KEHFEAFQSVQACTYNTQVQLDITAFLEK TVKKNKKFYPAFIHILARLMNAHPEFR MAMKDELVIWDSVHPCTVFHEQTET SSLW
4652	18553	A	4682	365	45	SPKFWFVASYDPYAGGPRTPRPNDSRDET GSHSVSESSSGSDSKRESTSSDREANEP SHRASPEPEPPPTNKWQLDNWLNKN
4653	18554	A	4683	238	372	SATPLISSFSFLFFFFFFREGVNLCHP GWSAVSRDCTTAAVWPG
4654	18555	A	4684	3	462	KTESREAVEKEFEPLLNWMDKRALDK IEKAVVSQRLTESPCALVASQYGSNGM ERIMKAQAYQTGKDISTNYASQKKTFE INRPHILIRMDLRIKEDDEDKTLDLDA VGLFETATLRSGLIPDTKAYGDIRERM LRLSLNIDPDAR
4655	18556	A	4686	410	0	FFFFFFFFFFFFLKGKGGFIKFL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4656	18557	A	4687	151	2	IFFFFFDVRQWHLGLSLQPLPPRFQQFS CLSLPSSWEYRHAPPRVRPRV
4657	18558	A	4688	342	183	FFFLFRWSFALVPQAGVQVCGLSLQPL SPGFKRFSWAEVGLHEPRSQRLQ
4658	18559	A	4689	126	404	NCQVWPLRPTGHSVFSVHPQWFLFYCF ALYFIFLEMGSYSVTQAGVQWHSLSLQ PPQWSYVLTFLWHPSSWGYFQVNHLP FDCKVPW
4659	18560	A	4690	2	128	GESLFYIVSPRDVVAKERDQDDHIDWL LEKKKYEVLILL
4660	18561	A	4691	407	2	YFFFLPRMKIFFPHQKGGFFFGGCPPI SPPPNVEVFFSPKEGGFFSPPKRVFFH NPPEGFPPPPFFMSPPPPPPPPPPSLF LILLNQKKKLSACVELRSCCTPM
4661	18562	A	4692	1	176	SRRLNPGGCGCSEPRSHCTSTWSTERD SVSKKKKRPFFALKPLGEANVKPTIGG KN
4662	18563	A	4693	1	403	SKAEIGRRLGLRLQTVSQVNAKEFLK EVKSATPMNTRMIKRNLSIADMEKVLV VWIEDOTSRNIPLSQLIQNKALTLFNS MKAERGVEAAEEKFEASRGWFMFRKERS HFHNIKAQGEAASADVEAAASY
4663	18564	A	4694	343	425	HCFLSLQLNSFEQLCTINYTNELQLQFL
4664	18565	A	4695	395	2	KNKGLFFFFFLRWSFTLVTAQSNVTAV CNVTILAHCNLHLPSSNSPASASRVAG ITGSCHQG
4665	18566	A	4696	429	0	VTWKCYITKKKKKKKKKKKKKKKKKK KKARG
4666	18567	A	4697	371	217	IPVFKQSSCLSPFRSWDYRHMPFCVTQ KKIEYQHISLYKPKSKCALFLI
4667	18568	A	4698	415	59	LOQQCECFISELTKKKKKKKKKKKKKK KRGGLKKKKKGFFAPYPH
4668	18569	A	4699	431	0	LKKIFPPGGRVLSPPPPPPPPPPPPPP P
4669	18570	A	4700	371	245	TLGDPPASASQAGITGVSHHAGPLFGI FIYKFTYICRKT
4670	18571	A	4701	410	0	KQCWFTQKKKKKKKKKKKKKKKKKK DRG
4671	18572	A	4702	340	402	PFAGGGYRLGAAPPEESAYVA
4672	18573	A	4703	188	2	TSLPKCWEYRHPPCPAHTLLIFFFIF VDMGSCHVQVALELLGSSDPPTSASQS AGIIGM
4673	18574	A	4704	423	34	LKKKKKKKKKKKKKKKKKKKKKKDL KKMVGNGYKNVGAQILGYKLCFSPF YRVF
4674	18575	A	4705	2	297	PRVREKEMASMKFEFTRLKEALEKSE ARRKELEKMVSLLOEKNDLQLQVQAEQ DNLADEERCQLKKNQLEAKVKRBN ERLEDEEENRSLP
4675	18576	A	4706	2	179	QENGMNPGGRACCEPLRYCTSSWATER DSVSKKNEKKRSASLRRLPFGALTGR KAS
4676	18577	A	4707	432	578	PRIVCPQELRKPYSAEICQRTSKEPPSS PLQPSSSSSSS
4677	18578	A	4708	419	35	GSFFFFLKDQFKKKKKKGCCPPPPPK IYPPPATKMGGGGKKPPPPKKRGP KNRGRKKKPPKKKKKKFPKKRAPQK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, /o=possible nucleotide insertion)
						TKKKPPPIETFFLYFFKNIFFFFFFFFFY FFPPFFKPIFNLLKFF NFFFFFFFFFXFFFFFXKXFFLFFF *FFFLKLLKIFF
4678	18579	A	4709	147	31	HASAHASDQPERLNAGTYFLFVTLVGLS PLLIALIYTHNTLGSINILLTLTAQEL SKKKKGGGAVLKNPWGAQS
4679	18580	A	4710	3	229	PTFRPTPRSCSELSHCHTAPAWTERL KLKKKKKKFFNLVSGVKILGLKG
4680	18581	A	4711	1	158	KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKHPSRGGAKK KGGGAQNRAGGRRRPSRGGGKQKN
4681	18582	A	4712	163	404	FEPEVYIKSRQKRKESNPKLVSOPHG LHDFPKKKKKKKKKKKKKKDGSGPLK KKGGAQNKPGGKKNFFLKGKKKNPW GFFKKKTFPGGKGKIGAKPKKKSLKKK KKFLRGKGKKT
4682	18583	A	4713	3	378	VSNPAVSVPHLFFSVYKSSPMASMTFSK KKKKKKKKKKKKKKKKKKKKKKGGPQ KKKPGAKNKPG
4683	18584	A	4714	2	208	SAPPTIFFLFFFLFLFFIFFIFFFFKQI LEKKGPPPPFFLFFIFFIFFFFYRMGC DRWNFILIQSTFHRKQKPVLV
4684	18585	A	4715	290	56	GGFKIKFLTQFLFLFSPMFLISKSP AYLWQSSPKQVPMVVGKTNFLVLSIECK KEGIYFFCIPFVPPGPHPKILCSLLPF LAFLLRRSLALLPRLECSGAILTHCNPL PGSSNSHAWA
4685	18586	A	4716	50	424	GRFGADFRVRPQLLQRFIFYLFTENE SCSVTOAGVQWCNGLSLQPLPPGLQ VYTTAMAEIEEYPAWGSVEVLVSVLVG LWMEVGSTRP
4686	18587	A	4717	161	2	GNQGGYGGGYDNGYGGNGYSGNPFSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS
4687	18588	A	4718	2	416	QPSGISSTRSFKTILPAAQDVVYRDE IGNVSTSHLLIILDDSVEMIRPFPLFG GWKTHYIVGNLPSYXYLVNLGQYALK MRFDVHVDFEODVSLTVKILPEGAKN IEDSPYEISRAPDELHYTYLDTFGRPV IVAYKKNLVEQ
4688	18589	A	4719	1	173	DAWAGPHYVQAGLELLTSSILPASASQ SAGITDVSHTQQLDVPFSPSLPLPHQC
4689	18590	A	4720	3	201	LKPGGGGCSEPRSCSTPAWRQSETFS QKKKKKGWGLERIGWGGSTNNAGKNQR GEKPGKKGGF
4690	18591	A	4721	2	183	LKPGGGGCSEPRSCSTPAWRQSETFS QKKKKKGWGLEIICWGGSPTNKRATNSP VEKE
4691	18592	A	4722	2	395	ODATSPITIEELITFDHALIIFLICFL DLHALSLTLPSALT
4692	18593	A	4723	1	3	SFSPLEENLGNITQIDIGRKDKFTSKTPK AMATKAKID
4693	18594	A	4724	388	44	WLFFFXPLFFFFFWGGIIFLLKKLYIF FFFMKIIFFFFFFFFFFF
4694	18595	A	4725	223	374	FFFF KKKKKKKKKKGGGGGNPKKKKGRMEK PPGKNRGEKKKNFLKKGGGLFKGK
4695	18596	A	4726	41		
4696	18597	A	4727			

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KPPKKKNGGRKPWKKKNFKKKKKAPFF LGPKI FKKKKRGLKKKLGFPSQSVGP
4697	18598		4728	323	69	FFFLRQSLGASQAGQAGGNLGLSQPLP AGFQLFLQPPPPGKQFGRNLNLGNKDL WGLPVLRAHPQAPPLAFIL
4698	18599	A	4729	3	197	CLALLHLSRQROYALPLGLGPGCPHIHT HSHTHAHDHITYTSPHAHRHAHTHTMM TLFYTTTCI
4699	18600	A	4730	309	443	VLTLSPKRLCCSMNIHAYSLKLLGSSDR PTSASQGGIGMSYHA
4700	18601	A	4731	3	172	DWAFFNGPGVSLGCGWSTFPQLKRST CLSLPKWDYRPEPLSPAPKTLFSLVLL
4701	18602	A	4732	98	232	QTVLLIWLALCSFGVQLTKRFLERF CIFSLIVFTICLYRN
4702	18603	A	4733	238	1	LGPPPPSFLGPPFLVIFKGFSEFKTDL FFSPFFPGPPPPPPPPPPPPPIRRSFAL VTQAGVQRDLGSLQLPLPGFKR
4703	18604	A	4734	121	424	LTOGHRVVIYFSQLRVRGRQACSTLL GHLPKVVRMFPFLSFTVAGLEPTSHYR MFVDVVLVDQHHWRYQTGKWQCGKAE TMFGAR
4704	18605	A	4735	319	8	NPPQKKKKKIFPPPKKKTTPKKIKKNPP PFTIFFFFFFFFFPPPPPPPPPPPPPP FFYPQHVNFCFEIIHVIFFLIEVLFLAF HVGDSIADAWSTKSNRTK
4705	18606	A	4736	297	442	TQGFPGGPRKIGFFRGLKNGGGGNPK LRFLKPGQLVGRGKTKKNGG
4706	18607	A	4737	430	0	CVLGSKDKKKKKKKKKKKKKKKKKKK KAKKKDS
4707	18608	A	4738	137	1	INYYFFLKQGFPLLRFLRCSGAI IAHCS LEFPGSSDPRPSASQVA
4708	18609	A	4739	188	3	ISPKALNPRREVGPIPPPPKKKVPQNP PGGFTTPHKEKNFLPPPNLGPDPKDP LKRPP
4709	18610	A	4740	188	2	TSLPKCDYRHEPPCPAHTLLIFLFIYF VDMGSCHVQVALELLGSSDPPTSASQS AGLIIM
4710	18611	A	4741	410	1	RRPGGGFCPPPPPKIFFSPPPPPPPFVGV LPQTPPPPKKFFLNPPPPGPPPPPPKKK KIFFSPPPPPSPPIFFPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP GKDRVSLCCSDWSTGPKPSLL
4711	18612	A	4742	225	444	ENLKLKSFCSHFWLWENLTIGALS SFDEAALLFFQNDTYNPGTVAHACNPST LGCGGRITKSDRNHS
4712	18613	A	4743	2	452	VSNFVSVPLHFFSVYKSSPMASMTFSK KKKKKKKKKKKKKKKKKKKSGSPQ KKKNR
4713	18614	A	4744	3	144	LAAVLLKGGYGIIRLTLLNPLTKHIA YPILLSLNPDITGSSL
4714	18615	A	4745	206	2	IQNPQTERVNSTSLKLISSKDTINRAK QPMDEWICKKHIFGKELISRMKELQL NNKQIVPPTP
4715	18616	A	4746	523	178	RHRRFFMDIEREOKVEQORQKEKKKDIE KIKDKREQECYAAEQRLRMNPHEDPYS GEKLSIILAQLQLEIKGTREKQOREKE YLRVVEALRAQIQEKMOLYNITLPLC
4716	18617	A	4747	3	518	ENRLNLEGGCGCEPRSRCTPTWAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4717	18618	A	4748	491	145	LCHVGAGLELLTSSDLEFLASRSAGIA GVSHRTRPHSHFYFFLYSSSFFFFFL AQRGNRAPRGKKTPEGLATLNIXNSGV FWFLPLGPGFLKREPTFALGLKDRGNL V
4718	18619	A	4749	6	362	NKLPNGTEFLSSLVPNTFFSFLFFPFF FFFFFWGKGPPRGGGCAKFPLEPPPG VPPPPKGGKGGPPPTNLFKKKEGGS PFGPGGVKTGPKGFPFPPSPORGKKGQ WAQKPP
4719	18620	A	4750	380	3	SLLLAFALLCLPWLQEGAVOTVPLSRL FDHAMLOAHRAHHLAIDTYQEFETYIP KDQYSFVHDSQTSFCFSDSIPTPSNME EPQHSNLELLRLISLLIESWLEPVRFL RSMFANNLVYDPS
4720	18621	A	4751	1	345	LFYIFKKTSSLFCLFMMCVFIFFFFL LFVFFLCGLGILVSFIPGGEKREKKR RGGEKKKKKQNVFKKKKNPWGGGGGL KKQRARGGKKKKKGGGGGGGGKKQSP LRG
4721	18622	A	4752	1	407	QEFETYIPKDQYSFLHDSQTSFCFSD SIPTPSNMEETOQKSNLELLRLISLLIE SWLEPVRFLRSMFANNLVYDTSDDYH LLKDLLEGITQLMGVVRVAGVNTPGTLP ASRAGGEKYCCPLPSNKARDQEN
4722	18623	A	4753	357	1	PLFFFKRNLFFFFFFFKKKEKAPVFFP FPPPSREWGQFFPRVGOVNTOLHPFFF SQNTSVFFSTLFFFFFFFFFFFFFF FFFFFFFFFFFFFFFLFYCFIYFSR DRGLTLL
4723	18624	A	4754	1	207	LGLAGVEEVEASRLNAGGGGCSKPRSH WTPAWAMEQDSMSKKTNEYQRRQLHL QSSTSGFLVHQ
4724	18625	A	4755	2	336	HEERERERERERERERERERERERES RAQFRANKNSQAPHPVCTLWTEEGGS FYPLTEKDAQACERAHFVCLVGSHPGW GLCKMNPCECARTHSLHGDAIDISGVL
4725	18626	A	4756	230	446	VGFSSLSFRYCTYLISASSLTKLECEK RSFLFCFAFWLLGLFLQSLALSRLVYN GAISAHCNLLHPGSSD
4726	18627	A	4757	3	390	QTSFCFSDSGFTPFNMEETOQKSNLELL RISLLIESWLEPVRFLRSMFANNLVYD TSDSDVHLLKDLEGIQTLMGRLDGS RRTGQILKQTYSKFDTNSHNDALLKYN GLLYCFRDKMDKVETFL
4727	18628	A	4758	234	387	LAKIFLSFSSTATGWENRQSPATGRTP VFVSPIPPLPPPPPPAFVT
4728	18629	A	4759	396	0	IYTHITHRTHHTIYIMYVFMIL
4729	18630	A	4760	176	384	MVIFLPLNKDTQHILFWGYVLIFFFLKR NFVFWAAGGGQGRYFGSLKPPPPRLKPF SCLSLGTDWYRR
4730	18631	A	4761	419	208	IYPPPPFPWPKGGSLKKKKKKKPGPG VPPFIPPLPGGQAGGFPSKIQTTPAPQ GKPLFFQKNQNYLA
4731	18632	A	4762	158	2	GNQLNPPFPSPGSFCLFFLRSLALVT QARVQHWDGLSLQFSPSGFKRFS
4732	18633	A	4763	489	398	AGFELLTSSDPPASASQSVGITGMSHCT QP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4733	18634	A	4764	420	1	FFFFFLGELFPFGGKGGVFPFPPPLKKFF FSPRGLFFLGGGGNFPFPPKKRVFFKKP RAGVFPPPGVLRKPGPGFLTPPQKEKN FFPPDPGVLGPPKGGFKGGPPFFFFF FFFLGKKKKKALFFTCKKGGGTVRKA
4734	18635	A	4765	167	3	IYFFFFLKKIFFYKKKINKLKKKKKKK KKKKKKKKKKKRAARDLELAHAS
4735	18636	A	4766	424	222	FONIHKKNFSPPLKLTGPAPLFKKPK KKKKYFFPPPEKLGPPEFLKGGPPPPF FFFFFFFFFF
4736	18637	A	4767	254	423	VTKSARRRNNKNDWGAVALSCNPSTL GPGQANFLRSQVGDHPGQHGDTLSLK
4737	18638	A	4768	363	0	KTTTSQARQPTSVIPAAQETAGDSSNP SGYGSYSSSSSP
4738	18639	A	4769	51	169	YVTHVDRITGVFKKKKKKKKKKKKKK KKKKKKKGGF
4739	18640	A	4770	188	3	ISTKALNDRREVGFIFPPPKKVPPQNP PGGFPTPPQKEKNFTLPPPVNLGPPRDP LKRPP
4740	18641	A	4771	1	131	KEDKENALDRAEQAEADKKAARGKQLE DELGSLQKKKGGP
4741	18642	A	4772	363	452	RLECSGMIIXHCSNLPQSSDSPTSASQ LA
4742	18643	A	4773	121	1	RPRRPVQAQGVQVHNLSSLQPLPPGFQ FHLSSLSSWDY
4743	18644	A	4774	31	226	MISSQLSIPTPTQEGGLKKKKKKKKK KKKKKKKKKKKKKKKKGGGLLKKILG QAKFLGGEKKNFFFF
4744	18645	A	4775	161	1	KPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP WGLKSADAL
4745	18646	A	4776	394	67	SPPRGEGGVAPPPPPKFNFFPRAVFLG GGGGPMPPQKRGFPFKTPGGVFKPPP GKFFPPPPGEGGPPPEFFKGP PPPPP FFFFFFFFFFFFFFFFFFFFF
4746	18647	A	4777	2	409	GVCIFSGHKHNKAPLFSVLYSTQVINS LEKKKKKKKKKKKKKKKKKKKKKKK KKT
4747	18648	A	4778	456	0	FFYKKKKKKKKKKKKKKKKKKSS
4748	18649	A	4779	438	0	LLKIDKKKKKKKKKKKKKKKKRTSKR GG
4749	18650	A	4780	58	330	SPFYQLKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKK GKKKCGGGVLVGKPHKEKKGKKKN FGG
4750	18651	A	4781	435	73	FFPPPPRGRKFFFKKPPGGKLFSPPELGV FFPPFLKLTFFPSTPFFFWGGFPFPP DPKKVFFPKPPGFFPPDPLKKKFFFP PPFFLPDGGFFSPPPPPFFPPPPFF FFFFFFFFSP
4751	18652	A	4782	420	109	LFKKFFSPTEREGVFPQPPKFFPFSN PLFFGGGGAQNFPPQKKNFPKNGPFF FSPPKKKKFFSPPKKILAPPGYFFKGP PPFFFFFFFFFFFFFFFFF
4752	18653	A	4783	230	2	LGLVVGALYSFLLGGLGRKFLLPWRPR VPLTPISPPPSRLGGPPKKKKSQAWHA PVVFTTREAEGGSLEPRRL--

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4753	18654	A	4784	271	440	VLYSRDNNKSKFMNTYTIGIPGAVAHACGPSTLGGGGQIMRSGVRDCKPYRHGET
4754	18655	A	4785	2	266	KKVGITIFCSFSLSLFLKQDGLAPLPRLEKSVVFAAHRGLGLLWSDPPKSAFLVAQICCHHHAWLIFVKVQPSNLMGPWSYTWSAVD
4755	18656	A	4786	216	435	HRSGDSSLKKKKKKKKKKKKKKKKKKKKKKKKKKIKKFKWFKGPFELGWGKKRSGGG
4756	18657	A	4787	249	437	MNNEVVLTKTETSREDDVAHACPNSTLGGGQGITRLGVDDQPCQCHGEAPSLPENRKYLAWSV
4757	18658	A	4788	107	368	AHGSLDLFLPGGPKKSHQWFPKPKDGKPPDPFKKPLKKKTPGKGGGHPTPGARSKKGGYPRGGDPGGPFFPKPKGQKKKTPFLLRD
4758	18659	A	4789	1	225	PTRPFTTNITFPASPOTITFLYLKLTALAVTFLGLLTLLDNLNTNKKLKSPLCAKKKKKKKKKKKKKKKNEG
4759	18660	A	4790	2	216	SGRNSRVDGRQEAACRDYQSSLEDLTFNSKPHINMLTILAEENLPFAKEIVSLIEAQTAKVFIHPAASYF
4760	18661	A	4791	389	30	EKKSPQKKKKKFPFPPQKKFFSPPNQKTCGGGGPKPPPKKKGSPQINPKGVKKPPPKKKKKIFPPPKKKGPPPKILKKPPPPFFFFFFFFFFFPPFFFYSLFFSFGFSYKIFL
4761	18662	A	4792	164	3	LFPGGFNPVGKGEKISFPPFFFFETESHVSIQARGQWRRLGSLHPLPGFKR
4762	18663	A	4793	550	413	AEMGFHVGVGAGLELLTSSDPFALASQSGAGITGISHRAQPHRIPC
4763	18664	A	4794	456	352	RSQDGLYLLTSSFACGLPKCWDYRRRFPCLAVFF
4764	18665	A	4795	242	3	KPFSGGGGAFQTAFITFGKKFVVSRLGLLKKKVLKLPQAFFFFFETESHVAQMGVQWRSLGSMQSPGPKRLS
4765	18666	A	4796	218	346	GFSCFVFETVSLCRKPGSAAVVSRLTATSASRVAAILPQPE
4766	18667	A	4797	383	80	KFFFNQIGGFFFPDPKNFFSLKPFPLGQGSFPPPPKKIFSKIPGFFFPPLKKKIFFPFRLILADRPFFKADPPFFFFFFFFFRRFI
4767	18668	A	4798	1	126	ILILKSLSTWEGIOGKELEEQHGHCNMTLFSLFAQAVACAE
4768	18669	A	4799	81	356	ILFFFFFFPGGGTFFKKSQVFFKNQNI GKPTRMGKGEKPPPPRGKKKKGGPPTLGKNNKVPWGGAFLPLEEKKKPPGPPPLKKKK
4769	18670	A	4800	1	99	GCSEPRSRHCTLSWATRAKHLIKKKKKKKKGA
4770	18671	A	4801	238	5	NHONSQVNYFNKLRIIFOLYLSLNMNLERSSFKLSMTHSISFSFLSFFFIQSHSV AQDRIKWHDLGSLQPPGLK
4771	18672	A	4802	166	62	IFLSFFFLRLDRVLLCYGVGWSVMVQSTQTPGLK
4772	18673	A	4803	102	6	AASTTESPSVAHAGVQWCDLGLSKPGSRRFQ
4773	18674	A	4804	17	374	FGSRAATLFFFFFFLGRGGFFLGRPGRKPKTPGEGFTRFFDVGWKGPEKTPPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WGKGKGGPKMNLWGAGKIKFLEIKGKSF PRGTTNPFPGPPLFFSPPKTQGGNGLD FSFKLKN
4774	18675	A	4805	59	175	SFYFFLMMKKKKKKKKKKKKKKRGA LKKKTGGGPN
4775	18676	A	4806	406	300	SSGVLSRAPTYFCGQTLTRFQVDIKTS HLPQEA
4776	18677	A	4807	123	1	KSTAWLGTMAHSCNPSLTGGQDQTTTS GVRDQPGKHGETP
4777	18678	A	4808	319	406	LYKSYSSWPNVVAHTNCNPTLGGQGGQI I
4778	18679	A	4809	236	351	GFWPAPGVHACNPSILGGQGGRVTPKL GNLLGQHG
4779	18680	A	4810	173	2	EVLFLGFRSILSLQMNLYLYLIAKFA FVAQAGVQHNLSLPPPPRFRKFSCL R
4780	18681	A	4811	2	94	TRILKWQKRKCSVKNGFLTISHGTVSI LF
4781	18682	A	4812	358	2	FFFFFSETESCSVAQAGVQWRDLGSL
4782	18683	A	4813	362	3	YSEVCTISLQQAHSLSVINFLAECVI QLPVLRELFGAVHSPGLSCFSDSG SVPSHTRSPFAKALRLTANHRGCTESG WPFSLVLPFERCMWPGTVAHTCNPSLTG AOGGOIT
4783	18684	A	4814	341	1	WNQKEAHITKSLSQKNKAGGIMLDDPK LYYKATVTKTAWYQNRDIDQWNRTPE SEIMPHIYNYLFDKDPDKNKKWGDLSF NKNWCENNLATCRELEOFLTPYTKIN S
4784	18685	A	4815	2	283	VYTGREILQKKEITIRDOEAPYLLNLS DHTVAISSSTLDCANGVPEPQITWFK NNHKIQQEPELYTSTSPSSSSSPSSSS SSSSSSSS
4785	18686	A	4816	266	3	AASTLQAHRAHOLAIDTYOEFEETYPK DQKYSFLHDSQSLRQPLHTHTGSGVTRT LAASLSGRTAHTRHMTHTQTRKRTAH TNA
4786	18687	A	4817	365	1	SFFFFFSETESRSIGLEFSGTISAHCN LRLPDSNSPASA
4787	18688	A	4818	87	372	ASYKKDRYCMPILRIVIKPOTERKKWL SGLGGGNKELLFNGCNMAVFLVGGGF ETEPSPVTQAGBQWCDLSLKLPLPHRLE RVSCLSLSPGW
4788	18689	A	4819	5	175	FAFLTIPLSRFLDNAHLRRLYQLAYD TYQFEETAYILKEQDQSFQNPQTSLCF S
4789	18690	A	4820	235	351	FEKFFKFFKFFKFFKFFKFFKFFKFF KFFKFFKFFK
4790	18691	A	4821	2	155	IFLLLLIESLEPURLKSWFANNLVYOT SDSDYHLLKLEEGTQTLNGL
4791	18692	A	4822	90	2	LFFFFFETESPSVTQAGVQWHLGSLQP P
4792	18693	A	4823	247	3	KVKGSPSHKRAMVAKGNLSLHMRKSPG ISNYMGSKILFSYFKNCWPGTVAQYN PSTLGRGWIITRSVGRVDQPOQYSET
4793	18694	A	4824	93	407	QHPKKKKKKGGGPGPLNKKKVFHKTFN FFSRQKKKKKKKKKKKKKKKKKKGGG GLLKKFWGGPKFFPGGKKKFFFGGGKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *≠Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4794	18695	A	4826	2	129	NPPGVFLKKNFFWGGEKKKKK TTAHCSLNLPSSDPPTSRSLVAGTTHV CHNAWNVFVCRKG
4795	18696	A	4827	342	140	GGFFFFPPPPFFFKFLPLPPPPPPGPS CVGGVQKFTFPFPQLSRLFFLFFFAP PPETDNPEFFS
4796	18697	A	4828	1	259	GGCSEPRSCHCTFAWVTEYDKKKKKKG RCGKKKLGKGGFQKFKGPNPHGRFLR ESHNSPKKGFKKKFFGNPPPGTSKKVPL PH
4797	18698	A	4830	125	1	KGTFTFETESRSVAQGVQWHDLSGLQP LPPGFRRLTCLSL
4798	18699	A	4831	1	323	ARGEREREREREREREREREREPPL SRGGSEYLSKAWERILLERDPLFFFG GKMGNLFPFPFPFPVGRGYTGGLITGGP FWWGCVSHTHTHTHTHTHTYMSV
4799	18700	A	4832	3	297	TRERERERERERERERTL
4800	18701	A	4833	1	150	ARERERERERERERERERERERKKKN HSRGGGPGPOPLGGGVKKFGGVG
4801	18702	A	4834	1	98	ARGERERERERERERERERERERE RERGAGGPT
4802	18703	A	4835	2	66	HEEREREREREREREREREREAR
4803	18704	A	4836	2	73	PEERERERERERERERERERTAR
4804	18705	A	4837	146	2	FGLVYSISQCLFFVRSLSLVTVQGVQ WRNLGSLQALPPGFTAFSL
4805	18706	A	4838	354	0	PPPPPPPPPPPPPPPPPPPPPPSP SSSP
4806	18707	A	4839	62	358	GLVHDKHSPhGGGCSHHVPLSNFSPFT FSTKSPSPPARALWPPDSRWALQVGH GLTPTTRQESAQAPRRKLALEGSQGQ AQLWTPVIPALWEAE
4807	18708	A	4840	121	13	RPGRPPEFTFPSCLSLPGSWDCRRPP RPAANLYF
4808	18709	A	4841	3	221	LVMGFVFGSSFKSPFYGGALIVSGVVG CVIILNFGGGMGLIVFLIYLGMMVVG GCILDLSLNFNVLNLF
4809	18710	A	4842	3	84	CHCTPAWTANLDSLRKKKKKKKKFRN
4810	18711	A	4843	33	230	LTVTISKAEEVLKHKKKKKKKKKKKK KKKTPKKNPPPPQKQKGLKKIFFFFWE RFLPQKKRP
4811	18712	A	4844	3	368	HELNPRGRSCGEPFCHCTPAWATRAKV HITKKKKKKKGFNLFKPGGSLSNFFPKK KETPWSQNFPEKGPFRFRSGKNPPLA LRGKKKGKSLSGKIFPPFPRGKTPPWA FNGTQKGEYS
4812	18713	A	4845	163	2	HGHISKSLTLTVSSPKSFNQLRPDAVA HACINASTLGRGGWITRSCVDQIV
4813	18714	A	4846	387	234	KCGEPRSCPCPAWATLAKLFKKKKKT KPKKNPKQKQETFPYMLNRVCY
4814	18715	A	4847	189	349	KFRFSQKALLKDLRLGTAHTCNP STLGGQCRWIMRCOVFKTSLAKVVK
4815	18716	A	4848	3	95	HENFYCFSGALGRNEGNIFNPENATFVK EM
4816	18717	A	4849	2	325	DSHTIIMGDPNTPLALDLDRSTQKVNED IQDLNSALHQADLIDYKILHPKSTEXT FFSAPHRTYSKIDHKIYSQGNHETDCRY GKGGGKWKDERDFDVDCSKFKSQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4817	18718	A	4850	241	348	SFFSQTQASEQLTKSQGLALRLTLPVQ FFPPPPRP
4818	18719	A	4851	2	176	LVETGFCHVGQAGLELLTSGECWDYRCE PPSPAYCFLHTIIVTLYPLLCLAFFSYLDC
4819	18720	A	4852	2	191	VGRVGLLELASSDLPTSGSFSAGITGMS HCPWPNFLFIGVFFTVLTPEEYYSYG MTVPLWL
4820	18721	A	4853	67	376	IKCTTFNKKKKKKKKKKKKKKKKKKKK ALKKKPWGQKKTKGKKKKFPKRGKK KRGPGRVLKKGERKIFFWNFKGNFFW GGNGLGQPPPKKLALGKK
4821	18722	A	4854	278	363	IWPDVVAHTCNFSTLGGQGRWTRMSGR
4822	18723	A	4855	3	282	RGCSPEPLRYCTPAWATEODSASKKKKK KKTKIWFEGPGGGVSPFKPHFFKPGGK KPGQGFKNPPFPQEKPLFFPKKKKTKF SPGGGCP
4823	18724	A	4857	382	224	PVIQLIGVGRGKPNFLVGKGFNEPKSP PCPPTWAKONSLSKKKKIKKK
4824	18725	A	4858	392	102	FFFFFPLRGSLVVQARVGCFCNSLGL LGSSNPPTSASLSCLNKKYRWENVTN KV
4825	18726	A	4859	3	111	FHRISQEGLLILLTGSAAHLGLPCWDYR REPPPA
4826	18727	A	4860	282	83	AQIYKQVNGSSGNKICVVCVVCVVC VCIIYIMLCMSRFYKCIKVCNMNDSYV VYIPNIQCYI
4827	18728	A	4861	3	417	NHSLNGRGCSDDPRSRHCTPAWTERDS ISGKKKKKKKKIIFGLREKKLTLPFPLG KKNENSGFPLNPNFFGGGKKATLGPL GLVLRGVPPFRGGETQNGENQKPGTTLE KFEKHFWGPPPLEKISPHGKQTKQ MEEMYKKAHAATLENPVYKKPKKKKKK K
4828	18729	A	4862	1	88	VSLCCAGWRAAVRSQITAAALISRAQAIL PPQP
4829	18730	A	4863	274	369	DPRVRSEKKIIFKILLIDNAPSHPKAL MEIYEEINVIFMPANITSIQPMQGV STFKSYLRNTPHKALAAMDSVSDGSG QSKLKTFWKGFTILDAIKNRDSWEEVK LSTLTGVWKKLIPTLIDDYEGFT
4831	18732	A	4865	341	210	VVMCHVGLLYHQPVIIYRNRIEASEITP HIYNYLIFDKPSHQF
4832	18733	A	4866	206	412	QLCLSQACTLARGNAKGLFYIHRNNVS MFSVAGHTWGPDLVKGQGETCPATIH SDSPSLKITYMTPW
4833	18734	A	4867	248	78	SHEAGLAAQLTVSNPQCTPVFVHAGP FANIAGNSIADRIALKLVGPEGFG EPDGRWQFQIVSSILGLHYGGRIDCWG WARQSGQCPVQCPQPCRGHCIGCNPK KCHPGYAGTKCNDDEHIPAPLDQGSBOP LQPLDHQATSLPSRDLNECCLKPRPCK HRCMNTYGSYKCYCLNGVLMMPDGS ALTCSMANQYGCDDVVGQIRCCQPSG LQLAPDGRTCVDVDECATGRASCPRFRQ CVNTFGSYICKCHKG
4834	18735	A	4868	637	2	VSFPLFFFVWGANPFPVQAGGQGGFLG SLNPLPPLKHFFLCTPPSSGN
4835	18736	A	4869	276	426	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4836	18737	A	4870	100	485	EERNREMTERC SVTQAGVQWHDLSLQF SPPGFKRFSCLSPSSWDYRLCDGMNL AHGKRLRLPGSSSPASASRVAGITGMCH HAPLARLVSNITLPQVILLPLGLQQAEL PRQVEVHNTPSLVT
4837	18738	A	4871	718	408	EVLTQLQAHFPGFLGAEHWNQDAALGR ATDSKEPEELCPDVLVWRTLHGQET YTPRLILMDLHYDVS LGALVLTAGYRA SSCSQSVAVCTGSLVLEARA
4838	18739	A	4872	392	246	RGGSSELRSCHCTPAMATRVKHLKKKE KRCKKIRPEGNE ILVNNAGK
4839	18740	A	4873	1	156	GGGGYSEPRSCSTPAMTAKRLRLKK KKKKKGVCVCGVGLPGRPKGGFF
4840	18741	A	4874	246	2	AHGISIVASMLAMSTFSRRNVSFRRAQ VKAVFVSVVFGPLHRHHLGHEFLFLR QSFTLVQAQAGVQWCHLGSQPLPPA
4841	18742	A	4875	72	2	CFPAAPDEDTNTITTKRKWTVE
4842	18743	A	4876	375	221	GLRLOENRLNPAAGGCGEPRSHYCTPAW VTEQDSISNICIYINIFSVVHQ
4843	18744	A	4877	151	2	RAFFFFFFFFFFVAQAGVQWVRVLSLOAP PPGFTPFSCLSLSPSSWDYRRP
4844	18745	A	4878	401	70	PHKREGGCVFPPPPKNNFFSPGGYFFWG GGGQNNPPPKGGFFPKTPGFFFSPPQK KKIFFFFPPPERGPPPGFRLRPPPPFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFF
4845	18746	A	4879	4	152	LPYSTPSTPFRAKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKRGNFK KR
4846	18747	A	4880	267	1	TPPKKKKKRIIPPPKNGPPPHFKTTP PLFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFRIGTKRGRTRGRT RGR
4847	18748	A	4881	2	408	LDATSPILIELITFDHDLIIILFLCP LVLYALPLTLTKKKKKKKKKKKKKKK KKKKKKKKKKKKKKGGGPKKNRG PKKLGEGKKIFFFFKGKKTRGVGKK KIFLGGGNGPDPKPKKPRGKI
4848	18749	A	4882	413	69	LPPPPPGFKHFAWPPPGRGVFGPPPP RVNPFVLGKGVSPPGGPGPRPLFPNPG GVGAGDLPDRGQGFHGPMPMPCPPAR TKRPPPPPKKKKKEKKEPERKEKKK EI
4849	18750	A	4883	46	394	KQYQVSVKLLFVTQNLGTRKKKKKKKK KKKKGGALKKPGGQKKKPGGKKKNFF LKRGGKKPPGIFGKKTLEGGGNNGT PQKKKPPGKKKILKGEGGKKTLYFGRG KNFS
4850	18751	A	4884	399	3	FFFKKFFSPNEFWFFPPFFLKIFFFFP RLFFFWGGLAQSPPPKVVFSKPRGF FFPPPLGKNFFFFPPGFWPPPGFLLRA PPLFFFFFFFFFFFFFVSIRNALAI RMGTMSRRRLAMGMLLRG
4851	18752	A	4885	391	47	PHFFWGGVFPFPFKKKKFFFLPQKGG GGAPKKKKKKKLPNFGGGFFFP GGPRFFFFIFFFFFFFFFFFFFFFFF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RRPFRPAVWAGLQLLTSSDDPPASDSQR ACITLHSLTLFCHLRF
4870	18771	A	4904	384	194	HWVGRFFFNWLGQKNPFPFPPKREYQG WGPPPPPPFFFKKTPFISQVNPFPFF FFFFFPG
4871	18772	A	4905	3	387	TIITPILTLFLITQLRLTNTNYHLPLP AQVPLDQKKKKKKKKKKKKKK
4872	18773	A	4906	1	327	PTRIPIEPENPKFVSPFITPHPKKKKK KKKKKKKKKKKKKKKKKKKKKKGALKK KTWGGPKKRGKKKIFFFLRGKKKPRG EFLKKTSGWGGENLATTTPKKKKARKKK KNF
4873	18774	A	4907	134	2	ALYSLKVKWPGAVAHACNPNTLGGQGEW IRRSQVRDOPGQHSSET
4874	18775	A	4908	59	449	ATRHVTIMLAYTSVGIFITAVVLGQKAI KQARFQVRRTTENYDQQLIHKGGRRPP GCHSTHTVLLPPTVTKTNGSTVANFV LILVCLSFLLLVYRCIQQLQSDNSQREG AMMMVVLSKRKGGYAGK
4875	18776	A	4909	337	3	LKTAWATRGNPLYKKNTQISGARGEFP FPLIGGGLSQKNFPTPGGENSINPDPP PSPPPGAKKETPPPKKKKKKPTTKELG KDWTLWELSDSQRAGKLAUVPGESSP
4876	18777	A	4910	14	162	AESGAKRETAFPAQOGATDKRLNITTY AAKKHMTCLFSLAIREMQIK
4877	18778	A	4911	331	2	LPLLPKPEGOGKILGYKKFPFPLPPFF GSTPPRNGEKGGPPPRGFNFVFKNGG FRLGGRRPPPGPKPPPRPPQKGGKQG GNPAGPFFFFFETEFHSCCPGWSA
4878	18779	A	4912	116	316	ACAHATLTFFFFLKKKPPFVLGGGK GNLGLKLMPLGLKKVCLTPPTGNYGG APHRILFCL
4879	18780	A	4913	93	16	SFGNFGTVAHACHPSTLGGRRGIT
4880	18781	A	4914	316	2	KPRGPNLRAVFNFKPGFETFPFFKN PKPTRGGRGGPINYPFGRVRFKNFLYP RGRSPHWNISICPPFANGTKNPFSSKKK KKKKKKKKLCSASVDAQ
4881	18782	A	4915	3	289	TSCNPSTLGGRRGITRVGVRGPDQHG ETPSLLKNYIYIICVDVYLIVCMYGA YIYICIGYIYIWRVLSLSEHTHTRAP QOYRVIVYFCG
4882	18783	A	4916	1	222	ARGERERERERERERERHOGGGAGP PHTLWGEQVVLSSPQTGVREKNAPIWG CAAPVLAFRVGRTPFQVD
4883	18784	A	4918	1	281	ARGERERERERERERERERERERE RERERERERGAPPPPRGGVRERTCP SARGARALSPITSCGDPHRGPKIYRGVG VHTQRYFSVGSSLCINTHT
4884	18785	A	4919	1	259	ARGERERERERERERERERERVFVEKGD MVTLPAGIYHRFGGKKYTKAVRVCVR KPGWRAHNRVADHPGARGPHVKFLAQTV YE
4885	18786	A	4920	797	910	NTMQPGVWTHTCNPSTLGGQGGRTTSG VQDQPGQHE
4886	18787	A	4921	2	67	LEERERERERERERERERERERS
4887	18788	A	4922	1	698	TLLLAELGTICDPYRSCSISEDGLSTA PTIAELGHVFNPHDDNNKKKRGGPF KGNFSPFVRASKNFFFGPPNLNSWARF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
4888	18789	A	4923	323	2	LTPEGKTPGVFPFNPFAKEL LVCRGTIHKFCVPHLTGRRFEHGVTD YTLFRDAYHLAIEMPDFHREDDWRNG QNLVLDNLEATGLYQVFLSAAQPGDVL CCFGSSVFNHAAIYCGDGLLH
4889	18790	A	4924	3	225	HEALHLFQITLMCMKKRLITVPHIGS DEHQDIDVAITALLKQKPLRTFLFVRP FILCMYCMVYVICVCI
4890	18791	A	4925	371	169	HTQTSVVVVERRRPHHSGOENLPFGGR GCGELRLCHCTPAWATRAKSLKTKTQT KKDAIKCSLCN
4891	18792	A	4926	2	352	ARAARAGRIIKELFFFFFNGNLKKKGL FWWPGGVKNPDGNPPFPKGGITGL TPRPGMGVIFKKFGKGSPTSPTGPKSL GPREFGLALQRGDGLGNHRGPPFFFG VLETH
4892	18793	A	4927	2	379	ARANMEETQKSNLELVRIISLLIKTGL BPRVILASMETNNLVYDTSDDDYHLKK DLQBSIQTLNGLNRRRTQILITQDY SKFDYNSDNDALLKNYLLYCTKDM KVETFLRMEOCRSV
4893	18794	A	4928	175	31	ILGDLFFPAWLPFLPLLPSPRSLAV TEVAVQWRNLGLKQPLPGF
4894	18795	A	4929	368	247	VDRLPFCPCGWSPLSELNQSACLSFLKC WDRCEPLCSVS
4895	18796	A	4930	2	110	ARGEPRSHCTPAWAMSETVSKKKKSGG LFFLPLRV
4896	18797	A	4931	150	1	KYVAPCRPLFLVLSPCRRSCPPFFCHD CKPPESFSEATMFFLOPAEPA
4897	18798	A	4932	2	155	ARDDLNPGGGCSLRSRCHTFAWATERD SISKKKKNPQNIWGNLKKKNLKK
4898	18799	A	4933	144	249	ETLYPQPPQSLNASCVCVCVCVCVCV CLCVCV
4899	18800	A	4934	2	153	ARESFVEGRFRHVQGVGLKLLASGNFPN LATQSAGIISISHCTQWRQGL
4900	18801	A	4935	1	355	GTSQBFEGKDRLASPLETNAGAGRER LAEVSTCPSGASKPLQTPRGGQEGTFG LGGRRMRHSAGSPNPAPWESIRDPSTLS TALLVACISFIHEDDPILHDVLSRCMS IKTSR
4901	18802	A	4936	112	358	NIIFKSXAFFFSFYIFILINSVGLASTF MWGGELKFSFTSGILLIIFQPFKIGHPQ RGILRTGTFKDDPDPEGNKVSLLQ
4902	18803	A	4937	1	258	GTSPPVTOQFFSGWGRQGLTSLPKLEHS ELRLCHCTPSWVTERDSISKKKKKLFP LGPTFFPPGGGNFNIALGRLLKRGGE KK
4903	18804	A	4938	380	1	FFFFFSETEPYSVAQAQVQMC
4904	18805	A	4940	255	1	LGNNLAGYKIRGLYSILNRRHPSFVI SLCNGLPYVIRFDMESCSVTQAQVLMC NIGSSQALTPGIAPFSFISLPSTRQNSR P
4905	18806	A	4941	10	173	KYIYDTNKKWNNCSQIGRINPVMSL PPKAIYTSVFPIKIPSVYLPVHLSI
4906	18807	A	4942	144	3	DKCIRRPQTVTHTCNSTFLDQGGVRMR SGVRDQGGHSETPSVRV
4907	18808	A	4944	484	274	PSSQSRPRTARMIALSTRPTTSMKFCH VQAQGLKLIGSSDLPASASQNVIGSVS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GGGFFRSILGNPIKPLFLNSPKISPLP WPGGFFPLPWGVMAGKNPLPRGGGFPLT KFPFLPSSLGKKKKFRFKKKKKKKGQAR WLTPTPTPREA
4930	18831	A	4967	79	346	DKIFSNISCGIVIDLLAIYNNDAYATRL GIYKHWDPIIIDKDTSSCRLSFSSYPRF LESLODFYILSSGLIILQTTNSVFNKTL LKQVI
4931	18832	A	4968	3	93	FLHVQAGLGLPTSGDPPASASQSVGLQ A
4932	18833	A	4969	158	1	SKSNFAYIFPIKDNGLTGKKTINRVVTK NWANDLNHRFSKVNIQMAKRYMK
4933	18834	A	4970	2	266	VGGQGVLLSSSDPPASAYEGAGIPGVS HHTWPKHFFPALFVACISSLVNCLFOLF ACISIGLSFFFFFREGLDGLNLLKLAGL TFLG
4934	18835	A	4971	3	96	GVKHAHLIFVFLVETGFPHVGGQDLNF L
4935	18836	A	4972	253	348	NFIFLLFIYFEMESHVSVAEAGLQWHLCS SLQP
4936	18837	A	4973	326	2	PMETPOHKLSLWPGFAISVSYPFERKLIF SADVSYKVLNRNETVLEFMALCQRTGLS CFTQTCCEKQIGLILVLTTRYNRTYSIDD IDWSVKPHTFLKRDGTEITVVDY
4937	18838	A	4974	3	244	DASLVFKVAETANEVEVKKCMKYVFGN KCOREGGREKKREERREGRKEGREGLR EGETDEEREEGEGLSYSPFFKNSI
4938	18839	A	4975	6	79	THFSLTITSLQPEDIGTYTCQQYD
4939	18840	A	4976	15	339	PGEAGNCLNPGGSCSEPSRHRCTPAWA TERNSVSKKKKKKKKKKKIPRGRLPPV SHFFWKAGGADWFDLGTLEPFWPTGETP VFKKKKKLTGGGAPLVAPTWGGG
4940	18841	A	4977	204	275	ITIEVDPTDKMKLLKLDGFSLSNLQ
4941	18842	A	4978	3	352	RRPSFHLGVAGVSGAGVMAVETLSPD WEFDRVDGSGKIHAEVOLKNYKFLEE YTSQLRRIEDALDDSIGDAWDSNLEPMA WRRLPYEQSSVLELIKENTKVLNRVVTG YAGL
4942	18843	A	4979	219	3	AASTMAMSEFWPQYRPPFFFTLQPNVD TRQQLAANCSLVLSFSLRHKQSSMTLM KSRLTSLITVMLDC
4943	18844	A	4980	142	3	FQGGFFLRDKVLCCPGWSRTPELKRSS CLGLPKCWDYRRELPLRA
4944	18845	A	4981	351	2	FFFFFSETESRSVAQGVQWRDL
4945	18846	A	4982	133	3	SFFFFLPETECCSVPGAGVQWCDLHPLQ PLPPGFRFRSCLSLP
4946	18847	A	4983	3	161	LGSLHDTANTLWRLRSLRTIMAHYSLD LPGSSDDPPTSASHVRGTGMRSRTP
4947	18848	A	4984	363	3	GPSNKKGRSKKAHLVAASVEQATENFL EKGDIAKESQFLKEELVAVEDVVRKQG DLMKAAAGEFADDPSCSVKRGKNVRAAR ALLSAVTRLILADMAVYKLLVQLKVV EDGILKL
4948	18849	A	4985	101	1	LQVCYGRVVMNSREYGANKQQVESKIM PFQDA
4949	18850	A	4986	341	1	PPPKSPDVLKTSFVADRAAGVDDVKET LOHORYPNVFGIGDCTNLHTSKTAAVA AQSGILDRISVIMKNQTPSKYDGYTS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CPLVITGYNRVILAEFDYKAEPLETPFPDQ
4950	18851	A	4987	86	1	KCSGTISAHCNVRLLGSSNSGPSASRAI
4951	18852	A	4988	124	3	LPWLCSRFETKTFQFQIYYKAGKGVKTVWYSHKDRNDQWN
4952	18853	A	4989	305	150	WLNRYRISHSAEVQVCQFLTWVFTLGSPOHFSKFFNFYFFKICFDYWN
4953	18854	A	4990	64	340	KKKKKKKLLKFGQREKPLSPNFGGLGGQGNQPGQKPSRDPDWPGIKPGEKKKNPLKKKKKKKKKPLSKGGGKKTPLKKKKKPPPKGF
4954	18855	A	4991	3	158	PSLVOTRLRHAGQAGLKLTLSTDSPPASASOSAGTTGVSHHAMPKDCSLNSN
4955	18856	A	4992	116	66	FFFFFFFFFFFFFFFFFXE
4956	18857	A	4993	3	107	GOAQWLTFVIALWEAKVGGSEFVRSRLRDAWFTQ
4957	18858	A	4994	1	105	KLDRLARHGLYEKKKTSRQRKERKNRMKKVRGTW
4958	18859	A	4995	110	3	RIRIGRYKTVFLCTQLEILMARYPLPSPKPIKIKN
4959	18860	A	4996	109	3	DEVSLCPRLCNGTLALHCNRLRPSSDSPALAP
4960	18861	A	4997	1	148	ACCPFTTYLLPMFMIKAPLMGTSSKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
4961	18862	A	4998	3	110	VILQGSNDVELVAEGNSRFTYTVLVDGCSKKTSTRP
4962	18863	A	4999	3	330	PIADRGAEVVSARENMTICFELQLLKAHKKAIRATVNTFGYIAQAIQPHDVLATLLNLLKQHERQNRVCTTVAIAIGATCSPTALPALMNEYRVPELVQNGVLK
4963	18864	A	5000	3	110	VILQGSNDVELVAEGNSRFTYTVLVDGCSKKTSTRP
4964	18865	A	5001	25	329	NSRRRRNDQGSFNLCTQTFMTFLPYLPEHRSLLKIRSCAERETKKDDIPEDKGNIKQCEINYYVKFQSGPOHKKLTKSKRESKILKKAQKQDGLHETLLN
4965	18866	A	5002	278	345	EDEEGYNDGEVDEDEEDELGG
4966	18867	A	5003	101	3	VRITISGTGKKKKKGLPKRNYDPKVTDPER
4967	18868	A	5004	18	350	VSHECLIFIQNVLTGLVISLSCPSVPFSRHKHHTHTHTHTHTHTHTFS
4968	18869	A	5005	26	147	KEEVRMALFANDHIVYLENFVVSAPYVLKLSFCCKRGLQ
4969	18870	A	5006	85	1	SASRVAGTIGKHHTRLIFVPLVETGQS
4970	18871	A	5007	370	3	RARPELLWKKIWSFWYKKKTRINFQKSKSPFSRPFPLFKKGFLPCGVFSRGFLKIPPPFFFFFETESRSVTCQVM SVQWCNLGLLOPEPPPGSKQLLCRGLPSSWDYRCCLSTRP
4971	18872	A	5008	1	85	TRILSKIKNALTFPLDGTPTPLIPLE
4972	18873	A	5009	218	93	FFFFFFFFFFFFFFFFFFFFFFFFFFFFF
4973	18874	A	5010	3	250	RFRRRRLQENHLNLGEGCESSESRRHCLTWTATEQDSVSKKKKKRVPPPHPRGKFFWAGGPTFFPLKTVPPFGGKPNF
4974	18875	A	5011	336	0	SSSSPSSSSSPPPPPPPPPPPPPPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
4975	18876	A	5012	2	80	SNQNGTGGESIYGEKFEDENFHYKVK
4976	18877	A	5013	53	324	FLVFFVPENSEKISLQLHLALTSSSSWV QSPSHLEMLNLCRHINIRVDPTGLREGM HYTEVCGYDIASPNARSLSFRGPITAVIA AQVNES
4977	18878	A	5014	329	1	FFFFFSETESRVAQAGVQWRYLGSLQA PPPGFM
4978	18879	A	5015	193	32	PLLILCSERLCHCTPAWAIEDRSVKTN KTKQQQQQQNQOGTKMFLALLQOI
4979	18880	A	5016	354	235	CGEIGMLLHCWCEKLVRLPWLTKNLFIRD GSTLTVGSKSSF
4980	18881	A	5017	348	2	RLLVGKMLHEGSSSSGKATGDE
4981	18882	A	5018	76	1	IFFLSQVSPLSKEDAGEYECASNS
4982	18883	A	5019	68	356	YFGGVGGGFFFFFVFWFGPSGGVFPVG VQAIFFFFFPLGGFFFLVRDVFVAVF WNGLLFFVFFVFCVFFVFFFGWKRK NIFYGWNFLFCW
4983	18884	A	5020	1	288	FFLNLEKNIKMLSYTDNGIVVATAEDF MQNFKNLVGYHNSITEENLPQLGANENL ESQSGNSVVFIFFNADRRKGMVLLLPN NEMTILKPTSV
4984	18885	A	5021	133	1	VVATEHMTSTKPKMWPGTGAHTCNPSTL CGOQOITSPOKFE
4985	18886	A	5022	2	337	RRSDENPKNHLREPRKKQKLAYERAGLS KLPLDKDAEAQKPFLEXIQLGEKLLAQ GEYEKGVDHLTNAIAVCGGQOQLIHVLQ QTLPPVPVQMLLTKLPTISQRIVSASHL
4986	18887	A	5023	1	325	VGGCPANLLSHRSVLRAETISLGEHF CDRGEQVTLFLNDCLEIARRRKVI GT FRSPHGQTRPPASLKHILMPLSQKKA LDIETEDCHNAFALLVRPTEQA
4987	18888	A	5024	135	2	ATMFLNSKVSYSYGLLGFHECREKGWM TWDGERDPSGILQLQ
4988	18889	A	5025	2	94	KTATKLIGGXHYDSXNKAIRDGLLARR HAL
4989	18890	A	5026	2	362	QELERSMAQRCVCLVALVAMLLLVFTVP SRSMGRSGEHQASRIPSQFSKEERVA MKEALKVFPVTVSTFSIQHEVVVEYSHL FTIQGSDPSLQPYLMAHFDVVPAPFEG WEVPPFSG
4990	18891	A	5027	222	84	AASFCHVSQAGLELLTSDPPASASQS AGITGMSHRTOPMVHLY
4991	18892	A	5028	366	0	SGRSKKKKKKKKKKKKKKKKKKKKKK KKKKKKRGR
4992	18893	A	5029	231	68	AGMGSRALPKPILLMSHSSSLKAVELPDSF SPELRSLLEGLLQDVRNRLGCLGRG
4993	18894	A	5030	2	366	LNLGGRGCSLELRSCHTCPAWVTETPFKK KKKVPHGGYFAVQLLPPRKMRTTHRRPQA QKERTGPWGAPVHTGLLPRRGQAFTQP PSAFKGFPHPTNKSSSSAKKKKKPRVG RKKVGYLL
4994	18895	A	5031	241	368	QVENFKSSCSAEAHICDLS TLGGCGGQ ITRSVGHQPCQHG
4995	18896	A	5032	279	396	DGGMWFTVAHANPGTLGGQGRNITRS GVRDQPGQHE
4996	18897	A	5033	173	398	SNESSLRVNPPFFFFFLKTNFSFCPPGG RQGNFNSLLDPPPKVKEIFCLTPPKRW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4997	18898	A	5034	2	143	EYRPAPPPPPRNFGFLIKTG SNFPALTSQSMGITSMTRHALPIACFLV FVLFVFEMESHSLAAEQV
4998	18899	A	5035	350	2	QELSSVQTSITQLPFGMTVKARATTREVM ATTIETDIVELIITQLPSNYPLGSIIVE SGKRVGVAVRLFIFITQKSFIFLSEFLT LCCLQHQHFNDFLLLIIVPILIAAFMLL TERK
4999	18900	A	5036	1	100	HECGSSQRTLSVQEAAYLKVSNSEIRI LIAIF
5000	18901	A	5037	247	334	LQIDISAVVAYTIAVKEDGELNLMKKAA S
5001	18902	A	5038	2	296	DKAPMLKIVVNSLKNMINTFPVSGKVMQ VVDEKLPGLLGNFGPPFEEMKGLIAVT DIPLGKVHLEALKKKVVKFFYPPLRCD IHTAKCTGLRYTAQ
5002	18903	A	5039	152	335	RPIWSYVLLFFFLFWGLYLDVNNKRITF ILSEKYFDMKKKQCKEGLDIYKFKLTRM TRISE
5003	18904	A	5040	336	1	GGLTISILLKEKEGSEVAKFTLEQLCLI CNIMSTAECVAATQQLKELEKQVDS LFDRINLSDGMGTFSPVSSSIHLLVQD VDAACDPAMVMSKMQCQNVQHVGVKSS
5004	18905	A	5041	3	204	LNLLGGGGCEPSEKCHCTFSWVTRHLHK KKKKKKRGNLQNGGKENTFKLIQLLVN PKNSLENLAV
5005	18906	A	5042	382	148	WCNHRGPRSRKKRSEGSTSKSRRLGATIR MVTPTTTRTCARDPELTSKEKCVYIEEH THTHTHIYIHTHTTCTIVRTH
5006	18907	A	5043	137	1	RPRRRYMKKFSTSLTIKMKIKITMKYH LSHLIPVKMAITTKTKD
5007	18908	A	5044	198	34	KPASRFCHVGQADLELLTSSDLPASASQ SAGITGVSHCSQPNFTLCLVVDTHFF
5008	18909	A	5045	11	357	LLTYFIIMFKILEIYEKEQLITKQISE QGEKVKELRQFKERKAKDSALQSIKES MLELTNLRLESQEEIQIMRKKRKNAAK QYWKFKYSQRWKSPPGPFQNGWGRKN FV
5009	18910	A	5046	2	193	GLQLLTSSDPASASQAGTAGNSHCTQ PQVHLMPSLYHFRFLQVTDKDLRASAD LIHRGIT
5010	18911	A	5047	1	196	KLCLVMSPMKAAPRNPFSCARSLSLKPF SFRKTTTTLTNTADDPAYFDLCKMEPC SMVLFFVFC
5011	18912	A	5048	386	276	AQAVLELLSSDLFPASASQAGISGVSH CTOPDSIF
5012	18913	A	5049	1	324	VDAAAEKLEASTGWLRFKERSCLINIK MHGEATVADTEAAGYPEDLAKITDKGV YTQOQILNGDEIAFCWQKIPCRIFLARE QAVPGCNASKARLTLLNANAAGD
5013	18914	A	5050	1	129	PRSCHCFPAWVTEQDSVSQKKKKKKKE KEKKKNPVEKSAKVI
5014	18915	A	5051	193	356	RSFTPSASASASTLCLCKSQNGQPGAVA HACNPSTLGGQSRLTRSGVQDSQGOY
5015	18916	A	5052	192	341	AKRVKRNFFFFFLKQFCVPGAGGRGP DPGSLKPLPGLKGFSCPTPLN
5016	18917	A	5053	340	1	KRIPDKQKELRRLATKLIREAPKGGQA QKKEIHKSIQEAKEIFKIDRIKKSQF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DRQEALDILVLMQNALESLSNRIEQVEBRNSELEDKVDLTRLSSKAGKRIRNYDHS
5017	18918	A	5054	2	383	VVKVATQPADNFDLVLSRKHLGPNVGRDVPRLSLPGKLVFPSSGTSGHFFMLGIGDIVMPGLLLCFVLRVDNYKKQASGDSGAPGPANISGRMQKVSYPHCTLLIGYFVGLLTATVASRIHRAAQPC
5018	18919	A	5055	2	383	GSVLSKKGGDYLRKYHNASLLDGLTLDSTWNLGKTYNIVLGSQVVLGMDMLKEMCVSEKRTVILPHLGYGAGVDGVEVPGSAVLAFDIELLELWAGLPEGYMFINWGEVSNLFFEEIDKDGNGEV
5019	18920	A	5056	2	383	AVIDEVRTGTGYRQLFHPQEQLTGKEDAAANNYARGHYTGKENIDLVLDRIKLADQCTGLQGFLVFHSGGGTSGGFTSLMERLSVDYGGKSKLEFVIYPAPQVPTAVVEPYNFILTTHTTLEHSD
5020	18921	A	5057	26	452	KLMSLRRLRQAWHEAALDEFRTGYRQLFHPQEQLTGQEDANNYARGHYTGKENIDLGVDRIRKLADQSTGLQGFLVFHSGGGTSGGFTSLMERLSVDYGGKSKLEFVIYPAPHVFTAVVEPYNFILTTHTTLEHSDCA
5021	18922	A	5058	2	385	AVIDEVRTGTGYRQLFHPQEQLTGKEDAAANNYARGHYTGKEIIDLVLDRIKLADQCTGLQGFLVFHSGGGTSGGFTSLMERLSVDYGGKSKLEFVIYPEHVCTAVVEPYNFILTTHTTLEHSDC
5022	18923	A	5059	3	390	GDAANNYARGHYTGKEIIDLVLDRIKLADQCTGLQGFLVFHSGGGTSGGFTSLMERLSVDYGGKSKLEFVIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAPVDNEAVIDICRNLNDIERPTYT
5023	18924	A	5060	103	3	KIFFFLKWSFALITQAGVQWRGLGSLQPLPRAT
5024	18925	A	5061	262	412	KKSPFRTGTAFGNGKTSYDLLLGNFGYTFGGITGCLKAGLETSYWTFETH
5025	18926	A	5062	293	406	VLIGSIFEVINAVIKFGTSGISVLRLRLRIKPKVIK
5026	18927	A	5063	419	15	NEEEGLPLPKKKKGSGFNKRGNIIMGPFILKRPPEKKPPPPPRKINIPFFFFKRGKPPPPRVKKGKAIKGRNPLPGSRDFFSPAPQKSGAPGGGPPPPVKNKQFFFFFLVE
5027	18928	A	5064	2	216	TGFHHVTQAGPELLSSSPETI GLTNLFICRDRILLCCPGNSOTPSLKQSSHLSLPKPMDWYMEPLCLYFLYPWFCLSLSLSPFLSHTYFFG
5028	18929	A	5065	259	36	SQPHWDYRASRAEEATFLEVLWQAIQVCCFLRQSPFPIAQAGVQWHLKSLQPPPGLKQFSCFSLLLVPLA
5029	18930	A	5066	2	404	GKGAPTSLISVAVFKIIKVLNEDNKLFGAICSLTCGGANIGTAMAKDERVNLNLSGTSTQVGKQVGLMVQERFGRSLLELGNNAIIFADADLSLIVPSALFAAVGTAGORCTTARRLFIHESIHEDEVNRL
5030	18931	A	5067	1	400	GENMITGTSQADCAVLNVAAGVEFEAGISKNGRTREHALLAYTLGVQLIDGVNK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						MDSTFPFYSQKRYEETVKEVSTYIKKIG YDPDPTIAFVPI SCWNGDNMLEPRANIP VTGWKATPIDCDASOTTLLDA
5031	18932	A	5068	41	392	GSPHHFCAHIERKKKPYNSNIGFYTKRN ALRVAEVMDDYKSHVYIAWNLPLENPG IDIGDVSERRALRKRLLCKNFMQVLDHV YPMRRYNNNTVAYGELRNKKAQDVCLDQ GPLEN
5032	18933	A	5069	3	395	GTETPRHILLQALPIRAMLPCPDYDDTD KTGLDQALKICQAMLEDAANQGLMTVL NNTNLIQMATQGRWVKDSSLTLTYPIEN HHHLFFKKRKPIMKGPBKRSSTSECLP ELIHACGGKDHVFRSLVQ
5033	18934	A	5070	3	405	FRASEVCGSCHITCNKAPTCTCPVPE QTKGPLGIDPQKIGTAYEGHVRIKPA GVKKGWQRALAVCDKFLFYDIAEKA SQPSVVISQVIDMRDEFSVSSVLASDV IHASKRDPICIFRVTASQLSAS
5034	18935	A	5071	3	393	ITRQEFIDGILASNFPPTTTIEMTVGADI FDREGDGYIDYEFGAALHPNKDAYRPT SDAPKTFHQGTRQVAQCICAKRFLVEHI GENKYRFFLCNHFQGDSSHQMLVRILRST VMVLGGGWALDQFLTT
5035	18936	A	5072	3	394	ITRHEFIDGILASKPTTTRIKMTVGADI FRDGDGYIDYEFVAALHPNKDAYRPT SDAYKIDEVTRQVAQCCKAKRLAEHI GENKRFPLCNQFQDSSHQLRVRILRST VMVPVGGGWALDEFLND
5036	18937	A	5073	1	393	GELAAANNYSRGHYTTEKETITDGLDRIC KLADQCTGLOGPLVFRHFGGTSGVTS LIMEHLSPDYGPKSLFSPYIPAPQVFT AVHEPYNSMLTTHTTLESDCAFMGDNE AIYDICRTNLDIERTTYTN
5037	18938	A	5074	39	482	LGLHSANRDKTIGYNPDVSPVPI SCWN GDNMLEPSANMPWFKWKVTRNDGNASG TTLLEALDCILPPTRATDKPLRLPLQDV YKIGGIGTVPVGRVETGVULKPMVATFA PVNDTTEKSVEMHIEALSEALPGDNVVG FNVKNVSV
5038	18939	A	5075	1	390	GVSMAVSLVITYQVYVVRNMPDPHNLPIV AGWKYPLFFGTAVFAFEGIRVVLPLEN QMKESKRFPQALNIGMGIGTTLVTLAT LGYMCFHDEIKGSITLNLFDQVMVYQSV KILYSFGIFVTYSIQPYV
5039	18940	A	5076	330	462	VNFFFRGGGTESPIAQAQPVWCSLNSL QPLPPGKFRFCSLSL
5040	18941	A	5077	1	403	GGWGEAEDEFYADVEPLEFTLSNITE QRSLKWIPLGGKGVGKTCSCSLAVOL SKGRESVLIIITDPAHNISHAFDQKVS VPTKVGYNLFAEMIDPSLGVAELPDK RFEEDNMLSMGKKMMQEAAMSAF
5041	18942	A	5078	348	1	RPGNNIERWQGGVLLITQLLRIAKSVK NVQLLWKTQFLIKHLILLFDPRIFFVS NYPKEKTVHKTATYQAQIFLSLPTFLF LROSLNMLPRQDLSS
5042	18943	A	5079	248	3	PQGVLEKERTCKRPAWVNVICILAGPA KPNREDVSSSQEESLQNSIPPTPLTFS TAVKSRQPLWGLKEMEEDSGSELD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
5043	18944	A	5080	3	192	GDGSELRSCHCTPAWLTERDTSQQKKKK KEKKTWNPAPELFFFLLEKKGGQNGKP NMKKVL
5044	18945	A	5081	10	171	CFLGLPVGVCRLSLKPOLCFLGFPWLQD ARQKFRSVLVEATVKLDELVTSTRP
5045	18946	A	5082	94	1	DFWPGKVAHACNPSTLGGRGGWITRSGV QDT
5046	18947	A	5083	142	3	AASTGSHSVAQAGVOWHDLSSLOPLPPG FKRFSFLSLPSSWGRKIA
5047	18948	A	5084	257	177	ISLGEVAHACNPSTLGGRGGWITRPG
5048	18949	A	5085	143	1	GGESHSDTQAGVQWCYLGSTQPLTLTF KQFSCNLPLSSWNYRCVPP
5049	18950	A	5086	3	87	HVGQAGLVLLASCDPPSLASQSDGITV
5050	18951	A	5087	375	220	LHLSQHIATRSKPPAPNLFAGTSLSPV STNWWGPNPISFEGMLIIFFFFF
5051	18952	A	5088	40	203	IFPLPLLVFFFYLLTWGFTFFWGLTLI NDLWLPFFFGNSGIFSWRGSAGELG
5052	18953	A	5089	1	145	MDMRVPYLAQLGLLILLMLSGARCDIQMTQ SPSLASVGDREDDGVDA
5053	18954	A	5090	146	328	FVFPFLLESLEIFSSKLFNPNLEFFFFE TESCVAQDQVQWYDGLSLQPPSPGFKR LSCLS
5054	18955	A	5091	338	1	PNLPSVOLPFTSTCTPLIGDLLVAAHAF AGWKHQGINSPLPMAPREGMEAPRNP HPHIFLCLIHGHILAVSKLYSLPYVYVY YPSRWSFTLVAQAGVWWRDLGSLQLPLP
5055	18956	A	5092	2	327	PPLTPPIFFPSSPKMKNPPPHYNPPFP FRTPPPPPYPLSPKSPPPPRVDPDL PYSIFPRNPLISPPPYSPFYLLPOLQAF P
5056	18957	A	5093	133	3	AQTCTPSTQINSKNITDLNVKGTIKLL KDNIREKLDLGCCE
5057	18958	A	5094	170	350	AGGQGGNFSYLPNPPPIRESSHSTLPK FWNYRHTPTGPPNGFFFLKMGGLVAQ TIFN
5058	18959	A	5095	133	274	RDYIIFLESIGIKGYLFFSDKITSELVS KIGDKNWKIRKEGLDEVAG
5059	18960	A	5096	2	188	RENQIKTVRYHLTARMVLKXSEKRN CWHGCSEKGTLLHCWCECKLLQPLWKIG NRVDA
5060	18961	A	5097	235	81	FPKKKKAQIKKPAQAGSLNSLSLYIYA FTYTHTRHRTHTQTHTYTHIS
5061	18962	A	5098	355	169	KILLITDSCAHISCRFSECMKYVNFPP HPHSVYVTDKIRLLEBQLPHVFSNKM PFKVCN
5062	18963	A	5099	160	1	FSASYFNSKKKILPFLLLKRWNVFCFF GMESHVSVAQAGVQWCHLGSLOPLPS
5063	18964	A	5100	364	151	QMGFCHIGADLELLTSSDPSASASQSA GITGVSHYASQELKKFPHSAHLIPLQ TCVQKTAQPSYAL
5064	18965	A	5101	205	3	AASFGVQWDSRLQRPFGVQKQFFPLS FPSSWYGRGAAPPFGHFFFPSSRDEIS VCLPGWSPITE
5065	18966	A	5102	349	207	DGASLCCPDWGLELLSSSGLPALALQNP EITGVGHHTQPTWLSLLIY
5066	18967	A	5103	425	0	CEFFPKNKDFCLSKKKKKKKKKKKKK KKKQSSQTSYS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5067	18968	A	5104	437	184	LELFFPPPPKKVFSQKTPRVSVPSPKKK KKNSPPPKLGPQPIFKTPPPIPF FFMFFFSFFFFKCHRRPRFISLMSPL
5068	18969	A	5105	401	10	NFSFFFGGPRGGVPLRGGKNGFGPKGK TPFFLNQNYLGGPLLYSPFLERLNKKKA FTLEAKGPNPNSSRSPPPGAQKKNPFP KKKKKKKKKIIFMQAHPAVYVCSGNQ LPITFPYSIISGPLSSFT
5069	18970	A	5106	413	2	PNKKSPPPFSPPHKTSSPSPPPPPNK PTPTPPPNKNFPPPQPPPKKNPPOT PPQKKTPPPPKKKHPPPHKKTTPPP HTKNPPPPPLPPSLSPPLFLYINSP FPFPFFFFFKIPFYLGKRVGGRV
5070	18971	A	5107	269	115	GFFFFFFFFFFF FFFFFIKKCHFIFKYGISTN
5071	18972	A	5108	238	4	QWLPLVDRIWVILLFFDSLNKMFQYO IGLQIKVKNNTTFYFLFSFLRWSFTL VTQAGVQCNDLGPLQPPPRFK
5072	18973	A	5109	496	0	STPSRASPKKKKKKKKKKKKKKKKK KKKKKKKKSSK
5073	18974	A	5110	1	243	DHLSLGGRCSEQRSCHTPAWVTERDS VSKKKSFRAIDIFFNGKKILGTLRGK NQKPPREVSSGNYFHKGLFGPCYK
5074	18975	A	5111	78	4	LGMAVACNPSTLGGRGGRITRSV
5075	18976	A	5112	2	96	AGVQRDLGSLQPPPGFEQFCSLSTMP NFL
5076	18977	A	5113	128	6	IYKDVLEPGVLRLLDVDNVVLPPIEPI RIIIPSDVLHS
5077	18978	A	5114	132	2	DDLSSLQPLPPRFKRCCLSLDSWDYR RPLRLPAIQEAEE
5078	18979	A	5115	1	146	AVETGFCVAKAALELLHSNDPLASASQ SAGITGMSHRAWPSLFSILS
5079	18980	A	5116	213	3	GAVGSSGCFLLYLALLGFPFPLPLLO LKFICWPGAVAHVCNPSLTLGGRGGRITR SGVRDQDQDET
5080	18981	A	5117	407	0	LGMWWFVPIPTLREVKAGGSPVRS
5081	18982	A	5118	215	414	KIRPKETRNNGSSQQRKRAQLGKLEQT NVLNFKAPFFGQGDYKSFYKTCLDNL PRRGKGVFFF
5082	18983	A	5119	40	326	KKKKKKKKKKPKKKTGGAKWAPFLNLK KKGIKPKQKKGFQGGKKRGGKKKIFKI LIQGFQKKKNFSKKKISQKKKNKGF LGKGFCKPKKT
5083	18984	A	5120	99	2	GRSTRHSPARTHTTLRHTGFLHLTHSH RHSP
5084	18985	A	5121	3	219	ELRLCHCTPTWATRVRLSQKKKREKKK NFVGKKKKKKKKPNPKKKGSLGFKG FLSKFFKTRGTII
5085	18986	A	5122	262	351	TRPGTLAHACNPSLGGRGGWIMRSGVQ DQ
5086	18987	A	5123	340	0	KKKKISQAWWVVPVPAWAEVGG
5087	18988	A	5124	94	2	LMPITPALWAEVGGAPGCEFTSLANN VK
5088	18989	A	5125	310	68	LSFFYLKGFNGRVYIPPPPKVSPFVFG APPPPEKKKKPPPPPKSSIKKTEKKI CLASGKGLVCFCKKPLIQSYFL
5089	18990	A	5126	343	131	SRPRKFDLELLTSDLPAPATQSGAGIT

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						VSNHTQIWPISVGLDMNTGVVPIENRIV SELLREIHFRLICL
5090	18991	A	5127	2	145	FSLGSSVGRLEGGTITSTHCTLPASRD SPASNYRLTPPCPADFLYP
5091	18992	A	5128	1	130	SRSVTRLECSGTISAHCNLPSSDSPAS DYRLTPPCPADFLYP
5092	18993	A	5129	1	338	VVRKEGRFRFEKSKDFKNHVIKYLETL LYSQQQVCILWVTFI
5093	18994	A	5130	346	3	DDFFHFHILGFFFFFKTLFFSPPEGNGG HLLFKNTPPGRIFFLFPFLLWGGWA PPPPKKNNFFFFFPPFFFPFFFPFF FFFFFMPMPQTSILFKDQGPVQGGEEA DV
5094	18995	A	5131	3	114	FLHIGQAGLELLTDDPPASASQSAGIT GMSHHAQP
5095	18996	A	5132	292	180	AASTDSIEGHGASLPKKTTPSEEDPETI KLISNGAYG
5096	18997	A	5133	338	216	RGENRLPPGGRGFSGPKSHCFPPAWATE RDSLSKKKNPV
5097	18998	A	5134	337	3	IVVLNGKGTIRNNQIFSNKEAGIVILY HGNPVVSGNHFVKRAAGIAVNGKGL ITENVIRENQWGVDIRGGIPVLRSTL ICFGYSDGVVVDGEGKGLIEGNPISAN
5098	18999	A	5135	227	343	NYVKEKLITWNWVMSIMDSTEQAQPVY SALTSVVDPGQ
5099	19000	A	5136	166	375	ATFVSLGVFCSAVILLYFKNNMKLDLSL TPHTTINSKWKRLRTPAIFKLEVNI GKKFFDIHGEIIL
5100	19001	A	5137	90	2	KTTLWPGAVAHACNFSILGGRGGRITRS G
5101	19002	A	5138	213	379	PTFQSVGETGSLLKMHILGPGAVAHACN PSTLGGRRGRITRSVGVDQPGQYGETP
5102	19003	A	5139	384	2	FFFFFSLVMESCSATQAGVQWCDLSS
5103	19004	A	5140	41	317	TMSRDRPSDKITVYNRSNVMPDGAFF RYSFSALKDRHNAVENNI DPNNGWETA TELVEDTQAIARYGRNVTKMDAFGCTSR GQAHRAGL
5104		A	5141	29	523	VKAEEAYKKADDIWNLRDDYFVNDEAR ARYWDDREKARALEAARKKAEQQTQD KNAQQSQDTEASRLKYTBEEAKAYERLQ TPLEKYYAROEELNKKALDGKILQADYN TLMAAAXKDYENTLKKPKQSSVKVSAGD ROBDSAHALITQASLELTKHAG
5105	19006	A	5142	432	144	GGFLPKAFLDPKKKKGAFFPPPKGAIF PLFWGGWTVFLIPEKNPFRGFPFPRGE KPVGGPFRIFAFPQKKIGGGGFFLER FFFDWDMGTGP
5106	19007	A	5143	403	6	FFFFFKQIGPRGGGFPQKSPPLGGGGRG GSPPRGVLTPLGPPQGNLFFLKKKKKLG GGGGPRPNPLFGGGPGKSLYPGGQRFG PKILPFFPPRGKKKKIFFPKKKKKSHR KLIQTILITGKLMKMLWRT
5107	19008	A	5144	115	427	KKKKKKKKKKKKKKGGGPKKKKNFSPG GGKKKKFFNGAKKKKPRAPVKKTGEKKK GGKKKKKCFEKNPFFGGGKKKKKCSSS YPCPKQ
5108	19009	A	5145	2	79	GCSEFRSCHCTPAWTEGDSISKKK
5109	19010	A	5146	317	444	IHQPVCAVAYNPFSTLGGRGGHITRSGLD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USNN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
						RDHFGHGETFYPL
5110	19011	A	5147	3	413	SFYHGFIVLQTVTVLIIGDPSLHGDAW SWMEFFLTIVFIALMMLPLIGLTIUVNA IWFQDIADLAFEVSVTKPHPPFVSQII ADMFLPILLQALFLIQIAVSLFPIHLV GQLDSLHMLTLLSYLCEYRLVIN
5111	19012	A	5148	409	247	QTKFRHVAQAGPHFLGSSDVTSPASQSV GITGMSLHAQHGFFTASMGRAFGEN
5112	19013	A	5149	284	1	AERASRAHMAHARTOGTPGSKAEGVGPV EYRIWRPPGDRAHVSDEESGEPGGP PPHPANFVFLVETGFFRVGOAGLEFFTS GDPASASPV
5113	19014	A	5150	439	120	FGSPRLCSCGVISAHCNLRLLGSSDSPA SASHVAGITARPANARIKAFAPSTCTV VWERHEQQTCTIQRSDLPAGRQKXTGPKN RPLGVAFPPFNASPLGGPGGRIA
5114	19015	A	5151	415	0	FFFFFFFFFFFFFLPFVQSYIYIMYI
5115	19016	A	5152	67	179	ICLSLFLTVHVCVCVCVCVCVCVCB VFGVSI PCN
5116	19017	A	5153	280	2	KTFPFLNLKTRAPPFLKTKTFKKKKPF KIFFSKKRNFFPPPPGKRPTLFGKKF FFFFQKKKNFFSPKKKKKKKKKGRRS RSRTSPRV
5117	19018	A	5154	296	406	DRVLLCHSSCSEVAESRLTAASTSWAQA ILLPQPPW
5118	19019	A	5155	114	402	VWRIKASVEKKKKKKKKKKKKKKKK
5119	19020	A	5156	110	1	QRFLTLTKSLIRLGAVAHACNPSTLGG QGGIRMS
5120	19021	A	5157	382	95	SSSSHHFLTSPQLRLFFPPPLKIFFPP KAFNCSGVPIIPSPPKKKFFPNQSGV FKNPQKEKNFSPFPVKFPKPPKFFKR PPDFFFFFFF
5121	19022	A	5158	2	350	TLQPGRGSETFPQKKKKKKKKKKKKKK KKKKKKKGGGFLNLLGGGKLVGVEKFF FFFGGGYKKPLGFFLEKIFLGGGIVA PPPPKKISFWGKKKFFWGGGKTLPLFC GGKK
5122	19023	A	5159	1	208	PTRTLVLRLGMPAEIFLSSPOEIRL IDYDKMVDHRGVRVAFQGWAGVAGKYA RAYITHFLNWLGE
5123	19024	A	5160	1	208	PTRLPYLLRLSLGMPVEIFLSSPOEIRL IDYEKMVDHRGVRVAFQGWAGVAGKYA RAYITHFLNWLGE
5124	19025	A	5161	419	25	AQKKKKKKKKKKKKKKGGGFLKNFGGGK NKRGGKKKNFLFKRGGKKKTGGLLEKN FFGGGKKGKFPQKKKALKKKKFLRGK GGKKPLNWGGKKKK
5125	19026	A	5162	475	150	KPRTSGTARVFGDPPPRCLDDKLRLSP VIFVFLAETECDRVGGDGLQLLTSGDHP HLTFPNCYNRRREPRTSSGFQHDIE HLRRGKADRFKAHLPK
5126	19027	A	5163	237	409	PHNOKTYLDSALCTLVYFVFLVRDGI LLPQLCESGTVMACHNLLKLGSRSPAL A
5127	19028	A	5164	373	476	LGFILLSFLETRSHSVAQEVQWCDHGL LQOPTP
5128	19029	A	5165	374	132	IFYSFLLYHMLGRYHKIKNLKIKHML DAVAHCNPSTLGGRGGRITRLGDRDHP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
5129	19030	A	5166	332	2	GQHDETPSLFLWTFASSLSGFPL RPQGLANCFPGALPPTKSEGFPGQSPGF QINGGKAFFLRGFPFPQVESKGAVSPP CKVPPGLRPPSAPTPPKNGDKRGPPPG RATGFFFFFVFLVETGPFHHVSNGLY
5130	19031	A	5167	238	1	GGFTGTGGKYEPPAGIVHRGEVFTKEAT SRIGVGNLYRLMRGYATGGYVGTGPGSMA DSRSQASGTFBQWNGHGSAGESRG
5131	19032	A	5168	1	89	FFFTKTESRSVAQGVQWCTGLSQLPPL P
5132	19033	A	5169	3	127	DEDFSDFDEKADDEDFVPSDASPPTKT SPKQVSYLIWVLS
5133	19034	A	5170	20	254	IAPPARIRHEERERERERERERERERER ERERERERDRAEWARLFFFFFPLPA DQCFFTKPSGQRFLLPGGGVGP
5134	19035	A	5171	36	479	TXGDXNKKDLLTSVGLVDVRAENAECL ELITFPFRAVRGNHEQMIDGILSERGN VNHMLNNGGGVFNLDYDKEILAKALAH TADELPLIILVSGDKKYVICADYPFD EYEFKQVDHQQVWNRRERISNSQDQIV KEIKGADT
5135	19036	A	5172	278	448	RFLCPLLHFFSSSETKSLTLLPRIGCSG VIAHCSLKLGSNNPPTSASRVAGMTG S
5136	19037	A	5173	205	1	HARLIFVFLVETGFHCVQAGLELLTSG DPPSASQSETPSPLKILKSAGCGGANST ALASGLLFSLGP
5137	19038	A	5174	409	194	FFFLRWSLALSARLVQWRDLGSRQAPPP GFTPPSCLSLLSISFQPSATYMRFLNTI TIVEYSFAYFPISQP
5138	19039	A	5176	339	472	AKFTCISSNIRLNTNRPCTVAHACGPST LGGRGGQITSGDGDH
5139	19040	A	5177	426	148	GGRGPPPLSHPPGGGGGGGPLRAGGQKN PGPKGETPFFGQTKKNRGATPPFSQK LGGEKHKNSTFGPKENSIFDFFFPAPPT MGEKKNFFF
5140	19041	A	5178	328	474	NNTEYNKRLGAVAHACNPSTLGGRRGW IFRSRDISP
5141	19042	A	5179	448	330	ETGEGHVGAGLELLGSSDLPASASQSA GIIGVSPHAWO
5142	19043	A	5180	259	14	LRVXATLCSWIRTTNIVKMAELPKVIYI FNAIPFKIPDMFCRIARFILKCMWVK VETIDKTIKKENRVGIPPRVLVV
5143	19044	A	5181	2	423	KFYATLVRYVGDGRKNLVCREMSWLLSN LAQGDALARAALVQKGSIGNLSFLED GVWMAQYQDSOHNLMHMQPPLEPPSVD MMCRAAKALLAMARVDENREFFLHEGR LLDISIAVLNLSLAVSVCIDVLFQIGOL
5144	19045	A	5182	182	312	FFIQGVGFHHVQAQGLKLPSSSSPPHLS QSAGITGVSHCAQPG
5145	19046	A	5183	301	472	GTPFFFFLRRSFALVADQGVWRDLGS PQPPPPGLQFFRNSTAWTKGLQFPRL
5146	19047	A	5184	216	413	KPXXXXXKKKKKKKKKKKKKKXGGAVG KKGPKQTPVKPPGGFFFPAPLVGSPPPG VFFAGGGAPP
5147	19048	A	5185	357	465	IKPTKTLAPGPGVAHACNPSTLGGQGG WITRSGD
5148	19049	A	5186	467	0	FFFFFFFFFFRFLFFFFFSEKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5149	19050	A	5187	346	3	RFLPLGGGVEILTLPSTCLGPPKRWWDY KGEPLRPAQKCFPFKKKRRRKQVNSVA VYMWYHSMCGENKLRWRWGI FTHTH THTHTQKKQNILSRTHKKLVITGSSEEG TL
5150	19051	A	5188	11	109	GETPSLLKVQNIKWAWWHMPVIPAMWEA EARES
5151	19052	A	5189	3	151	QLLRPRQENHNLNPGSGRCSEPRLHCT PAWATVQDSISNTNNNNKCP
5152	19053	A	5190	2	373	AVAADKGVPLRYHTIANLGNPDILPVP AFSVINGGSHAGNKLAMQEFMILPVGAS SFKEAMRIGAEVYHILRGVI KAKYKQDA TNVGDEGGGPGPII LDNNDALELVKTAIQ AAGYPDKGATGR
5153	19054	A	5191	55	421	ARVADVCESMKHELLVLVERAKYIPGFC ELPLDDQGLVTAHAGEHLLLGATKRSM VFIDVLLGNDYIVPSHCPLEAEMSRVS IRILDELVLFPQELHIDNEYAYLKAI I FFDPDKETEA
5154	19055	A	5192	163	466	TCLFGSQSAGITSVSHCPSEVFFLKLI HWQGGQVALLVATPHSPCCPYRLAPI PRARHDFACASLFPACILLVHVLMPRV SACRGVGVPRAGIQAG
5155	19056	A	5193	470	0	ECLWPGTVAHASNPTTILGGRGRIMK
5156	19057	A	5194	491	281	RGLALLPMGQCSGHWLAHSLDLDLSSD PPASASQSVGIMGVSHAWPSLVNISFV CLIHRSPTKTPGGR
5157	19058	A	5195	3	222	LSFSLHRCLYMLGTTSENVSPPFSLLEL LSRLATLLGDYCGSLSEGTISRNVALLVY ELLDEVLRLESRCVAQA
5158	19059	A	5196	20	191	STWNWSSRRGGGCSSEPSHCTPAAVTER DSVSKTKKKINNKPALALPAVHPTSRPG S
5159	19060	A	5197	460	350	RRLRRENHNLNPGGGGCSSELRSCHTFAW VTERGPSD
5160	19061	A	5198	174	41	SLGELLTECLFETKSHSVTOAGVQWRHP GSLQPPPGQFKRIPPH
5161	19062	A	5199	131	454	FEYFKNRKPFYFFFFFGKGVSFCAFGK AGDPFKLREPPPRVKGFFGPPPPSGGK NGPPPPPRVFVFFFKRGGSPFWPGGVL TPGGGPPPPAPQRRGGINGLDPPAR
5162	19063	A	5200	168	51	TVKTPIRPGAVAHACNLSTLGGRGWMT RSGARAQPNR
5163	19064	A	5201	414	497	LLFXXXXDNGSINYNEVLDTITETLHNR
5164	19065	A	5202	381	614	VQPGAPPEVVALSTCFSAAPGGQQPYI PPTFCFFPVKWLSSLVTWLYLFYFLSWI SVAQAGVQVCMHGSLOPPRSRL
5165	19066	A	5203	377	485	PKEPGPOPCAPQOPHAPQOPAPQOPQ PCAPQOPQ
5166	19067	A	5204	54	434	MRTPENLELTNPQEFSSSWAAVECPDTL DPRDMCVLNPLREPFPAKKECSILLSEVF EICHPPVDVTWFYSNCLTDTCGCSQGGD CECFASVSAYAHQCGHGVAVDWRTPR LCRCPCQSPGTE
5167	19068	A	5205	201	418	GDAGAHAVLRLLPQHPGTSHLFPSSLLT SPLGLKRVYGGFNSKNRCDARTCYLLP TFAPAHKDRQVDETY
5168	19069	A	5206	27	177	NSFAHAGQSGLELTTSSDPFASASQAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5169	19070	A	5207	6	1175	ITGVSHRAQPKAGTFLSPFHR DLGPHTPAWTRPKREDLVQSTVRLPEV RISDNPGYECHEVGIYDRATREKVVLASG NIFLNVMAPPTSIEVVAADTAPFPSRYQ AQNFILVCIVSGGKPAWPMYFKRDGEPI DAVPLSEPPAASSGQLQDSRPFSLLLHR DLDDTKMKQKSLSLDAENKGRGRPYTERE SRLGTPPKNLLQSTENLFFTYVSRETF PRWHSIAEPTYFLHRSRTSSDQTEVEV ALLTWTNLPOIDNEALFSCVEKHPALSM PMQAEVTLVAPKPKIVMTPTSRARVGD VRILVHGQNEVFPPEMTWTWTVGSRLL DGSAEYDGKELVLRVPAELNGSMYRCT AQNPLGSTDTHTRLIVFENPNIPRGTE SNGSIGPTGARLTLLVLTALTVILELT
5170	19071	A	5208	401	3	FFFFFSETESHVAQAQVQWHHGLSLQG PPPGF
5171	19072	A	5209	402	229	GFFFKGPPPPPPPPPPPPPPPPPPPPPP RLSGSKVENVWGSQKLYMFGCCRCGRSW FT
5172	19073	A	5210	198	2	PPQAKILSSSSPPPIRPPPKKGFPPKNPQ VGFYSAPHKERTFTLPAPVKFGPPKDP KRPPP
5173	19074	A	5211	516	222	GSTLRLTQSRMPASSSTMAPSSKRLLLE RPERSVPAAGTAGHHEASRNCGRGAG ADEGPATKGDHSHKPGYCAAHPSAAPW PPGPEKNFMVRG
5174	19075	A	5212	103	203	DKVSLRCFGWQPTPLGLKQSSCLSLPKCW DYKCE
5175	19076	A	5213	409	249	RRNOVGPPROLNPGKRIKSPGIDPYIYG QLIFDKAVRAIWRKGSFLQKALE
5176	19077	A	5214	2	170	ERKILGYIQLRKGPNVVGPIQLLQPFAD ATLKFTKEPLKPATSPYPLQSPAFPLKP
5177	19078	A	5215	270	464	GGLNKRVWGWDPQKVTFRDGVSLYCLHW NAVAIHGHRHVSVPQQTGFKQSCCLRLP SSWDYMFPLY
5178	19079	A	5216	136	248	PDKSYITCVCVCVCVCVCVCVCVWVME CP
5179	19080	A	5217	412	2	PPPPQIFFPPPHFFSPPPKGGFFPPPPPP KIFFPPDPLFFWGFPPPTSPPPKKFFFP PKSPPPFFPPPPKKKKFFPPPLFFPPFP PGFFLTTPPPPPPPPPPPPPPPPPPPFP FRMGCDRWHGEFNLRLDGF
5180	19081	A	5218	165	1	QVKYHNKKTNPFIKIGKRSEOTTFHEKDT QMANKYMRSPTSLRIGKIQITIMRY
5181	19082	A	5219	408	88	PSSSPHFFSPDPLGCVVFPFPFFKIFFFP PGLFFFWGVFLFSPDPKRVFPFNSPPG FFFFPLFGKKFFSPPPFFPPPPGFFLS PPPLFFFFFFFFFFFFFFFF
5182	19083	A	5220	3	259	NLLLLIVPILAMAFMLLTERKILGYIQ LKKKKKKKKKKKKKKKKKRGGAFFKK PRGQNPPEKKKKKFFLREVKKPRGN F
5183	19084	A	5221	10	479	KLMPAESDGRHRERERERERERERERER ESSSARARCVSLSLDRYKNRVYMVAZA LCECRLLAYISQAPTQMFLLRLINIIH AHTLTQENDMCLHTLTLEILARQERV PLYLRVLQRMHKKKHGPGVFLNASHLV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
						RLNQQLYLHRDRDSTC
5184	19085	A	5222	142	56	KFQFGAVAHTCNFSALGGWGGQIKRSGV
5185	19086	A	5223	14	471	LEMRSETDSQVNCNCADAGENWTSFTIV LSQKEHLPTVQIVMTDAGRPHSEAAAYTL GPLLCRGDSQFWSNASFNTETSYLHPPA FHGELTADVCFFFKTTVSSGVFMENLGI TDFIRIELRGKLTATLDSQGTLYLAICA LTQKKKKKKTRG
5186	19087	A	5224	480	0	FFFFFFFFFFFFFLVAQYFL
5187	19088	A	5225	16	422	VRRTARIRHEGKPYECNACGKAFNRSAAH LTEHQRTHTGEKPYVCCKEGKTFRSRTH LTEHLKINSCKVPYQCNCEQKLFYCRYS LIRHQRTHTGEKPYQCNCEGKSPSLSSA LTHKKRIHTRERPYQCKKKKKKK
5188	19089	A	5226	99	436	GHPSEFIPATMTAAPAGFPQVPWEDVR YLFDEIMYGGHITDDGDCKLCRVYLEEF MNPSSLAAALSGTHACGEKPLPANSHVS EPSWKWILQPOSSQLMTAALANTLTATS
5189	19090	A	5227	473	9	FQITATPHLAVDPTVQGFEPWFSEKQIA DIRQVEASTRYLGALYWIAASINIKPG HDYFYFIRSNTVGKSAFVEAVGRASDD AEGYLDFFKGKIAESHLGKLEKVELT EDIASRLEEFSEKWKDASDKNAMWAVK IEQTQVGERDVTSG
5190	19091	A	5228	1	473	PPPIIDRLFNCTACRNSARVMTDAGQPHS EADYTLGPLLCCGDKSFWNSASNTETS YLHFAFHGELTADVCFFFKTTVSSGVF MENLGIIDFIRIELRGKLTATLDSQSQT YLAIKALTQKKKKKTRGGAGPPFPLIGS RITIHGPPFNNAAMREK
5191	19092	A	5229	170	25	KTFLLGPGTVAHACNLSLTDQSGCICMR SGVRDQLRQHDETPSLKKRI
5192	19093	A	5230	465	0	VVLVPPQKAQKKKKKKKKKKKKKKTRK ARG
5193	19094	A	5231	419	56	CVLLRSTKKKKKKKKKKKKKKKK
5194	19095	A	5232	79	451	AGSNLQEHRLRPESPFNPGGCGCREPR RRHCPAPAAKRAKRLKKKKHGKNQEA QQRHGFPFPGLPGLPREGFLPRRPGSRKRR GRNVGPELKGPAVLFSRHRRGADLR PPRKGPRGGGG
5195	19096	A	5233	39	467	VQOQQAQSQOQHPVLHLQPOQIMOLQ QQQQQRIQQQPYQQPPHFFSQOQQQQQ QAHPHQSQOQLQPPQQLHPQQQLHRP QQQLQPFQQQHALQQQFHQLQQHQQQ QLAQLQQQHSLLQQOQQQQQIQQQQLQRM HQO
5196	19097	A	5234	194	45	MLTKFFNFNFKIHFFFLRQSLALVAQAG VKNCNVGSSQPPPPGFKRNST
5197	19098	A	5235	204	475	ASITVHLWYVEKCYQSSTKVTMPSSNS WFGPQPDALQKGLRPGAVAHACNPSMT GGRGGRITSSGDAHP
5198	19099	A	5236	59	357	NHWRKIYCKVYNNRKIKGNTNTNTINQY NFORNRTKSSFTIFRIQSHYNKHIKKH KQKQSSLETDLMTQMLELVIFKVVIV ILTKIKPTKTLKNG
5199	19100	A	5237	447	166	ELLAPWGTQYNNNAVNLFFFWIKAPGI PTPSFASRTHSPFSPFLFLFFLQKK GPFLCGPGGKSLNLKTPPLGPFKGGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5200	19101	A	5238	34	296	LSVAEFLAFWQYNNMNAVNLFFAWIK VPGIPTPSFASRRTHSPFSLFFLFF LGKNGFSPCGPEGPKFLNLITPPLGPK GWE
5201	19102	A	5239	340	472	SLNETHVRSFAHHRPGATAHACNPITLG GRDGLIMRSGDQDHPG
5202	19103	A	5240	460	0	PKKKIFTIYFYFFYYYYFFFFF
5203	19104	A	5241	161	46	SFYSTRHKPCWPGFVAHACNPITLGG GGRTSRDR
5204	19105	A	5242	175	36	LKYLIIFYLLSFFFLQKRSVVGAGVQ WRDLSSQLPPNSTALQYR
5205	19106	A	5243	11	442	DTIRWGLPTLGSKSTINEKKREKKRKK EQQOSEANELRNLAFFKPKQKSHAVCN AQHDLPLSNFVQKDSRENNQEWQRDE QLTSEMFEADLEKALLSKLEYEEHKK YEDAEINTSQSKVNNKKDKRNHGGKDR PLTV
5206	19107	A	5244	459	333	FLRVTAQGLKLLSSSDPTLASPKCWY RHEPLCPAQWSV
5207	19108	A	5245	229	436	FNSTVVRKGLGGIHLNLITGSFFAHL VVSLLTYVLCVSFVCLFLRQSHFVTAQ VQWNLGLSLQPLP
5208	19109	A	5246	227	30	VFFARWFLRQDLDSRLCECSNVLVH CNVRLAGSRGTPSSVSQVAGTGMLYHT WVFFYEFHR
5209	19110	A	5247	173	442	FLGSSSKAAITLYCYQMEFFFFF KNFFSPGGGEGNFILLEPPPLGLK ISCPTPRGWDYGVAPPLVNFVFFKKN GVPPFW
5210	19111	A	5248	255	358	TGPGTVAHTCDFSTSGRGGQITMSGDR DHPGQH
5211	19112	A	5249	3	130	QPQLAAPSIWAPTSASQVAGTIGVCHH AWLIFLFWVESRRG
5212	19113	A	5250	90	1	STRLENNGTMSAQCNRLTGSSNSPNSA SR
5213	19114	A	5251	358	447	SFISYRRRSFSPYYSRYRSRSRSRYTP CWNTSMRGPWEAAEAGESLEPGRRSCG EARTCHCIPAMVVRALKLVAA
5215	19116	A	5253	330	3	EEMGFHVGGGFKILASGDTPAWAFQK GGISGVSPRAWAGFIIFTWVPSGGQPTG FPFYPPRGIFFPRAKINIRVLNPKGLC QKGVFFFFSGFPHYRCRLQISV
5216	19117	A	5255	175	3	MYLRFPGLSLSERPGWVAHACNFCYTW ESKAGGSLSLGVQDQPREHGGTLCLQKS K
5217	19118	A	5256	263	1	RPRRFNRDKTALLQEMFFPTALGKL ISDFKDKDGLTYFYFYFATSRSVVLACL ELLTSSDPTASQSTGIGVSHFSQFG LAF
5218	19119	A	5257	1	103	CHVSOAGLELLASDPPASASQSVGIG VSHRTW
5219	19120	A	5258	128	2	IRKWRDKCNVQFLMKRAQPLMNLNHL SCDPTVLLLDILTQ
5220	19121	A	5259	381	2	FFFFSEMESPSVAQGVQNCGLSLQA PSPGFT
5221	19122	A	5260	2	173	ENYLNMGGGGCSFSLHCSPALAIERD SVSTTTTQKQQQNNQLGLFSYPPNFI I

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
5222	19123	A	5261	1	175	1KGNQIGKKEVKLF1FDNNILYMENPK DSAKNYYKQSKTFCLPVVLGRSCKRTCP LA
5223	19124	A	5262	2	145	QVSLKLLGSSDPALTSQAGIMVSHR TRPRNTDFKNNTQKSKNTQ
5224	19125	A	5263	182	3	SITTSPLNFLLTEWVSHVVSQAGLKVLGS SDPPSSASHSAGITGMSHHTRPQPLLN LKV
5225	19126	A	5264	183	369	WNSLDFFFFFSPFRGYSMSGKVQDAFI FYRRFIDKSKPRANTWGSIGGLYQQQIH PMDALR
5226	19127	A	5265	329	207	RGCSLELRSHCTPWWVTEQDSVSKRKK KSPCHLQLGTSQ
5227	19128	A	5266	177	13	TLTILLNFLLRQSYSAQAGVQWNNLN SLKPPPPGFKRFSCLSLPEFQQGHNR
5228	19129	A	5267	474	122	FICSPHFGGFLTLGPKNLTLGFSOPLFP LRGSKKKQIGIPFYSYKIKGPPGAGPPGS ARYSNPFGYGGRVPLPEFPDPGGEHK PRFPLKKKKKGHVPTSXYLPEYLFAYY NASLE
5229	19130	A	5268	55	311	GIQTFGNVVVAGRSKNVGMPIAMLLHT DGEHERPGDQATVTLAHRVTPKEQLKIH TQADIIIVAGSLSLSHAGVQWRNHGS L
5230	19131	A	5269	238	133	NKNIWVQKCKVFFYYTLPLLCVCVCVC VCVCVCV
5231	19132	A	5270	336	517	PVLYILEHSPYNASIIYQLALKKYQSRFG AVAHACDPNTLGGRRGIRTRSGDRDHPG QRGE
5232	19133	A	5271	262	467	VLSMRPRIHGSAAAREDEHPYELLTLAE TKKVVLVDCKTKGTPPTPGRTNSKGIF KVCDPEWKGKMS
5233	19134	A	5272	213	2	MKIYINVVYLLFSLKKRQOPTLSPLRELC SGMIIVHRSCLKLVGSSDPALTSRIAWL IGARHTPDSCVCKF
5234	19135	A	5273	284	105	YSCSVSYFDEPVELRNSSFFRRNHSSDS YWKKKSSKDTEPVLKPPGYSARYECKTV GSS
5235	19136	A	5274	290	449	IFYFSGRVRAKLASPLAGMGNAKADSRG RSRTKNVQSQRMYCLSLALLYLSLC
5236	19137	A	5275	248	423	NKVNITLMTKLEKDTTKENYRPISLLN IDMKILSKILQNIQQYIQSI IHHDOVK LL
5237	19138	A	5276	425	30	TRRGMPHROGSPRKPAPSVRRQRVREEC GREPLLWFLQSQLGLRQETHLNWGR GCSEPRSCHCIPAWATRANSIFCNFQAS SVEVRSARKKLFSDILKRHNITITVRVS GLLLVDSYFGRLATPVRTQ
5238	19139	A	5277	25	185	SLFSVAEFAPNAYKVQTEKEEKEEARSK YKEAKESQORFLENHEKMTSTTRYK
5239	19140	A	5278	263	483	VFTVVVFQLFCVYKLLFSLTECRSVAQ AAHAGAHWNHLSLQPLPSGFKQFSCLS LPEFFRMYSVLSPSP
5240	19141	A	5279	25	252	LETGLMTLVQCGGIPGFCHVGAGLKL LTSGLDLPASASQAGIAGMSHHTRPILL HFIFYILLYHPCLAYFIIF
5241	19142	A	5280	326	203	TEESCYVAQDGLLELGGSNPPTSASQS AGITGVSHHTWT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
5242	19143	A	5281	210	459	NKNNKKFNEKKKKNYKKWARELYRHFSK DDIHVANRYMKRYPTSLIIRKIQIKTSM RYHLTPIRIATIPR
5243	19144	A	5282	262	454	LLFTDYHEGMLHSVKLLFCFLGWSFTLA IQAGGHWDRGLSLCPLLPRLKQSSCLNL LSSWDYKR
5244	19145	A	5283	451	303	GTEFHHVGAGLELGGSSDLPLVASKSAG IIGMGHHAQPKQYSFVILTQ
5245	19146	A	5284	217	489	PVTSITILRCLSLPTFGSRVLCMLEGM GISLQWVPLPSLPVPLHFLDLSLPVCRQ VGQTKTVGVRYVGRTDFAKGEGCVGLD KPLGKND
5246	19147	A	5285	247	99	FFFFFFFFFLYGFFCFFFFFFFFFFFFFF FFFLKINKTQPYFIYKRNILSM
5247	19148	A	5286	2	117	PRVRPRVRPRVRPRVRPRVRPRVRKKK KKKKKKKKKKGGG
5248	19149	A	5287	121	3	KFWPGAVAHACNPSPLGGRGGNITRSGD RDHPQHSSTP
5249	19150	A	5288	416	48	IGKPGSFFPPPPSRGAPPPPPKIFFFLP PPPPFFFRAGFLPLPPPPQIFFFKIPPP FFFTPLPKKKFFPPPPPIFESPLGLFFF PPPPSLSPSFFFFFFFFFFFFFFFFFFFF FFFFFFFFLGV
5250	19151	A	5289	503	0	FFFFFFFFSPFFFFSSSSFFFFFFFFFFFF
5251	19152	A	5290	70	236	IFCNSQLTSPHRQKKKKKKKKKKKKKK KKKKKKKKKKKKGGGDFKKKIGGAK QFTKKKKKKKKKKKKKKKKKKKKQKTT IPKPLP
5252	19153	A	5291	443	287	KNPNALFFFFFFFFVDRIISLRQWNHLS LQPLDPGFTQFSCLSLPSNWDYRCEPLR PALLFFSSKSKIHKPL
5254	19155	A	5293	413	3	SSSPPIFFPPQKKKIFSPPPPKKFFPPP KTFFFLRGFFQIFPPPKNFPPKQNF FFYPKKKKKIFPPPPKIFPPPKIFLKT PPPPFFFFFFFFFFFFFFFFFFFFFFFFLV LEKGFPAWADAWADAW
5255	19156	A	5294	291	11	IQPYIKRLMHRDVLGSSEKQSNWPRIYI YINVPGFNKGPIIIGSSQKAQMIFFFI LDRVLCHPGRSTVVQSQPTAALKNNAQ KTLPPQSE
5256	19157	A	5295	2	401	NPRSTAAIKYFLTQATASILLIATILF NNILSGQKKKKKKKKKKKKKKKKKKKK KKKIGGGKKKPGGKKKIFPIRGEKQNP RGEFEKKTFFWGGKRRANPPPKKTLGE KKKILGGGGKKKFFVGGKK
5257	19158	A	5296	49	363	RLQKNNKKKKKKKKKKKKKKKKKKKKR KKKKKKRRNGGGKLLWKGGQILLTKE KILLVAVSYTCNINNLQRQRKWIIGG KSEPNYEFKRNIGAGRGSSLL
5258	19159	A	5297	100	323	EVLNTCVRICHSHAFILFPSYVSFALLE RFLFKVLLVMQVFGEGTEAVKKSLEGI FDDIVPDGKVKINVCFLF
5259	19160	A	5298	595	0	VVCVCMCACICIC
5260	19161	A	5299	412	141	TVDTSYSEKILFQILLIDNGFGHLRA LMEMYKEINVSMNPANTSIMQLNQGV ISIFKSSYLNRNACATAAHSFDES QGSNLL
5261	19162	A	5300	216	2	SODRLRKFCHPRVFORQPIQLRLMGFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5262	19163	A	5301	368	3	FCLPLRMVWKGVFFFEEMEGRSVVQAEVQ WHDNSPLQPKPPLGK IFFPPQKKEGGGLFYIFFPPKKGFFFK KKIFFFYPPPKKKKKIIRAEEKRGPPLF FLKKTNRNFFFFFFFFFFFVFLVREK VFNSTISTQ
5263	19164	A	5302	389	2	AMQAASGSCCLSRLLVDGFIWGVFRYF IVEAGSCYVDGGAILASSYPTTLVSQ SAGMTGLSHRRAPPLNGPPPLTSLSM VPKANVFSLLKPTGLTOALRITLANVS NAPGQTRSGLEWGCFF
5264	19165	A	5303	84	333	FHDCCRPERSTLRNPLLSSAGIQSIAD AYRLALPQGLLYGPTNFAP1INHVAF AHAAHQGTASVVRVVGSGSGGQNGQLP
5265	19166	A	5304	485	93	PPLFRFRSPFPFPKFFSPRAFFFGGGF FSFFSPPKKSFFKNPPGFFFPPLKKK KIFLPLPLFAPKDSFLAPPFFFFFI FFFFFIIFLDRDLFCCLG
5266	19167	A	5305	157	2	PPPPPPPPPPFFVWVITLNVLEFSF SPNTESIQGPREAMERLOENRVE
5267	19168	A	5306	1	133	TQESIMDLNDKQQLDERLKKKKRPAV LKNPWGGGSLFGMARE
5268	19169	A	5307	239	2	PPRNWGFSPPLSPKSSSPPKAFNWGG VGNFPFPKKRFFSKNPPGFFFYPLKE KNIFSLPPVNLGPPRVFFKGP
5269	19170	A	5308	454	116	FRLPSSNSFAPASRVAGISGRCVGR GLQLLTASDPPASASQAGIADGVSTQ CSMWPRLECSGMI SACYNLHPAACLGP PKCRDCSLCLATPSGK
5270	19171	A	5309	123	1	CSVSKWYFIKFLKNTIMLWAEAGGSRG QEIKTILANTVKP
5271	19172	A	5310	153	33	WPGVVAHTCNPPFLGGRSGLTRSGVQP QPGQHSSEPSI
5272	19173	A	5311	350	3	NSRNLTITQHSPEKNEPLFSLPLQSV SMNTTHSPLLSNSLPHFIIISFLPTRFLV GPSPTRSFPPAQSDPDISFSSRLSCSGT ITAHRSNLPGSSDPLISVSQVAGTTCM CHI
5273	19174	A	5312	1	392	RTRGRTGICKSITIIHINKTNEKKNH MIISVDAESAPLQIHSAKLKK
5274	19175	A	5313	1	239	LKTSFHHVGOAVLEFLASSDLPALASQ AGITCMSHCAQPYISNFI PAETQSS PELVLPASQKTPSFSTPLFSLP
5275	19176	A	5314	345	237	LYFYIYFLKSACVILSTLCVCVCVCVC VCVCLCM
5276	19177	A	5315	268	412	GMISSNNSSDSFGNCLNPGGKGCEPGS YHYPPAMATDTFSKKKKKKL
5277	19178	A	5316	112	224	PWMLNGLGHASYLAMSTPLSPVEIEC ASKKI FTFC
5278	19179	A	5317	377	139	KPPPRIFYLGPQKKKLFYPPFPKNCFF LGPPPPPLEMIFFFFFFFFFFFFFFFFF PQWVMLFFLLSASQNSPWS
5279	19180	A	5318	216	385	RQVLCCPAWSQTPGLKGSSCLSLPKCW DYKHELPRPATSCNSILFNLQAGMYH
5280	19181	A	5319	376	3	RIDFGGPKKKILLPPPAVKIVSLKGGP LEFFFLNSFFAPAGGQGVQLLISSGDP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						PPAPESVRIPGVSFCAVGQFFFFFLL NSSVAQAGVQWRDLGSLQPLPPRSKRVS CLSHPPSSWDYSH
5281	19182	A	5320	377	287	ELLTSSDLPALASQASAGITSMHHTQPG SF
5282	19183	A	5321	381	65	SSSPSSRTSGPFFFFSPPKKKKNQKPKK NFLYPFFFFPPFYKNPPKKKLGPKKK KKISPPPKKNLSKNPPPPPPPPPPPP FFFFF
5283	19184	A	5322	132	396	EGGFVLKIIREGIGPHFLGLEEGSKFH EHI FWEKHRESFPKGGPIPHFMELGTWG LSKNPYFRVKQRVEHIEGFKNFNEKKD FLKE
5284	19185	A	5323	366	1	GFLKKGVFPFPFGKGGGNQTPPKPFVL GKGQPPPPPLKKNFKGPPQKKIIF FLTRGGVSLFGPGGGGFFFFQPKKPP GGFPFFFLKKPPPPPLFFFFFPFTGE CSCRPGRTRG
5285	19186	A	5324	131	1	DGALSPLREWCSTYLACHCSRLPGSSA SCVSAASVAGITGVC
5286	19187	A	5325	112	1	DGILLPLRLSNGASIAHNLHIFSTS ESTASAFLS
5287	19188	A	5326	404	18	PVSPHGNHKEHHTVTCVSTSGAFLHGE EHCHGNTHHPFSPSNPQACQSQANRIR HCNSFKNLRSWAWRTPVVSATQDAEM GRPLEPRGLSLAWATQDDPSLKQKQKQK KPTHLWSYILGHQPL
5288	19189	A	5327	109	3	KCVLTPVIRALWEAETGSGRQDIETIL SDTVKPR
5289	19190	A	5328	1	117	ETGFCCVAGSLQLLSSNLLALVQSA GVTGMSHRSRP
5290	19191	A	5329	3	120	DAWVAEAEQNDTIEEFNKVQRRKRI NDNVPAQOAH
5291	19192	A	5330	105	2	RSVVVAHICNPSTLGGQQRWITRSQVD QSVQDG
5292	19193	A	5331	204	411	SKKKQKKKKKKKKKKKKKKKKQDKG
5293	19194	A	5332	185	2	FFFTESHSTIQAQVQWRDLSSLQPLFP GFKSLPSSWDYRCLPPCANFCIFSRDR VSLCW
5294	19195	A	5333	561	325	WSTLHSPFIWLLNTGYYPKELTGFFFL TVALSPLRECSDTIAHYSRLRLGSRDP PTLVFGSTKITSVSHCTQPSVRF
5295	19196	A	5334	3	96	EKKAASQKSRVRKEENPITAVSASTI PE
5296	19197	A	5335	375	228	LSPHLECSGTILAHCNRLPLGSSNSPGV FGFYFFLLTLIGSGVHVQLC
5297	19198	A	5336	403	0	NISVFAKSHISFPFKKKKKKKKKKKKK KKSQKKSRG
5298	19199	A	5337	397	80	ITITSKKKKKKKKKKKKKKKKKK
5299	19200	A	5338	406	34	KRTLLKSKKKKKKKKKKKKKKKKKKKR EKKKKKPKKKKKKKKGGAQKKKNHPAG GKAYFFLGOTKKKRGQGDTPKLGKNS PAQTKLGGNNPPFVERGKKKKKTPI KKKKKKKKDAPGGGGGKKKKGGPQKK KKGSHLKTPEKKKTGGA
5300	19201	A	5339	410	0	
5301	19202	A	5340	306	392	IQYKILPQKENDWDNIQGLATPVSSLN F

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
5302	19203	A	5341	3	173	TFATLLELIFYIFPETLLTLLAITRG QNQPERLNAGTYFLPYTLVGESLLARS R
5303	19204	A	5342	247	426	GRANWFTFVITPLWEAEAGVQWRDLSSL QPLLPGPKRFSCLRLPNNDYRHVPRP ANFL
5304	19205	A	5343	3	149	SWFLHFGAEGLLELLTSGDFFALPKCW DYRLVSNWPEVILQPPQPK
5305	19206	A	5344	464	147	LRLRLRWENRLRFGGGGCEPRSHRCTLA RVTESLSRVQCQRPRRLAQTSRRRPGAS SFFAGPAFSAVNSTYQALPPAAGAPW TPRLPLGPHGTSTSSSYLPV
5306	19207	A	5345	228	1	VIRLEETYFLFFVLFLFFRQTRSGS FAQAGVQSSHLSLSPSWDRHYTPHLANF CIFLQKQLAMLRLVSNTK
5307	19208	A	5346	2	106	FVLELLGSNNSSPSSASESAGITGVSHCG QPLNPF
5308	19209	A	5347	140	436	FLCDMRVLVYVTTTTFGKGVSFPPGWRA GGEGFLIENPPGFNPFLLNLKKGEL RAPPPAPIFFFFEKRGRFRTLQEGLN FWTWPPPLTLPRGG
5309	19210	A	5348	1	465	LESRRFEDGTRVPGSTISWDPEEAVCP FSDLOLRAGRTTTLFKAVRQGHSSLQRI LLPFVWQCPAPRGVYRGRQASLSCSGL HPVRASWLLCFPSAWAMSGTTPPASLP PCNLISDCCASNEQGSVIGPSEPGEVY NLLLRHLLKPEEKRS
5310	19211	A	5349	183	58	ERDYEEGPAVACACIFSTLGGRGGWIT RSGDRDHPDETVDP
5311	19212	A	5350	288	404	LEXNGWLLAHCNFPLGSSNSPASASPV AVITGMNHYAR
5312	19213	A	5351	413	305	AEAGLKLPSSTYLRAASQSAGITGVSH HTOPLFF
5313	19214	A	5352	91	356	TVPKRNTFSPKNVAITAGTVSTSVLAL GNRESALPTRLGWLACCFTFWGGRGHRV PLCHPGWSTVARSLTATSTSQVAILL POPP
5314	19215	A	5353	2	410	FVQWQPLKTGSDRSHKAVESLGVEKVER AMTVNYSFRLNLTGKLELLGKISVNLV AKWKHFREKGRRYNTLGPTATAAPYST EKTEFLPVVEQTCKPFI DSFNKYLPGA ADHACNPSTLGGRGKITSRDRD
5315	19216	A	5354	3	288	SLDDDLKLLPLMLQYSDPEFVQSAYLES RRLAYFCARRLSLLSDSPNLLAHS MMIGFNNISIGAPSGPPGPGMSPVQLA FSDFLSCAQH
5316	19217	A	5355	187	3	KKILWQTPGVNLFVSKGAPLFFFLRRV LLCCPGPWSAVARSELTATSASRVQAILL PQPPK
5317	19218	A	5356	383	261	GKYNQKQSQAPLYTNRRQTESRLWYCY DSPQRLIHLISK
5318	19219	A	5357	367	241	FFFRHVAQAGLQLGSSNPPASPSQSVR VTGVSHCTOPLCFV
5319	19220	A	5358	217	1	SCDRENTGLKLLSILLIHCETDTRISL LCISLSIKREIWLGAVARACNPSTLGG GGRTITREDRDPGETP
5320	19221	A	5359	255	412	TOLCRKNAPFFLATNHSQKQSRWGT AHACNPSTLGGRGGRITRSGDGH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
5321	19222	A	5360	391	271	RSCHTAQAGLKLASSNPASASQNAEITGVSHHLTPIC
5322	19223	A	5361	232	397	EGLKEPAGLFTMEYYTARKNRKIMPFVV TWQLEAII LGESTQEOKTKFCMFS PV
5323	19224	A	5362	213	392	LFIKVBEKFFLRSINILNESLFLSSNG PGLLKKLGWVPGVVAHACNPSTLRGGGG RTA
5324	19225	A	5363	306	418	SDGITGTLPASQESAVVEDLLYLVLGV DGRVVSAP
5325	19226	A	5364	347	48	KRWLKKGGGKNNPKKGGKGGTTPFFQ KGGFFPPFFLEKRDLSPOAGGKGEK KKPQGPWKABGKKPMPGNPPQRGYKGN PTPPPQGFPPFFFL
5326	19227	A	5365	412	172	PDSNLSFGAHYQASLLGSFSLMPLLSY KCSGQWDVARSAETCSKSSQNKERKKER KKERKKERKKERKKTRKQKNPLT
5327	19228	A	5366	400	296	LVEGGFHHVGRAGLELPTSSDPPTASQ NLGLQA
5328	19229	A	5367	162	1	APSSLDDETPILLKKTLEGGVLVAGICNP STLGRGGGRITRSGVRDQPDQHGTEP
5329	19230	A	5368	152	403	TTVLCLEVLKKTWRFLKEVLVDLPF NPAVPLLGIIYPTKEKSYEGTCTHVFIA AQFOIARIWNSKCPPINEQKKKGAPV
5330	19231	A	5369	170	367	IUVFELIVISYFKSPPOKITEWNTFFPH FKVFNPSTVAHACNPSTLGRGRQITR SGDRDHPAR
5331	19232	A	5370	396	1	QMCVRHTFAGGRARTRHTHTHTHTHS VVATPRVSHNHCVCVCVCVCVC
5332	19233	A	5371	139	3	PKLECGASTIAHCSLELLGSKDPPPSAF QVAETTGCAFPCLAFF
5333	19234	A	5372	1	341	PLINILSHLILLCRNYFSFVKFCIRHTS LLYVVVISLPHVLLCVSPLTDRRAINAS VTYGFVLVPTFKNSPLPGAVAHACNPST LGRRGGQIMRSQVQDQPGQARSRRPALF T
5334	19235	A	5373	280	449	ICHNLQLCPSKDTTEKVRKQPIEWEKIF ANKISHKGLSS
5335	19236	A	5374	170	1	QKRGPSMGTPMVSI FRPQDLTLPFGPKA WDPVRNWPWGPWPCPLFFKGNPQLFOAPG
5336	19237	A	5375	462	165	PPTRFLHVVTGLELPTSGDLPASASQG AGITGVSHHAQPRGHVFDVLLYSQQGV FLLSLFLGSPVFEPLC
5337	19238	A	5376	3	451	PRAKLGTTRGLRLNDITGVAVDILLLER ELRVEQSSLLTAPCOGLQFLRNIA SRHE DSQSIGWHVAFPPVWVCLSLPPPHGTS SSSITLPLLLPHRPHPPHSHPPMATLS RPPYPPPPPPHPLPLPSLSPALSPPP PPPPPPSL
5338	19239	A	5377	460	300	KVLLCCPRLECRGATMAHSHLELLGSSN PPTSASQAGVTGVSHCRSPVVEFL
5339	19240	A	5378	452	191	DSRFHHVQADLEHTPSDDLHASAQSA VITGVSHRTRPDIAFAPISISSYFSCVAE ISLLHLSSEFPKQFL
5340	19241	A	5379	240	395	LATSSVANLRNTFYLLKSSVLGVEARS CNPSTLGGQGVRTKSGVRDQPGQ
5341	19242	A	5380	210	411	TSVNSAPNSGQKASVEECFQGVTKVKIKI NVFLGWAQWLTPI PALWEAGAGGSRDO EIDTILANTVR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
5342	19243	A	5381	406	300	FHVVGQPGLELLTGLSGTCLGLSKCWDR PRHPQA
5343	19244	A	5382	364	479	INDGTISKISLFLSHLKDQAGQVWKLTPV IPALWEAEG
5344	19245	A	5383	182	395	HLRLGSAASFLKSAQEPDTRFHTGKPRF SCLSLPSSSWDYRCPPPRRGGVGLRGR RTVQSWLTTTISIQ
5345	19246	A	5384	37	478	GGTHSYPTICLPIFLMGSSVSLPFSSVAC LLAWLLPSFLPLSLPSFLPSFLPSLTGR AFL
5346	19247	A	5385	201	458	WNPFPLSPRKWAARADTEGVGKTAQEP GLSSRLQAYEERQRHWQREARELREDA AYAQAQARAQQLLQLQVFLQEQEKLQ DD
5347	19248	A	5386	206	407	FFSPGGRAGEKFGFMEFPFGFKTLTLW NPPGKWKORAPPPIPVYLFLEKKGKGGV NMVQVGLNPRP
5348	19249	A	5387	468	0	NEFFPRPAPPPFFFFFVFAQGVQMRVL GSLQAPPFGFTPFSCLSLPSSSWDYRPA RVSPHC
5349	19250	A	5388	136	2	LEFFFLFETGFCSVPRLSCSTTIAHCS LKLPGSCNSPTSVSQV
5350	19251	A	5389	397	0	ILYPSQKKKKKKKKKKKKKKKKKKKSQ
5351	19252	A	5390	299	3	AQPLAPFGPSFILMYFFMILLFGIPILLY MEVIMGQWLHVDNTRVMQQLVPLCSMG YAHSLVNEGSPSRPSPISLCGLQVSAHR VHPQVCASVLYNS
5352	19253	A	5391	264	202	FFFFFFFFFFFVFSSENKI
5353	19254	A	5392	2	150	PRVRPLTETBFCHVGAGLKLITSVDPP TSAQSAGITGVCHLVREKS
5354	19255	A	5393	382	0	NSRAQAQWLMVPVSPHWEAEVGGSEPT S
5355	19256	A	5394	395	239	SLPSCFDRYHAPQCWANFILVETGFSS VLVCSFRIAGGGPGLSNIILCSLKS
5356	19257	A	5395	24	265	LLPHRKSNNYRTRPSTRSLKQKNMNLGG GACSESRSHCTPVWATERDSVSKKLLG TIELVYVFLKKNKSGEPLFKVLGOL
5357	19258	A	5396	174	118	FFFFFFFFFFFVFFRSS
5358	19259	A	5397	406	134	PSAPSSPFFFLIWGPFGFPPLFLPNK PDKVFFGAPKKKIVLPALRNFLVLKG PDPFVFVFSSSF
5359	19260	A	5398	294	64	IFEFFEFFEFFEFFEFFELHILWGALF LLKSRIIPGKKKTKCIFLCTPLTSYIP LKCFQKQKNKKSQSQNTLKS
5360	19261	A	5399	1	211	LLLPFPYHITNQDSNNKYHETKKKKKKK KKKKKKKKKKKKKKKKKKKKRGEKKKK KKKGGGGGYKKKK
5361	19262	A	5400	305	1	SPFRPPLFLFLFLPSFPFKAPHTINH FFSPPLPLFFFFFFFFFFFFFFFFFF FFFFFFFFFLKLYLFYKMRINYTSNI LKINIFVTSSPGSGRR
5362	19263	A	5401	416	3	ENTERDRGRQRREDRSRAETQETNRAGO QUESTPPQKKNYTSIPSSSSSSPTPOK KGKGGPPGPPPPPAGEKGKPKKKRGPQ KKKIRPPPPGKKKPPKTPPLFFFFFF FFFFFHKQTFIVGVNTYILLRSSV
5363	19264	A	5402	154	416	KKKKKKKKKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
5364	19265	A	5403	327	2	KKKKKKKDSGGGAF PPQKRFPLGCVFFPPFFFFNPPPPFFFF SPKKKKYFPPRGKIFFFFPFPPPPFFFF PPPPPPPPPPPPPPPPPPPPPPPPPPFF LRWSLALVAQAGVWNLNHSLSLSL
5365	19266	A	5404	372	181	YKGLAHTRCSTRNPLNFILITIEGSRFV AQAGLEPLGSSDPPPTSASQSDGTGVSR RTRPINC
5366	19267	A	5405	110	1	PVPVSSTEVKKLVLPQGTVHVACNPKTS GGGGGRIT
5367	19268	A	5406	2	401	GFHLLTYGNKKMQQRHVREASARPLQGT PPGHHALEWLTENVLLAARPRKAQVLF AIVASSETSSNDREKMLTSLAKCKGKIT LFVLALPGVGTHELALAEVLVAPSEIQ HLRLRLQGVSKPEVNYAQGFTF
5368	19269	A	5407	3	181	OLILFHDKLSPKLLSNCNVLLINPFLS HCSPERARRLQAKMMTNLVMAKDRQLQL GIN
5369	19270	A	5408	371	222	SVEMGFHIVAQPSLEPLGSSDPPASASQ SAEITGVCHCARPNHDSYRRS
5370	19271	A	5409	204	416	NQVGEWLVRKGTLDGLTMSMLFHFVLR SKDEKNTKWPGVAHTCNPSTLGGRG QITRSVGRDQGRIG
5371	19272	A	5410	236	308	AGRPGTVTHTCNFTLGGGGRTT
5372	19273	A	5411	375	216	GCSEPRWCHCTTFAWTVQDSFPKKKK RKEKKKKLLTTENSKKALKRNGYL
5373	19274	A	5412	1	381	RFHIVAQAGLNLGSDNLSASASQAGIT TGMSPTQP
5374	19275	A	5413	144	3	RPPPIFFFLAKKLALFFFFHSVIQAGV QWRNLGSLQPLPPGFKQF
5375	19276	A	5414	412	32	LFSSKKKKKKKKKKKKKKKKKK
5376	19277	A	5415	414	2	NNNSVFVFSKPIFLKTVGGAPPPFSIYN PIPIFLYIYPHKMGGVYIPTHMYGGD IWGYMTPPPPLFIYFFPPPPFYIEKK KKTVCFFAQGGVRLCKKKKNKDRGWG DTMTMGGHGRLEWVANVGLKRYVV
5377	19278	A	5416	1	240	GGEGCS EPRSCHCTPAWATERDSISKK KKKGPPFKRTHFSSPGLPSFFFPGAPK FNSRARFLTREGKNGLPPFPYA
5378	19279	A	5417	2	63	LCLKNNNNNNNNNNNNNNND
5379	19280	A	5418	322	1	WPLCFSRCSKKRGSPLGFPFSPPLGSK KFVRPACKTSPAFKPPPSLSFPQRWAGP PPFLQGLGELPKGLFFQOCFFPPFLRW SLTLVAQAGVOWHDPGSLQPPPL
5380	19281	A	5419	1	392	FRMAGSTPEGAPALLADKROQGGSRFLS DPA RVFHHNADNVMS EEQAAAERKV QNSIQRCQKQVDEINAHKYNDY KIHENGFKDRHMLFTFPELAPSONQN HLKDWPLENKSEAPSKK
5381	19282	A	5420	273	91	RWYIVLDNLFTILENTCCETS LKYIAGP GVVARACNLSTLGGQGGQITRSVGRDQQ GQHGE
5382	19283	A	5421	1	149	GGGGCSEPLRRCTPAWATERDSVSKKK NLKKFFCPGLGLYOKONTWTL
5383	19284	A	5422	381	179	SSCLGLFKSWDYRCLEPCPARTALNLT IKKSKDNRRWRGCGEKENLHMCWNECDM VMLCVPTQISC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H-Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
5384	19285	A	5423	195	369	CSLSFPIKECKLHISGLQDSSISLVNLGLAIRNRIRKPGVVVAHSCNPSTLGGAQWIT
5385	19286	A	5424	253	414	KKKKKKKKKKKKKKKKKKKKKXKKKKKKKKKKKKKKKKKKKKKKKKKKPKHSPAPAERDL
5386	19287	A	5425	160	2	NLKGSAPFSKKTSPFLVKENPLFFFFEMESLSVAQAQVQRDLGSLQLPLP
5387	19288	A	5426	53	426	ASSSFFFFFFLLSGGGSIFFPKGGEGEKNFFLWKPGAGGGGGPPPTPRGGKGKGGPPPGQKIPLGMFFEKRRFHGGGGGFKLRGKKKPPLPAKPRVKNNKGGNPGGGQPLKFKKTLPKMGCLKK
5388	19289	A	5427	60	1	KWPGTVAHACNPSTLGGRGG
5389	19290	A	5428	87	247	KKKNPQKKKKKKKKKKKKKKKKKKKKKA PAGAGDLSLYYPRAGRNLFFNYLP
5390	19291	A	5429	209	405	KLNVLFSSSLKAMISAILLKLSVPITPMKIVILSTLNSGSNPGAHAHADCPSALOGRGGRT
5391	19292	A	5430	324	237	VVNAPVCVCVCVCSCICVCVCVCVYFLF
5392	19293	A	5431	409	3	FFFFTSETSRSVTAGVGQWRDLGS
5393	19294	A	5432	270	402	MKIIIFHLIRITGWAQWLTFVTPALWEATGSGRGQEFETT VKPC
5394	19295	A	5433	107	277	YNFNHRHYREAIQKWDEALQLTPNDAITYEMKSQVIIMKNPTIFMLKLCYCVCSSEQ
5395	19296	A	5434	95	1	RNRKNNQSGTGVAHCANPSTLGRDGWITRS
5396	19297	A	5435	412	105	GGECSSELRSCHCWPAAWARARLHLKIKKERMDLAMLRVGYSGRHQVCHTDHTQLQFPF
5397	19298	A	5436	276	488	PLPQPKNDSRLPLLVLCLGFLFAPLLMLGHGPKRARLPIFFPQEAYFITFRLVFAEKKGYRGPLTWCLAPR
5398	19299	A	5437	179	2	GISPLKGGTPSLKKKKKKAKDFNRRVSKEDIQTNHMKRCITLLIIQMQLKITMR YLP
5399	19300	A	5438	3	156	TPLYSQLILSLRQEHFYKAEGRGCNELTSYCHTIPAWAKQCDSDSVSKNKQNT
5400	19301	A	5439	47	173	SLQGFLTEERKSDDEKSDRNRPWWRKREASMPKNGFIKY
5401	19302	A	5440	3	122	TTLATSLIPILTTLVNPKNKNPPKLIIRLVLPOTTEK
5402	19303	A	5441	390	489	KKYSYSLQPPPPKFKHFSCVTLPKHWNDYRRBP
5403	19304	A	5442	86	275	ROGFETTSQQOGETPCLLKIQKLAGRAHLNPGRCGCEPRLCDTAANVTRAGLSQIK KIKKKKK
5404	19305	A	5443	424	166	CFFVS PKAKSGGVVLGSPFPFPPLGSLKHFSAPTIRGLPLFFFFPRGVPLLGKGSKS PPPGVFPNPPQKGGDSGGYPYPPRAKIF LF
5405	19306	A	5444	356	3	AFNFNTNPFPPGKGFPCPHPLSGISKSG GPPPRGNFFFGKKAHFSFPFKFLPPIFLPFLAPQKVGFPGFPKPSQGVFLFF FFFFFSFLFFPETESSVAQAQVQWRDPDAW
5406	19307	A	5445	198	86	PWPLGAQAILLFQSSCLNLPKCWDYRREPHTALLNS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, =possible nucleotide insertion)
5407	19308	A	5446	198	86	PWFLGAQAALLPQSSCLNLPKCDYRRE PPHTALLNS
5408	19309	A	5447	143	3	TMIFYFYFFFLSQSLALLPSLEGNGTIS AHCNLRPLGSSDSSADAW
5409	19310	A	5448	324	1	KKNSATSPFFSVEPFPSTGGVLANKGALTO EKILPCPKIKKIRKRVGAVAPARNHFLP FSPFFKEGLQGIYVYFFFFFELESRSVT QAGVQRNLCSPQPLPPGFKRTRG
5410	19311	A	5449	403	0	LFFFFFFFPPFKENH
5411	19312	A	5450	114	409	LNIWTKLYLISKHLILVCLPDTLSSLC LKTYIGLQKQVLIFFPKQFSAIDKLQGN TAVVGKFGFASYSLLTKKKWLFGNITQE QNMIVTGGLSWWD
5412	19313	A	5451	192	406	RNFFLGHLKYVKRFQIGWRDSEKFTF KARATKNKMDKGDILKLSFCPAKETTF RGTHPTKGEKIFAT
5413	19314	A	5452	254	48	NAFGWLGVHYALQFDKSVKNSVCWLGZ VAHACNPSTLCGGQGWITRSVGRHQPOQ VGELTRTRASTR
5414	19315	A	5453	1	288	PLLEFILPSFSPFPFPGGPIKFLP KKKKKKKKKKKKKKKKGGGPFKKKI FPRGGKKKIFFWAQKKIRGGVLKTTGG RKKPGGKNNKSG
5415	19316	A	5454	285	415	TSGCCFVFLVLKLSIFCKGKVLNAIDN GLKNSTFTYFTSDHG
5416	19317	A	5455	372	125	ITPAFSFSPMGKGVFPFPKFFGFPFPGF PPPPFFKPPGIIIFLGPKKKKFFSPPPR VYFFFFKRPPFFFFFFFFFFF
5417	19318	A	5456	3	159	AHASAHAYDTIKDALGLLITLSLMTLT LFSDDLGDQKKKKKKKKRGGP
5418	19319	A	5457	109	392	NIIIRKSTSLRLRPIFPHLFPFILVL FISLRTLFFFFFKRECFPLQVGGQGP FLNSLKPLPRGLMQFSCLTLRSNGYGP PPPPPIFFF
5419	19320	A	5458	243	402	FLKIGFIHKYLKEFVWGLNIVFNRFNS HERAPHAIVFVNGTTIEGHVKECYW
5420	19321	A	5459	394	105	IPPPSPRGGFGAAPPFGGGGSTTPPK KKPPFFPKNNKQPGGGGAPPSPPPRGL QPKPLTPTGKTVEKETKPPFPFPRGAP EKLSSKKKKE
5421	19322	A	5460	56	379	VCFSPSTYGAUVLNKSPLESHGSSSTSG WGLPSPFPAQRLPLASQVQENGHVFA SYQVSIPOSECQCLSVIWLMDKALLCSG EWLPHQAPKPSMSPPTPHCSRGLQ
5422	19323	A	5461	184	420	FFFFFFLNNNLFFFFFFFPPPPFFFLG RN
5423	19324	A	5462	295	384	LGAVAQARNPITLGGRGWITRSVGVDQ PG
5424	19325	A	5463	413	257	FLNFGRGCSBPSPKSKSTLAWTERDLI SKKKKKEKCNIPORMPERGQWSPD
5425	19326	A	5464	2	181	SLYCSGSQSTPGLQSSCLSPFKKCDYR CELPFRPVYVLLYKTSFPKRYVFGHLCF MSQ
5426	19327	A	5465	1	229	TGSCYVAQANLELLSSSDASTSVSQNAG TTGVSHHVQPYTSSFSQVPLRAGSAAT ETTSILWQKRLQVVRCSV
5427	19328	A	5466	1	368	KERETKEREERERRRRREGKPKGRK ERKEREERERKREKRRNRLGQSAGIT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						GMSHHTRPKSHRVLSKPTNLCAAFKAT LGHHWGRDLKLNVEQCFSTLSALFSII ATSHMRLWVI
5428	19329	A	5467	183	3	VSLCYGEKFSQFMNESOLVFRPGAVAH CNPSTLGGRGQITRSQDRNHPGQHG ETGRV
5429	19330	A	5468	1	128	GGAGYSELRLCHCTKANATRLAKLKKK KKKGPLRALKKITGG
5430	19331	A	5469	1	155	NKFPVLISNVINIGMCHCTPANATERD SVSKRKKKKRSLARHSVLC
5431	19332	A	5470	113	1	FFFFFQKTSRLGTVAHACNFTSLGGR GGRITRSGD
5432	19333	A	5471	407	281	NGMIPGGRACSELRSRCHCTPAWATEQDS ISKKNKSKNPGK
5433	19334	A	5472	1	177	GGGCSEPRSRHCFPAWATERDSYLHKMK QSKTKGKMEVACYCIILFPLMTDALE V LMA
5434	19335	A	5473	76	267	KERRREEKEKKRKRSEKGRKKKEGRDR EKEKEERKDERREGEGBEGRKEKKEKD IKRRGVVE
5435	19336	A	5474	133	2	LCRMVVLFCFEAGSHSVTQAGVQWCGLN SLQPLPPGFKQFSCL
5436	19337	A	5475	5	394	YGVGTGKFRAGVKFEQALFLITVHSOL CHIEGTRHSHRIIVVDFINQIENGTF FPLVLSNGCIWLLIVYLFNIFTRQEGQ FFYGLKSHYSVFVFCFLRRSFALAAQGV RWCDLGLSLQPLPPGFKF
5437	19338	A	5476	163	2	SEKPNVVALTMTFSHFYFFIYFYIFI FQMESCSITQAGVQWRDLNSLQPLP
5438	19339	A	5477	111	2	FLFLKQDLPGAVAHACNFTSLGGRGQIT TRSGDRDH
5439	19340	A	5478	232	0	HLVWRMESGSVAHAQWCDLSSLPFP PRFKPPSS
5440	19341	A	5479	388	225	ALFSSKKKKKKRKRKKKKKKKKESM QRKGHLPRVCCGASWVSPGHKLSL
5441	19342	A	5480	150	2	HRVAVIYEVFFVCLFFYFLFLRQSLTLV TQPGVQNRNLSLQPLPPGFK
5442	19343	A	5481	156	395	DSVCTCVLHTCHSSGLSCGRSCLCGLSLG LPNSNCPCVVCVVCVVCVVCVVCVCS PLHQGVVCVVCVVCVVCVFLSAHPTKC VCVVCVVCVVCVCSPI
5443	19344	A	5482	391	115	RACPDRCVRFPHTSPFLCPCGPAEFGP GPALRELVOPLPGLOPPFGMPFSGLGA APSPAPPACATRPPIHHPSSFSSSVQ ISSFLFCF
5444	19345	A	5483	392	2	FFFFFSTQFRSCCPRLCNGAISVHCN LRLPGSNNSP
5445	19346	A	5484	381	282	PVPWQQAIFLPPPPPYLIGPFPFPPL FLFP
5446	19347	A	5485	407	3	FFFFFLRRSLTVAQAGVRWCDLGLSLQA PPPGFT
5447	19348	A	5486	2	417	QENHLNPGGVCSEPRSCHCTPAWVTEY DKKKKK
5448	19349	A	5487	3	413	VYLHPSLQPSLSSLVPEQALSHDIWLKK KKKKKKKKKKRGGISPPSPVGVGVP TWVWGPANLFRQGGGVRELFSQKKKG EKGQRNPEKKPPHKGPGGPKKFIFFE KKKKKKGKPGKTKPPPPRVNPGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
5449	19350	A	5488	229	411	IHGPGFRNGGRGKTLGLPLMALKKIPF SPGGYKPNP
5450	19351	A	5489	190	50	YHHHHCHHHHHHCHHHHHHHHHYHGD NDYSSHHRSRSTCHVAVT
5451	19352	A	5490	615	402	RWCLTLSPLECSGMSIAHYNLHGPSK QLSCLSLPSSWDYRCPPPGKTTFSRGIR DALKPRKPRINLI
5452	19353	A	5491	338	53	KGPFPPFFCKKGLPESNMFLLPGKWFE SPPTPPRSGGKRVPPGEGGKGFSLFFV EGGSGCHIAQAGLKLGLSSDLVTSASQSA GIMGKSPHAWP
5453	19354	A	5492	266	412	NFNFFERKSCSVSQAGVHERELNSLKA PSGYTPASCYSLPSSWDYRRP
5454	19355	A	5493	285	412	RDGVSALSPGLECGGMIACHNLELLGS SDPSALASQSTWNY
5455	19356	A	5494	1	1350	MGFMTGICIEDNVGSPSPESGVLTVGG VRIQMLDRCHTAHCPVLPGLRLGOLWTE NLAERNSHDRFPFPTVVCSHFAQDLWFE QSIKDSYQKVLIRKFEKCGHGNLHFKKG CESVDECKLHKRGYNGLNQLTQTQSKI FQCGKYVKVFHQFSNKRKRKRRTTEKPP LKYLEGDKAFNQSSHTHTKKIDTGEKP YKCEECGKAFNRSSHLTHKKIHTREKP YKCEECGKVFYFSSFTTHKKIHSGEKP YICEECGKAFMYPTLTTHKKIHTGEQPP YKCEECGKAFNPAATLSHKKIHTGEKP YTCDKCGKAFISSILSKHEKIHTGEKP YKCEECGKAFTRSSHLTHMKIHTGEKP YKCEECGKAFTRSSHLTHMKIHTGEKP YKCEECGKAFTRSSHLTHMKIHTGEKP YKCEECGKAFTRSSHLTHMKIHTGEKP YKCEECGKAFTRSSHLTHMKIHTGEKP RT
5456	19357	A	5495	4	146	PPIRPTCYLLSFYYSYPTQYKEDTRM/V KHKRCSTSLVYLLWINPY
5457	19358	A	5496	5	388	CGCFFFSPPFKKKYFPFPFPFPFAGFPF PPLFTTFFPQFFFWAPKKKKNSPPPGK KIFFLKGPPPP
5458	19359	A	5497	231	163	FFFFFFFFFFFPPFXNTKNWF
5459	19360	A	5498	163	2	SVKFTLGKVSQFLKKHTFAGWAHTVIPA LWEAEAGGSRGOETITLTNTVKPH
5460	19361	A	5499	229	388	RTHLQASSDLFCFLYSLKTGSCCVAGV QRHDLSSLQPPPPRFRKSSCLRPPE
5461	19362	A	5500	405	289	HVAQAGLKLASSDPPTPASQSAGVTSV SHCTHPRCLFV
5462	19363	A	5501	286	375	GDVFRFSFWPGGGAHSCNPSLTGGRGQ VT
5463	19364	A	5502	20	374	ILQFONFWIVLFGKFNHYFGKFLIYLWN FSGLFWYFSELSFSLGSKINILNLLS GILNVFSPISGVRKKIPLIKRYCWLGT THACEPSTLGGGQRQITRSGDRDHGQR VVKIQN
5464	19365	A	5503	1	185	PHHIGQAGLILTLSSNLPASASQKAGIT GMSHCTQPIIFLYSLFLQLSFSWQDFV MRKKF
5465	19366	A	5504	202	402	NSFSSTAKLREKRYQFLYTPITPTGTQPL PLLTFCRTPDTVAHACNHSTLGGQGGQ TRSGACNPPGQ
5466	19367	A	5505	118	7	IKKENNWPGAVAHACNPSILGGDRGRIT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted ending nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						RSGRDHPG
5467	19368	A	5506	205	422	ANHFTSTRMAIINNKKOTENNKCWQGG EVGTLVHCWNECKMWMRLQIVWSFLKK LNLIQSRDPATLLAI
5468	19369	A	5507	3	425	RSCHCTPAWATERDSVSQKKKKKKKK
5469	19370	A	5508	3	86	EKKQLVLLNCMTETIYQFKKDAERSK
5470	19371	A	5509	395	108	GVLECNDDTTAHCSLDLVGSSDPPTSAS QVTGTTGTCHHAQLGLPKCWDRHEPRL PANNTKTLRRKNWHSLLPVVPAIQEVLG GSLRPSRLLE
5471	19372	A	5510	421	59	FFFFFLRRSLAVSQAGVQWDLGSLQA LQA
5472	19373	A	5511	168	3	EICKMCFVPVPGVGFLLNIVFVVFVFL RWRMESLSVSQAGVQWQCNLSLQPP
5473	19374	A	5512	446	149	FFFFFCCFFETESCVRLESSGMISA HSSHNLCI
5474	19375	A	5513	74	398	DRIIDAGPKGNRYARFMNHCCPCNCTOK WSVNGDTRVGLFALSDIKAGKNHFILO LTSEFGQFCFLQTASSDYNFKHFMYS LELSFTFLCNHHHHPSPFLFSS
5475	19376	A	5514	73	335	EGGSLFCPGWSAGALFWLAPASRGWG GAPGVVVGVEGQKNCWNGGGGCGNELG LHHCIPPWGTGKTLSPKKKKKGATDMG GAS
5476	19377	A	5515	416	0	WLGPGAVAHTCNPTTLGGGRWITRSRD
5477	19378	A	5516	242	423	AGSPLIHQGGQAIILTNPTFGWGTMF QPVLRPVKGLYNANHVTSSPVASQPIIF TTAG
5478	19379	A	5517	2	151	GRVGFVGMGSHCVAQAGLELLGSGGPFT SASQSAIIAGVSHRAWPYPPS
5479	19380	A	5518	312	405	GQVRPGAVAHACSPNTLGGGRITRSGV PDO
5480	19381	A	5519	3	387	ACSGPRSCHCTPAWATHQDSVSKKKKKK KREKFLLEKKKGPTLTWGEKKGIPLG ERNGPSHFKGPFAPKPPGGNLHPEI AQGPSSTDCNKKDLNPTVPYFKFKPT EQAINWAAPPPFSEK
5481	19382	A	5520	292	140	KKGPFARPGGGSPFLFFFFFFFFFFF FFFFFWESTLKKRELHRSDLVCV
5482	19383	A	5521	1	399	KKWLFLSSAQITPKLSRRRRNRRTWKE RSKINLHKPILKQKHLELPDKEFKTAL KMLYELKVTMHEQENINKEKENTKKKK KKKENPPLFGTKNQSPPEKFGMQGQPP PPPPQKKKPPPNRNFVFSPP
5483	19384	A	5523	316	399	MLLYWGTVAACNPTTLGGGRITRL
5484	19385	A	5524	400	0	FFFFFCCFFFLFFFS
5485	19386	A	5525	3	429	TTNIGRAMGATTSIVGSDTSQARPPGT TVVSPGASSTQSSSRPGTSVTPDSSAGE SETVITKEFGTTAISRSTHTGTPAASG GOATGSLTATTGVAAGTTVAPGSNTA TTSVGEKKDKQKKKASSP
5486	19387	A	5526	135	3	GGKICTLIKQSVIQESWPGTVAHACNTS TLGGGGWIMKSGDR
5487	19388	A	5527	105	5	KKKKKKSGRWFGAVADACNFNLGGGG GGITI
5488	19389	A	5528	411	31	GQVPLSRGVAKKKFLNFGGGAGKNG GKNFLKKKPPGAPPSSGGPKKGPPDP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKPLILVSPPPREGGAHNMHFRQKKS KGEGSTKGGKERIFLGKFKVQKNFFFF DPEPHSCCLGWSAMP
5489	19390	A	5529	411	142	PRFSFLSPPRKKEVFPFKILGGPRFF PPRFLKPPPPFFFWGPKKKKFPFPG EKFFFKGAPPPFFFFFFFF
5490	19391	A	5530	174	401	QVQFQKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKASPGGGKKKK ROGCGERNNIIVPLLFPP
5491	19392	A	5531	410	0	QPGSKKKKKKKKKKKKKKKKKKAS QKKKKKKKKKKKKSSGGGPFKEV
5492	19393	A	5532	383	145	CGFFENPAKKGSSFPQPNLGGPVFES PVPFKTPRNIFCGAPKKKFFPPGAK KYFFKKAPPPFFFFFF
5493	19394	A	5533	418	328	KTGFARHVGAGLKLASSDLFALASQA GL
5494	19395	A	5534	169	3	IILIHPCSHVPRRTGLGKACTFKNLF WPGMVAHANCNPSTSGGREIRITRSGR
5495	19396	A	5535	1	254	PTRFCKPQTSNNGKLSPSSNGCMNTL HISSTNTVGEVIEALLKFLVTSAPAK ALYKRCREDQVYACKLSDREHPLVLD
5496	19397	A	5536	43	404	QGGITVLPLVLNWSWPKRSSRLGLEP WDYRYEPPHQAN
5497	19398	A	5538	2	212	KENHLNPGGGGCSLRSRCRTPAWATER NSVSKKKKNFRGGGLKGGKPGFYPLEK KFFGVGFFPKTNLV
5498	19399	A	5539	2	387	IFQEHKNCGBMSETEAKVKYVLARSLR TYGVSFFLVKEKMGKNKLVRLLGITK DSVMRVDEKTEVLQEWPLTTVKRWAAS PKSFTLDFGEYQESYVSQTTEGEQISQ LIAGYIDIILKKKKKD
5499	19400	A	5540	317	407	GLSHHVFFEEGLKKPRIKDKDKVPEP DN
5500	19401	A	5541	120	3	NFFFFFLRRSFALSPRLECSGTISAHCN LHLPGSSDSP
5501	19402	A	5542	430	0	OKAQSNPGKEQKRGVIONFKRTLKSKK FIFNPLIHFSFWFTTKFGCPIVLFLRQS LALLPRPGVQWRDLGSLQPPPRVRPRV
5503	19404	A	5544	149	2	EKDIQELNSALHQADLIDTYRTLHRKST FFSAPHRTYSKIDHIVGSKAL
5504	19405	A	5545	84	276	TLKKRPKEIRNQGSPQRKRAQLGLKQQ KYPVLNFKAPFFGERGDYKSSFFKTCLD NLPRRGK
5505	19406	A	5546	2	914	NPANHEOKSKNEPEDTEDKEGQMDKE PSAVKKPKPTNPFVIEEKELKSTPASE KADPGAVDKASPEPEKDFSEKAKSPH PIKDKLKGKDETPVTHGLDSDSESE LVIDLGEDHSGREGRNKKEPKPSPKQ DVVGKTPPSTTVGSHSPETPVLTTRSSA QTSAGATATTSTSTVITVPAPATG SPVKQRPLLPKETAPAVQVRVWVNSSK FQTSSQKWMQDSSSSSSSPQNOQQQ PQSSQGRYHTRQAVKAVQKEITQSPS TSTITLVTSTQSSPLVTSSSGMSMT
5506	19407	A	5547	2	244	TRLIFVLVETGERRVQAGLKLITSGY VGTSAORMTAHLCLPRCWDYRCQLHP AQRFFKRLNSVAVDAALLHTSGGM
5507	19408	A	5548	406	1	FFFFFSETESCSTSQARVQCNLSLSPK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5508	19409	A	5549	417	43	TRPARKCGSSGLPCAPLAGGQAPPPPP RQTSPPPPHTKGGGGGPHKPPPKKKRPP PKKKGGGKKNPCKKKKNTPPPKSADP PAAKTDPPPPPLTVPPFLPPYITPKKIPF LKSYPFFFF
5509	19410	A	5550	3	136	QPRFPPTLTNNINENNPTLLNPIKRLAAGS LFAGLITNNISVHSP
5510	19411	A	5551	75	194	NKELSRNKKKKKKKKKKKKKKKKRGGG LKKKKGGGAKT
5511	19412	A	5552	343	493	IFSFPPPPFLKGSFVFAPOAGHGNGF GPLKPPPLGLKEFSCLTLLSSN
5512	19413	A	5553	148	3	DAVSLFCPSGLERSDTHIAHYSPLLGS SSLSASTSRVAGITGICCHA
5513	19414	A	5554	407	252	KKKFLKKLAGGGMRLOSLRLRLROED HSSSGVQSCSELWGGHLIYSNR
5514	19415	A	5555	3	231	HEFVFLVETRFHHVGRAGLELITSSYPL ASAFREAKARREDLLSPGVKDPQYRD TLTLKKKKKSFYILGECW
5515	19416	A	5556	3	131	SVVSVWEESKDAKELVGYYIEASVAGSG KWEPCCNNPFVKGSR
5516	19417	A	5557	3	131	SVVSVWEESKDAKELVGYYIEASVAGSG KWEPCCNNPFVKGSR
5517	19418	A	5558	462	255	RSHHSAQAGLELQASSDPPALTSQAGV TNVSLRAQPIACSSVEVSSRCQVCLHV RRGKCPRAESYR
5518	19419	A	5559	445	29	KSSNLTLLQKVENGDLSNKLKITDFGL AREWHRTTKMSAAGTYAWMAPEVIRASM FSKGSDDVWSYGVLLWELLTGEVFPFRGID GLAVAYGVAMNKLALPIPTCTCEPFAKL MEDCWNPDHPSPSFTMILASQAWR
5519	19420	A	5560	225	475	GAVSSSTCEHHWIFKAVGESSLTPTPE SRVVAHGVQWBNVSLQPPPPGFRFSS CLSLPSSWDYTSAGEGCAYSRKSVLK
5520	19421	A	5561	248	142	NKNINVOKKCVFYITLFFCVCVCVCVC VCVCVCV
5521	19422	A	5562	262	456	NFFLKTTFYFLKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKASSPPLIKRGPKN
5522	19423	A	5563	314	444	LKSMFCFVLCFFIESRSVAQAGVQWC HLSLPQPPPPGFKRS
5523	19424	A	5564	220	486	LNSSHPEPLPLFGLVLQFPFSPNPKSF NKKNLERMLLTVDRGNNHPSLDFVHS NVDTVFLPQEGPSFLQPLQGGITEAFEH NQAYV
5524	19425	A	5565	176	492	CTKTAVASKARYLQALLALASVTTAAT ATRLASISGASPIFRSFYLOPTAGLV LPSILILVDVGLRKEKGPDTVAHACGPG TLGGRGGITRSGVDRDRPH
5525	19426	A	5567	24	470	PMDXKXPKXKTFPLNGAGENQDDMFAK LKEKLFPNEINKIPLPPWALIAIAGVAGL LLLTCCFCICKCKCKKKKKKKEKGGK KNAMNMKDMKGGQLPQDDDAKTGLTEG EGEGEEKEPENLKLQFSLDYDFQANQ LTVGVQLAA
5526	19427	A	5568	45	485	GXDGRLLRHGNQYAYDGLDYIALNEDLS CWTAAADTVAQITQRKNEAREAQLTAY LEGGLCVELRTHLENGKETLQRADPPKT HVTHHPVSDHEATLRCWALGFYPAEITL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						TWORDGEDQTHDTLVELTRPAGDRTFOK WAAVEVP
5527	19428	A	5569	221	422	FFFLTGVRVQSLADLEQKIEVHSMPPFF SLALSPTLYCRGAILGATSASQVAGITN ICHHAQPSLYF
5528	19429	A	5570	401	477	IFSRDKDVMLEPRIVLNSWAQVILL
5529	19430	A	5571	102	36	EVENDDIISHHHHHHHHST
5530	19431	A	5572	106	407	AGRQGVLEGCCHPAAPTLTTPATSSK GASRPPTATCTPPAPATTTMQPWPFRLWAGVQVHDLQSSQPPPGIKQFSCLSCPSWDVYGRRAVCHH
5531	19432	A	5574	253	363	YHSNQCVLKRWFGAVVHACNPTLGGRGWIMRSGA
5532	19433	A	5575	1	132	MECHYVQAQLELPGGSDLPASASQSTGITGVSHCANPGFFFF
5533	19434	A	5576	18	378	TPGGGGCIEFRWHHCTPAWATRAKLSYK KKKKKKK
5534	19435	A	5577	21	232	ILRCTTITLLKVDQNHNLNPGGSGSEPRSHHCTPTWARERDSYKKKKGGAALWDPOGGQPSAGSQTR
5535	19436	A	5578	377	2	LSLITQITLCLGATTLTFAVCAVTONDIKKIEAFSTSSQIGLIIIVTIGINQPHLAFLIHCTHAFFKAILFMCSSGIHNLNNEQDIRIGIGLLKTLPTLSTSLTIGSLALAGIFPLTGFYTRG
5536	19437	A	5579	2	227	IESWLEPVRFLRSMFANNLUYDTSDDYHLLKDLLEGIQTLMGLEDGSRRTGOILKQTSYKFDTNSHNHVDA
5537	19438	A	5580	113	3	NFFPFFFLRQSLAVAQAQVQWCDLGLSQ PPPPWFKQ
5538	19439	A	5581	184	3	IMPPHSRLSPTARFCLQKKTNNNTPIEMASIQCPGWSQTPGLKPPSCFVLPCWDYRCE
5539	19440	A	5582	381	3	FFFFLGDRAFPGGKEKNPLGGGLKTPGKPGGQGVSPPPQKKMPPNFFPPGKKKSFGGGGPIFFPGKNFPPTQKKKRGGGGFFFFKKPCGQFFFFFFFFSSFFLGKSPFKISFKRRRG
5540	19441	A	5583	314	389	FSCLSLSSNDYRCVLPHLGNFLYF
5541	19442	A	5584	131	1	FLWTSEQVGRNKQTVTWQADKRENAQGDYVTFPPQPTFV
5542	19443	A	5585	484	3	MTEILLKQAMVIGVSGSAGGAVGGASASGCTAIAAAAKFHPATGCTCTCGKYEPAGIVHRGEFVFTKEATSRIGVGNLYRLMRGYATGGYVGTGSGMADSRQASQTFEQNNHVVINNDGTNGDIGPAALKAVYDMARKGARDSNSAGDQIFHH
5543	19444	A	5586	136	48	NTMQPGVVTHTCNFTSLGGQGRITGSGR
5544	19445	A	5587	306	479	DSFFPGVGSFYLQVAAVVTTKYFKRRVALSTDIAERSEMRLTFLAPTTKFLIDVDW
5545	19446	A	5588	201	2	ILETGPHHVAQAGLNLASSNLPASTQSAGITGVNHHAWPSFLIQGTKHSFKNSKPVFHIKLSKN
5546	19447	A	5589	30	477	TFSLARGVYPCWLYTGFLHDLFLSPKPIERFMDVGVLRATEPSNSLFAIISTPIELAKSWHIIGDGLSLTSLVAVERGNRTTI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
						ISRLPEFEKSSLSQSLVLTLSGYPVAVY RVKLTAKKLEIHEGAFQITTDYEIITI PVKARNALC
5547	19448	A	5590	208	91	KGHFWVTGKKKVPKPPRPFPPFFLGGI SLCYPGWSAVV
5548	19449	A	5591	325	467	ADLCSPCDILQDLFRHIRTVDLTLLALG EKAPPTSAISRDLISFCF
5549	19450	A	5592	332	403	LSLCVXHTHTHTHTHTHTRETFIY
5550	19451	A	5593	292	26	FILDMEGAEGAELGLVHCLLCWETPS RLAVLQHLRTFAHRDAQARRLLQLLQNG PTTEGLAALQSILSFHSGQLRTFGEET GTGE
5551	19452	A	5594	387	51	LKKIFLGRGGVSLFFSPPLGGPGGRFL GLEIGALFGLPGKTPPPFKIKKNYPGLW GGALFPLPLEGLGGKMAFPRKGGAPFSQ KNPPPPPLGKGTKPPPLKKKKKKKVL
5552	19453	A	5595	88	362	AETSPGGSYODGLRRPGFAEGPPAGNR PRRKKKTQDRRGGAGSQPOACADGVRL CTRLQCSGALSACNCLCPGSSDCPASA SRVAGIT
5553	19454	A	5596	92	365	DQFWPGQLPQRSPEAIGRGSTSRKKPQ EEENSDRSPGRORGIPASGVRGRCAALY QAQVQWCHLGSLLPPLPGFKRLSCLSLP SSWDYSH
5554	19455	A	5597	3	138	TRPRTRGVQAGLELLTSSDPPTLASQS AGITGVSHRAPQSSS
5555	19456	A	5598	150	3	SCVIYSNMKFFSFLRMSFTLVTAQGVQW CDLSLQPPFPFRLFSCPG
5556	19457	A	5599	148	3	TOHNLAKKSGITPGWVAHSVAHAGRW CDLSPKPLPCLLRASCLP
5557	19458	A	5600	195	1	MVYFKKFCGFELFVRSRIACSVAVQVGMQ WCMHSSLQPRTPGLKQSSHFSFPRSWNR RHMQPCPGA
5558	19459	A	5601	228	415	VNVSTPRDVFLLIITILFFGAPAPQAG RGCNLNSLLPWPGGLKQFSCLTLPKSWN YGLPPP
5559	19460	A	5602	405	2	AATGVDRHAQRTQAGLPLKTPQTPCNP TSKARGTPSAQHPSCTQRHQASNPQR RRRRPQAEHSIRTDHAGPLFASGHMAG ERPTRKAQSRDVSVLRLALRLPRLCT SAISAHCSQNLTGSGNPPVSC
5560	19461	A	5603	3	236	RQENGMPGGGACSEPRSRHCTPAWATE RNSVSKKGIKIKGHCSSAMHQVYLSPF GWRQVCSHCVCPPKPLLVGRH
5561	19462	A	5604	184	2	RPFLRTQGIKIRMFSGSRIFNFILET SHSVQARVQWCHRSSLQPKPLVFKSS YLLP
5562	19463	A	5605	261	2	GWFLKGPPLFLGPKPKGGIGFFQKLLVL QKKNPPFGIGPKPKLKTPLFFFFFLRR SLALSRLCSTGTSIACNLRIPRTNS PA
5563	19464	A	5606	134	2	GSFFKNLVFLGQSLTSLPRLCSTGTSI AHCKLRLPGPHQSPAS
5564	19465	A	5607	3	269	RQESHNPGGGGCGEPRSRHCTPAWLAT ERDSVSKKKKKRKNFLNFIKKKKPCPLP FKLTKKKKGGITALLVLLKLYKRAIAPK TQGY
5565	19466	A	5608	36	380	PPFXPPGGTETGGTGRGPPPKKKKSPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KRGGGGKKKPPPGAGPPPKHLGGKNRGG GTPPPPRKTPPLNPKKRGGGKRGVFFP PKGGIQKRGFFFSRGGGGGAPPPHPP GGG
5566	19467	A	5609	3	411	SSRSRAAALFYFFFSRRGQKEKEPFLG GKTPPVVFPPGGVGKKNRGFPFPPPPAG KGPFSGGGGREQTFIWSPPPPPRGKMGK PPKPVTFNPNFLRGVGLGKNPSFGGVC PPKPTPIFFFORPPPGGFFWGGGG
5567	19468	A	5610	364	483	ISWVLFLLFKWISFVLVAQAGEQWRGLG SLQLPPLGKGF
5568	19469	A	5611	399	285	GGCESEFKSRFCTPAWGTERTDFVSKKKN NNYLKVKSN
5569	19470	A	5612	408	3	KEVFSFPFGLERGVYSFLPLDPRAVKG FSPPPPPGGGGPRGPPPPPGVFLFLPKK GGFPPPLPGGFSSQIOWPPRPQKVGVPK GAFRPGPNFFFFFRFRESFPFLARGPPKK KKKTWNVTIHSASVQSSVLL
5570	19471	A	5613	1	112	LAQHVFFLLNTIASPADSSSELLMEVHG NGKRFPSPER
5571	19472	A	5614	2	389	FVREGERKKERKKKKRKEGTKEGKE EGRKKERKKKVKKTVDRRRPQVTFQA VNLESEGAPNGCVTAPPGGHILWQVE VQTHLENRCHRLKATVTTTRPGAEPRS PPFIITCGEIMNVFSOM
5572	19473	A	5615	385	3	KPPFGDPGKTPFFFLKSKQITGGGGGAPL FPPPKQKVAKKRGVPRQSFKRARLGPC PPSRGGKKKAGFKTNPPTKKNQTKKPM KAKTSKLLQENRSGPGTVAHCNPSTLG GGGGIMRSGDRDTK
5573	19474	A	5616	218	402	RSYSFSQLGVTIVIKARKPESSCWLCAPN RKNAFWPGVAHTCNPSTLGGRGRIHR SGDGD
5574	19475	A	5617	2	235	KSFGCASRLQMHGRTHITGEKPYKCKQCG KAFGCPNLRHGHGTHITGEKPYKCNQCG KVFRCSSOLOVHGRHCHIDTP
5575	19476	A	5618	347	421	IYLVKXKKKKKKKKKKKKKKKKKK
5576	19477	A	5619	92	1	ENLALLFRLECNQTLIARCNLRLPGSSD SP
5577	19478	A	5620	3	402	APPPSFFFKKLIMASPTLGAIKLINF LFFFKKGGKKKKPPLEKKKKKKKKKGA PLKKKKFSPGGGGRKIFFKGAPKISBA RVKKORRGKEKTRGNPKKKRKKKRPFN TVSR
5578	19479	A	5621	420	3	HPFPQGSANFFPPPRKIGINGPPFPAGI IFVFLRCRFPQVGGQGFKIRPPNKPFP PPPKNLGLQKSSPPPPPIFFFFLWRNG LMTLPRLVSNLQKSHLGLLKHWDYM SEAPHLAKNFKLEYEVVLSLHFVEGS
5579	19480	A	5622	246	132	EVAPHLLGCTISPTMCVCLVCVCVCVCV CVCVCLCSW
5580	19481	A	5623	219	424	ILNVMLVIGITFGRLLGLEGRALINGIK ALIRDMGPGVAHTCNPNILGGREGWI MRSGDGDHPGGH
5581	19482	A	5624	32	454	GLEKVSMTXDRNSRLSVQLRDWDGGGE LLQFSVHLDGEDTAYSLLQTPAVAGQLG ATTVPFSGLSVPFSTWDQDHLDRDKNC AKSLSGGWFGTCSHSNINQYFRSIPQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						ORQLKKGTFWKTRGRYYPLQATTMLI Q
5582	19483	A	5625	166	2	LFGLVKLTALKGLKMLPSQVWMLTPVI PTLWEAKAGGSGQQEFFTSLANTVKP
5583	19484	A	5626	120	406	GEAATQENLAELRPEPELLSPSTVLSRE DELPSPTVLSREDELPSPTVLSRKPD LLSPTVLSRKPDLLSPSTVLSRKPDLL SPSTVLSRKPDLLSPSTVLSRKPDLLSP STVLSRKPD
5584	19485	A	5627	324	16	LSPPPPLFKTAPRPOKNNPPPKKKKPA PPKKNNLFFFFFFFLVFFIWCMSRLAE WNETLGECDMRWGQAVGTGTSRELRPGG SRSPRRLAGKELGPHCAP
5585	19486	A	5628	378	72	GRGGERPFPPOKSGAKKPGVLNFPFOR GKRGPPGPPGPFKKIIFSQAEPGFSSFF WGRSLALFPSWGARGGFLVPANLGPPAG APKGNPPSKKKKEKIED
5586	19487	A	5629	3	204	QESCLNMGGRGCSSEPSCHCTPAWATEK DSVSKKKKKWKFQGFYEIVIGNFLHLFPK WSYPPSPRIF
5587	19488	A	5630	177	1	SPHEMRFWKLIFIRIYVHFERRSCVPV QSRVQWHDLSGLQLPLGKRFSCGLLL SNW
5588	19489	A	5631	154	3	KWFMGMSRSVTQAGARQCDHSSLRPPTP QLKRSCLSPFGGNDYRHVPDC
5589	19490	A	5632	239	17	EGVRNYLILQPSLRCINLCSFPNREKE LCHISSFSPLAAAKESQKEGRLLSQD EGLLLVVEVFVEDVEINS
5590	19491	A	5633	2	110	GCSEPRSHHCIPAWVTEGDSVSKKQFPF QKKKCIAG
5591	19492	A	5634	433	0	FFFFFFFLLKIPPEGGGF
5592	19493	A	5635	306	433	FSISIEKSSSRAQLLTFVMPALWEAEA GRSSQBIKTIILAN
5593	19494	A	5636	2	285	QSRSTVIFNSEKAERGEETTEKFEASR GMLVKFKERSCLHN IKVQSEIASADVEA AASDPEDLAKIIDEDGYTKHIFGQALC LMSNPTTLGG
5594	19495	A	5637	160	1	LYCGKIVYVKIRLNFLLSQGLTLPKLE CTGTTIATHCCLKLISPNPPARAA
5595	19496	A	5638	3	261	KIOLNPGSGCSGLSLCHCSFPAWATETL SOKKKKKNNPPGFKIKGEIEPLKEFGTK KKKGGFLKKFPPLGFFLEPFTWGFWN
5596	19497	A	5639	2	121	SELRSCHCTPAWRQSKTTSHKKKKNIKK KNNFFLPFREN
5597	19498	A	5640	370	180	VEMEFCHVDQSGLELLISGDTPTPSASHN AGITGVSHRTWQSPFSPFKERNLKS V TSLNVSP
5598	19499	A	5641	254	1	FYLIRKRVVFLFPAVSYGKTYFAVDAS YSAKDTYSKPDNSGRKHMYVVRVLGVF TKGRAGLVT PPPKNPHNPTDLDFDSVTNN
5599	19500	A	5642	292	106	NPVILFYLEFKQGSHTVVAQAGLEPLSSD PLATASQRAGITSVSHRAQTKAETVYV PPSLFT
5600	19501	A	5643	3	100	DTFFVEVEMEKEVCRDLMCTSPKDEEG FLII
5601	19502	A	5644	1	282	EKVPEAKRLYKGRGDPFYEAQENHNHIG VANVFLECLFCVKLQYAVPIISQQGEV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						STGQPWRTHVQVFCFGLFWFSFYLSVY LEVQDETKAN
5602	19503	A	5645	142	67	NKNRPGTVAHACYPNLTGGGQQGIT
5603	19504	A	5646	350	213	GLELLTSSDPPASASQAGITSMHRPW PPLASRLDLCCGTLYLI
5604	19505	A	5647	3	180	EHNAERAFLAQAHLGPGAPCTPGFPSEI PTQFPFRSSGLPNIPVQTIISRAAAEKL FG
5605	19506	A	5648	366	1	RSWFTTYKERSLLHIKIVQEAASADIE TAASYSEDLAKITHESGYPKQIIPNVD TAFYWKMIPLSTCIAREEKSISGFKASK DRLTLNLGANAIGDIKLPIMIVHEKTP RALNVASSL
5606	19507	A	5649	1	355	QIQSSQSGKGLLTSTDEETKLFEPGN KWFCEIPPGGKLCFKKKIKGLYDGG GGFWGPOTPLPLTFFPGFPFPPGNGNS PRGFPKMGPALRGPGKKKPEKTKPA KGGTGP
5607	19508	A	5650	348	124	RAPPVFFWVFLGQFPKKKSTNSPRGGGP PRSFPQPSLPPFRNVRFKKPPFFFBG GRGPPADPFKNPFFFFSL
5608	19509	A	5651	194	43	KKKFFFFFFEMESHVPTQAQVQWHLGS LQPTPTTFERSCLTSLIAIP
5609	19510	A	5652	27	244	KKQOSTLFLFYFLSTLFFFLVKITGSHY AAQAGLELRASSNPNTSVSLPKSWDYGH EHTVPSPTWFLAAKTP
5610	19511	A	5653	38	429	GLFLSCLFFFFLEKGVPLTPPGATGENP APKKGTGQKLLKNRDFFLKAMFGKQK QKFFFPAPTITGDORAPRVFKGPGAQKE PFAQKKKRGKKTRAAPNKKKKPGAF FSLKKTPLWAGGGPPPPF
5611	19512	A	5654	391	68	NLYPHGGVPGVSPGKSLPKAPNPLIGI PPSGEPPLPPQGFPPCLPKKRLGKAP GPPFFFLAILLGGWFIQISNTSCVQVFI IQTIWIIFTIIKGCHLHFTLFL
5612	19513	A	5655	159	34	GARLFFSPVLSPLTEHCVCVCVCVCVC VCVCVCVCVLCACMCT
5613	19514	A	5656	88	388	SIFCFYVFFLRGSETLVAQAGVQWRDL GPLQSPQKQKQKSTPSFLGENRYLQPK NEPTFTLVQCFFKIPPNGLINGKRPKW IGCCFLTKTLVGPVW
5614	19515	A	5657	176	371	HYFCFSDINLAAEPKVRNGKAGVKRSA AEMVGSVTEHPSKLLRSQTLLFTAL CPVGVIFSP
5615	19516	A	5658	3	113	CSEPRSRHCTPANATERDSVSKQQTKN LSYKKINH
5616	19517	A	5659	409	67	SSSNKPTPRVFLTFFGHGVLPELPGK KDPGPPPGPPPPQVQVMYGRKGFPALNL PPRRQNKMLYSPELGEK
5617	19518	A	5660	2	377	GRISCSRNTPLRHRLMLIVCGLRMLPS GFLPWGQVFLALIPVNPQPSLGVRTI MDMLRCRDFIYGQFWGQFMARLWACS QOYTEFFRKIIIFISLLFNIVLEVLAR AIRQEKELNGMLQ
5618	19519	A	5661	256	381	NFTGQAWMLMPVILAIWEAEAGESRGO EITILANTVKPHL
5619	19520	A	5662	19	313	LYSSLAIGFLPLLLNFIITIIFFFFER DPGQONQNFVSLKKRETPPPPFSLGVPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, -possible nucleotide insertion)
5620	19521	A	5663	78	365	KESLLFPFPGPKRHAGPPVLPAGLWGGPE PPTWGAGAKQKREI
5621	19522	A	5664	159	28	DTSTLPTPTGFKRFFCLSPSKNDYRRP PICLPNFFFFLVVTGY
5622	19523	A	5665	350	151	IRCLCPDKFLAFCDGVLCCSGWSRTP GLKRRSPCPSLPKSDHRLCLADYIYIF LKDTSTIMSF
5623	19524	A	5666	394	248	LTPGGGGCGKLRHRCTPAWATRANLPL KTKKKRRFLPTLAETSKVY
5624	19525	A	5667	1	194	RLNPGGRGCSSELRSHCTPAWATRKLH LKKKKKDQDQGRGDHTKNIWLPFRVFLP LHSLNTLK
5625	19526	A	5668	2	312	RGONSARGIITIIAILKKVCVYIYRCSLT LSFPLKCRGTIIAPCSLELMGSCDPSST ASQIARTADMHHHTRLIIASLTFCLLKK KKNVFCGTYNHCPKPGFYL
5626	19527	A	5669	1	245	RLNPGGGGCGEPSSSHCTPVNATRVKLS LKKKKKRPPFFFGIRQPPQGGPQTLL TPLNLLKNLITLLGAKKFFFTGGK
5627	19528	A	5670	1	135	ARTPSLSSESEDEKPTKKHKGKALR LKRRFVWVLMALPCIH
5628	19529	A	5671	97	2	KKFTHVWPGVVAHACSPSLTGGRGGRIT RLN
5629	19530	A	5672	362	173	VFSPPPPFKTPPPPPPKKIFPPKKKKTTP PKKKKLPFFFFFFFPGTRIVIND ILSGNRV
5630	19531	A	5673	237	13	SGGGGGFADYVWFFLDFERQSCSVAQA GVQWHLSSLOQPSPRPYFYSRDGVKNR PVPRVAPSPKGISLRPYK
5631	19532	A	5674	245	14	ANFLKHTVSTGLQITWSLLQLLNFAL VFYFLRQSFALVAQGVQWRDGLSLQL PPRFKRFACORFSEAEVAVS
5632	19533	A	5675	2	249	SHPTSHPOHLPTPTKNSSTPVDFTE RKAPPPVFPWQHHRAGPGTSLIPTDAPQ EASPPPPYSPSPSTPTTIPRETFLRQ
5633	19534	A	5676	115	241	SSTLGGGGSITLAGELRSHCTPANATG QDSISKKKKTLG
5634	19535	A	5677	460	2	RLGVTRWOKLKPQERMAWRENGKGP ALPASWEGPTVNLNLKHEHRANWSCHCD SGFCACWQGLGSEGSGLPSLPSWDGLV LTPSPNPPTGPPPLKTRSVLRGDDVLLP CDQPSNLARALWLLNGSMGLSDGQGGYR VGVDGLLVTDQA
5635	19536	A	5678	2	346	ENCLNSGGGGCSLRLCHCTPAWVTERD SITKEKKKKKPKVLEKFGIEFFLGKWK FFQLNPLKSSKEMEPFNTTLPLEPCFNG NKPFWAAKIWTLNFFOTOKGSIFKKGGR KK
5636	19537	A	5679	181	4	PKVRTLFGRRFFFFFFHSMESHVVQAGVQ WCNFSSPQPPPPGFKFCLSLPISWNS RHM
5637	19538	A	5680	549	410	FFVQTDPFCHVAQAGLQLGSSNPASAS PKYWDYREPVCPWSPGF
5638	19539	A	5681	111	403	SRQINGFFVSVTRKVAIGQFLVGPVKYI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						FENNNEICMIKTSQSYIVLNHKLKVYS SNIWQLKNILLRGGVAHACNPSILGGR GRRITRSRDRDHP
5639	19540	A	5682	189	3	NNNRKASWKKKDRVLLYCPGNCWDLGS LQPLPPGFKRFSCLKLPKCWDYKHEPLH PAPHV
5640	19541	A	5683	2	227	IHVCVCRVVCILREDSAQPARCVCVC VCVCVCVCCLDPRELSPTSQLESSCH FLYVPSGGSRINRYPGGC
5641	19542	A	5684	318	421	DVPCFFVAFCCDCKFPFASPAMLNCEM KPLSFI
5642	19543	A	5685	213	398	SLCCILLCCCCYFETESRSVVQAGVQWHD HSSPQGPFFRLKSSSHLSLWRHDHSSPQ PGPRL
5643	19544	A	5686	398	1	SFTSTSYSSSSVGGGGGAHSYKSCITAP TAQPHDRPLTASSSLAPQVRQNLHAYO SGRLSYDOOOOQQOQQOQALQSRHH AQETLHYONLAKYQHYGGQQGGYCPDPA AVRTEPQVYOTFSPSSSHRE
5644	19545	A	5687	2	288	SDRPRSPSPSPSPSPFAGVGRASSIFPIL SATLLLLGGVCVAASRVYKSRNIIILGA GILFVAGERQREGATGAHLGAHVVC VCVCVRARARA
5645	19546	A	5688	314	2	CRPGSQLQELGGGGESFVGGHGGQHP GAPQGRYLQPLLMCGASPHASPROPLA ILAAGVKFRVLREAGRPLRLMLQINPL PYSRVVHTYRLPSGGCLTCI
5646	19547	A	5689	122	3	MGGGEFSKKMNIQGVVAHACNPFSTLG GRGRQITRSGV
5647	19548	A	5690	144	1	EAVKKYTCPTWAGAVAHACNPFSTLGGRG GWITRSRGRDNNNGHGEIPR
5648	19549	A	5691	377	65	LGVFPPFFFLRGEGLSPPPGGLVKNQF FFPPQKGFPPTPERGQGGFLGPKFFPP LPPQPGKIFFLKKKKKKIPICALAVL TYQHPCYRTGQERVDGLREL
5649	19550	A	5692	12	147	YERRFCHIGAGLELLTSGNPPASASRG AETIGVSYHALMRNIS
5650	19551	A	5693	183	395	GHRFGFLHFPFPPGPGGFFRPPPKTEGK RAPPPPRFFFLGGGGSGGGPRGVLF LEHNPFGGAPKGVG
5651	19552	A	5694	177	283	THFLNRTDGRRLSLASLPSSGYGTNTPS STVSVA
5652	19553	A	5695	266	460	LSQKRTAFPPPPFGKKIFFSSPGGEI RQFFLETPSPFWKGFSPLEPLFKTWDY IGRDDPPLG
5653	19554	A	5696	1	412	MQPLKVNILEQKNLGLFVAPFTWHCP SWMSIAYNVYFSQYSFIWVCTWFTWY IPSKKKKKKKKKKKKKKKSSSPGSP GYAPKAPKNNKKK
5654	19555	A	5697	379	0	FFFPSSQKKKKKKKKKKKK
5655	19556	A	5698	1	187	PTRPPTFRFENGVNLLGGGGGCEPLKLC CTPAWTVTERDSVSKKKKKKKKAVGPPWF FOKKKV
5656	19557	A	5699	374	0	DFLLQKKKKKKKKKKKKKKKKKKKKGG
5657	19558	A	5700	219	413	FFCPOGGGGGPNFVFLGPPFPLKEIP PPPRGGGKKKPPPPPRGGFFFFKKGVS PGGPGGSP
5658	19559	A	5701	381	249	FFRAGQDGLDLLAPGAPLGLPKCWDYR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5659	19560	A	5702	382	197	REFPRPAFFFFF IANPCLIFSRDGLPCCPGWSGTPGLKQS AHLCLPKCWDYTHKPPCPAPQVIRPSIN LLIVN
5660	19561	A	5703	1	381	ERGSKHPPRGLKHI RGRTCFVLKGCMIQ LCVVPFGQKKKKKGGGKKKDKKREEE GREKKKNGNOGERVKKKSKRKKKKRSS SS
5661	19562	A	5704	291	167	NGPFFFFFVLKMGFCVHQAGLEFLTP GDPPALASRLGL
5662	19563	A	5705	367	23	KNFCPPFPFFFLAPKKKGGPPFRKTRF VPPPLFLIKGPPPKRGKGGPPGGFFPLF CPLGGKRGVFLSPRVGKPRGKGNPLF PKKKKKKKRRRRKKGKGRKERQGYIH TV
5663	19564	A	5706	411	116	FLKRWGSHYAAQAGLELLDSSDLPVSAS QSAGTTGVTHCSRLSYALACQCPVW RIPWRGRGVGRETSFRGWGRYGRWSS SGGGAESLPGLSPG
5664	19565	A	5707	162	2	SYCFPNSDDFIFFQPLPHTWFLWPRPFF IFKTAHGWARWLTPVIALWEAAG
5665	19566	A	5708	1	416	LPLLYKIPPPPALELFIDSPPPPPPP PPPPPPPPPP
5666	19567	A	5709	403	142	LSKEKKWGWPRGFSRPIFEKPPPPKIFF APPKKKIFFFFPGEKKFFFKGAPPPFF FFSFPPPPFFDCYNSSTWNSAWHIRCSI SIC
5667	19568	A	5710	339	461	PSTFILFILRRSFALVACGGVRWRHLGS PQPPPPGFKRVA
5668	19569	A	5711	408	42	TGARIIFSFGPKKTYSPPPRAPIILSFK RAAPQLIYFYLNLPAFKRLVKLTIVIMR RRPTFLLFKTFLFVPEFGFCHVAQAGL QFLGSSTCGSLPQCWDYRCEPQLAKRS TFIKESAV
5669	19570	A	5712	277	9	GVCCVCGGVVPPMGLTFSPAPWGLSLA PFLGTLCSVQWLAEISHLICQALVEPL RRQLQVVPVRKLLASSIVSGFGDSIWN GSYLR
5670	19571	A	5713	411	0	FLQIILLFIDIAFFLVFFFPNKK
5671	19572	A	5714	205	400	HYLTQSSSSMASESVDVWNKIPLTWP GAVAHTCSPSTLGGRRGRRITRSGDGDHP GQDEAPSL
5672	19573	A	5715	1	89	FFFFKTESRSVAQAGVQWCTLGSLOPPL P
5673	19574	A	5716	176	392	GVHLVLEWKLSHVCAEDDELFLCSNKK FFFFLFLQRSRVTOAGVQGRNFGSLQ LPPLGLKRISCLTRPSS
5674	19575	A	5717	1	89	FFFFKTESRSVAQAGVQWCTLGSLOPPL P
5675	19576	A	5718	306	42	GSGLRRCALNSVKCLNTLECLLGIYLR QIKICVYTKTCTCKFIIVTLFIIAKKEY PSVHQLINKMWHIQIIFLVIKRNEGCGG SCL
5676	19577	A	5719	1	263	PTRPGRFLLILDRGCSSELKSCVCTPAW VTEGDSISKQNKQVELSRPAAHLGLGL VPRNPQASTRIDGPTCKLLELISKFSK AAA
5677	19578	A	5720	3	278	NQRIKKNVSSRTQPHFLELLSLGWS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						VDVGRHPGWTGHVSTWSINCCDDGEGS QEEVVISSEDIGASIFNGQKKSMHI IKQ IKYFLSH
5678	19379	A	5721	127	3	KKKKKKEEEQEGERRRRKKKKKEKK EKEEDGECKEKEGE
5679	19580	A	5722	204	96	VTSRSSLFSTFGIKRASCLGLPKCWDYR PQPPHIA
5680	19581	A	5723	3	261	QIVRQWKYNDDDDDQLEFYTRYVLDPLGR VGKAEWAHFAALWEWRQAEWDLGSKG GCKEKNVCLGVVAHACHPRLLGGLGRI A
5681	19582	A	5724	134	358	PEPPPPFXLLFFVASVPPSPSLSLFFP HRPCYSPPSPTLSSLPPPLFPPPSSP PPPPRPSAPSPPSSPPFS
5682	19583	A	5726	248	470	LLNVQNGIRNVCSPHYTPFHKKVRYLS VFLTEVDSSQLRRRLCGGSAIERMHI FGREKVQILHALIYFLV
5683	19584	A	5727	1	281	NQHNRGFFDSCDGFNTYNNWREEHLERM LGQAGERRADVYLGVDVFAWNNVGGRF DTDGKGGLFSKQGRPSASPGTSFPHPG SIPVCTSK
5684	19585	A	5728	460	3	SCFTFTLADREITLPSSGTAISLVLDGS GNPVSVEQVTDGVKKVKSVPDPAE YSWELKLPTEQLRFRVCYSIRENDGT YAITAVQHVPEKEAIVDNGAHFDGQSG TVNGVTPPAVQHLTAETVADSGEYQVLA RMDTPKGGPVT
5685	19586	A	5729	70	465	SQCSFHHSVLCKQVODLESGLQSNWKK ITPMDENVVCVCCVCCVCMCVVCV YVCLCVCVCVTCVCMCVCLYIKGLLFLA KKETAGSFFHSQLTCLGVPCAFTIHPVP FLPQCRSHCVSGGRFVPGVL
5686	19587	A	5730	281	427	SWLTAAPNFOLQMESSRVAQAGAQWHD LSLQAPPPGQSAETQKQIV
5687	19588	A	5731	418	194	TKFHHVHGAGLELVTSGDLLSSASQAR ITDMHCSWPASVLSMNRPSGSTRCLRN GIFGLPKDFKPNDLTVQL
5688	19589	A	5732	229	2	PGGAPPLVRSFGPCWGAPPFVFVNGE PPKNFFFFFDGVSLCRPGWSAVAGSOLT ASSTSRVHAILLPQGI VA
5689	19590	A	5733	435	138	PPRYPPPLNGAPPHLSRGGGSFTPLTPO GKPRFFFLIKIKINPGGGPPYSPFPGGG PRNFFS PGAKGPLVLISPLFPFPGQKK NSFPKKKKKERE
5690	19591	A	5734	113	409	KDVCGGVLTGLSGVLTSPEYPNNYNSM ECHWVIRAAGPAHVKLIVFDVQVEGNEE CTDYAVVLVGGSPPTVHQYCGSISAPY LFLAKNIMSYSLPN
5691	19592	A	5735	3	122	GGWQVQVSEPCSLISINGVIFGLTSTDL LPHLCABEESR
5692	19593	A	5736	14	428	FLALRWGHIRLPASGPRDTATLFTSTLOT QLLMTLVGKDETCGFVYSKALVHTGVAL VPRGLTLADPGPTTDEVTLVQSGEREG SPSTAVRYPGSGVALPSQWLLIGHIELP PVLHTMLRVHPTLGSQGTAEPRPEN
5693	19594	A	5737	415	1	QRINTLQFQWTKAFPLPRMLELQNGHIV CLNSVLALSATPGADYCTSKASAFAPM ESLTLGLLDCPGVSATTVLPHFTSTEMF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QGMVRFPNLFPPPLKPETVARRTVEAVQ LTQALLLPWTMHALVILKSLPQAA
5694	19595	A	5738	335	152	GVEMGFHHVQAGLEFLSSDDPPASASO SAGITGVSHQASPFPLPSGITLPLSIY SSGSD
5695	19596	A	5739	35	462	LDASDFGECSCQAANDNVIVYELLEEM VDNGFPLATESNLIKELIKPTILRSVV NSITGSSNAGDILPTGGLNIPRRAGV KYTNNEAYFDAEEIDALIDKSRSTVFA ETOGVIDACLKLSGMPDLSLSPMNPILL DD
5696	19597	A	5740	429	325	NFGGRGCSSELRSHPCTPAWVTEQDALIG GRSGRIT
5697	19598	A	5741	344	423	RWFGVAHAHCNPTLGGRGGRITRSR
5698	19599	A	5742	431	103	RGFPPFRPROKKGSGPGGPPONKKNKP PLHTGGAGKGSFFKKKKKKVPPKGPPL FFPGPQGRKGPVGAAPVLIENRLGPFR IPFGWEPGRQIFFLAPVFFFPKPKF
5699	19600	A	5743	31	224	EEMGFYHAEQADFELSSNDPAALAFQG AGIASMHSCHSWFGKXNFMFCCINMRL AIHWECIA
5700	19601	A	5744	217	400	HSVMGSGSPFFFFFFFEGEGLFFFCF GGPNLKGKNPPPGKKGFPPPPPKGKN NGAPP
5701	19602	A	5745	4	455	DGLEFFGRFRFGRCSSPFREGRGQVEA LLTSQTGRRGRGAPHVSDGRRGRDAPH FLDGLVAGKKRSSLPIDWGGRAETLLTF QTGQPGRGAPHVDDGRPGREAPHFDP VAAGQRLQSRHFGGQRRLLGGGGCIEPR SRHCTPAWAP
5702	19603	A	5746	381	212	PRGGGGGRYSPPFGGGGRGNSFYPPGGG LNKPHFGPCPPPGGPRMKPPPKKKKSL
5703	19604	A	5747	334	432	MFCENYKEIAWPGVAHSCNPTLGGRG RHITC
5704	19605	A	5748	190	1	IPPKKGLNFPSPPTPKKGVSKPPQK VFFFLRRSFTLVTHGVQWRDLGSPQP APGSKHE
5705	19606	A	5749	425	297	ESAFHHVAQAGLELLGLSCDLPVSAQSV GVTCNSHHTRLYCS
5706	19607	A	5750	425	0	KKKQKKKKKKKKKKKKKKKKKKRT KSDE
5707	19608	A	5751	136	3	AQSSRPAWLTLFLVLVETGFHNVGQAGLE LLASGDLPSTQVPRRP
5708	19609	A	5752	3	237	GCSEFFSRHCTPAWVTEGDSVSKTNQR TQRLGKSLALFPAIHSLPLVVIKLAMPI LAMDI FHPDIVEPSYHVWQOM
5709	19610	A	5753	1	358	GDRGCSSELKSCHTPAWVTEQDLESKKK KKKKGGKTRNPGPTCCGDLPPPLGGG KNFPKGETFWFHSGKKKRFSLGKGEK FFIPRAEKGPKTLGGPNRGGGAKKLLK RPPGPVY
5710	19611	A	5754	2	191	QGCSELCSYHCTPAWETRARPVSKKKKP KTKNQTKNRLGKKPNLIFPPFQKKKK WVQIPGK
5711	19612	A	5755	42	408	KHAAPPASLSLSLLHHQGRACRFPFAF CRDQFLEGSAMPVQPAKLTRSTPP HPCSLENDSAHFFN
5712	19613	A	5756	179	410	LQAFLRPSPPVLFLYADLSNQLWFGM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
5713	19614	A	5757	166	2	VARACNPTTLGGGRGRIT GRGPFADFRVRPQLLQRFIFYLFTFEME SCSVTQAGVQWNCNLSLQPLPGLP
5714	19615	A	5758	334	3	EEKVFGLESPFILLSKGGGAAGPPCP SPRAMGPQKKGWETMVFITKAPSPG LVKQSPGIGPVPRNFFFLRRSLALS AGVQWRDLGSMQAPPPGTFPSCNLT
5715	19616	A	5759	373	470	SSCWLSRNSPFGAVAHACNPNTLGGRRG RITR
5716	19617	A	5760	210	384	EALDTTIFFFFFETKFCFVQAGGQGG NLGSLGAPPTGLTFPSCITLRRKTWDCG FP
5717	19618	A	5761	257	400	SLGSEYTWVCFCVPTESRSVGQVGVQW CNLSLQPPPPGPKRPSCLR
5718	19619	A	5762	400	2	ARAVSGVEDPGLGTGFSFRETWEAV VCRACRSGQLLWGLKLELRHWDLRKVL RNGTETDCLKQWQCCGAGMRGPPGGL KGPVGCICSSREVFVFLFLYLRDRVSL CHFGNNAVKOTRLTAASASQ
5719	19620	A	5763	34	440	RVRAPLWGEENGYFVLRAKPRSGKRSCL PFLRCGHQEPDLLWIGISTASPLRLVGAS QICGVFLFCFQVSLKPGASWVIGNNG ERKAQRLCPLRATRVEGIFCFRFRVFLRN SFTLVAGAQVQWRDLGSLQPPPL
5720	19621	A	5764	297	468	LVGAVPTGCGGRGVVNSHKSVOAQWL MPVIFALWEAEAGSRSQIETILANMV T
5721	19622	A	5765	1	205	GFKLTDSFASGAKAILRSQLLGRLRQEN RWNLGGGCGMLKWHNCPPAWIEGNLL FKKKKKGGGTF
5722	19623	A	5766	307	1	KERDFPPTPFCKTFFFFFRNCFEFP KEGQGGILGPRHPFSSRLSFLRGVPRG FPFGPRNFFFWILVKMGVPHVQADFK LLTSGDLNKTASQAGIK
5723	19624	A	5767	2	319	LLNGEELSRFPFSSQAWVFESSAGI FGGKAGATGLEKLTGSFOQLTGHPDPRT PEELGDPKSSASEKTRGLQANGVPEI LKAVTYQAWPKKAVDPITP
5724	19625	A	5768	787	1118	EAARLEAEARQQLQSQLOREQEELAR KRAKEQGLSEIAALQJHEDEGLLAES EKQVPEPRWGLCCSCSSSSGAGPCSA TWOLGALGQATALLGASVSLPAGGD
5725	19626	A	5769	2	452	NGAGTSVSLSEADENPFAQGLKLSDC FLDHGDKDKIFVWKGKQANTERKALK TASDFITKMDVPKQTVSVLPBGGETPL FKQFFKNWRDPDQDGLGLTYLSSHIAN VERVPFDGGLDFTTAMAAQHGMDDDT GOKQIWRIG
5726	19627	A	5770	2	130	GTQGGKIVDLVKELDRDTVPALVNYIFK GKWERPFEVDKWS
5727	19628	A	5771	422	8	HTARWGARAPGGWALLKABLCLNPAEP PIGARTAPLWPGCCFSLRPVFLLLFPFF SLFIQSFRILYQPPWPLQGRSTTLRM GTTDHVIVLASTNRADILDGALMRPGR DRHVFIDNPTLQERKCMRRLGASRN
5728	19629	A	5772	432	3	YSLNLKKRVFLTHNSVHYKSSSEKAL KLGTVVINSCLSVVPPDEKIFKETEYVN VAVYGRKHCVRLYTKLSEASRWSSAIQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						NVDTDKAFIDTPTQQLIQDLKENCMTSH VVEQIYKRKKILRYTHPCIAAAVEDHDND
5729	19630	A	5773	20	432	SRAAALLAVTETLEFYVEVAEKIWSNRA NRQCADCSSRPDWAANLGVVICKQCA GOHRALGSGISKVQSLKLDTSVWSNEIV QLFIVLGNDRANRFWAGTLPDGEGLHPD ATPGPRGEFISRKRYLGLFRKFHPQ
5730	19631	A	5774	433	2	KGAFOTLQKKDLQAFVLSSVOLQVLGTS CFKLRTVHNIPVPSNKVDECEPGLYGLF HVIHVFAKGFQKQATLSCALEVDSFGYF VSKAKTRVFRDTAEPKWDEFEIELEGS PSLRILWYEEYNNKSKVNNLYSAVGFSA AWO
5731	19632	A	5775	133	436	MLISLPHFSTHLTSLPFCADFGTRQTG AASHVLTLSAHSSVSCCPPLMGEATTSR AQDLPADEHTAFAHELEAPALSKQQLGS ILRLTGHFLPGQEVNL
5732	19633	A	5776	397	58	KGTISIGKLEELRGAARQALADAIIEF QLLPASLCTEDTPTGMQVKRSLGSRCH RSKQDSVAGERAKVGRGSTENYIIRT TYSQSLSVLSGHHFGATLAANGCSCSP T
5733	19634	A	5777	1	324	NRRCVSAGGVLEEYVPAFLDMVRSMLE QSIDPTQYEDTLRMEFTIHAQVGTMDK LVGNIAKQVSRAGVGRPALRTAEMALPSF HSLPGRGPVVSTANLSCFFLIETK
5734	19635	A	5778	1	398	RLGSRFSLHQSFLELRSIQLKGDVK KTVKLFQTEPLCAIQDAEGAIHEVKAAC REEIQSNAVRSAARLFTETSLDVINQDP SQVRLIRGISLEEGARPDVSAATRWIFDT QSLDAIREILLVDEKDFPSP
5735	19636	A	5779	281	12	VACNLGWRVRTPTTASYPCCVPQLSVRG KNRKELGGFLRNIVKSADEALITGMSG LKEVDFFEHERTNLLYHTLYCGRSED HATSR
5736	19637	A	5780	406	23	DSQATGPGISRGRRISSPSSLCTRFSTS IVKCSPLEHVLKYLDPPPPTRCSRSPAS LRSSPKHCVOQGFPIACRPGAAAPPPPP AQCNPFGPAAASARHEPKWGSRTTEGPPA RARRREGTGRKKRR
5737	19638	A	5781	415	18	TSQAGDDLLHGSLLRRGPEMGYLFQYDP DPTLATPPAGQTLAVPSLPATEPGTGP LITAVTPNGVRGAGPSAPELLTPPGT APPPSPASPGPLGPEGGEPPPTII TTTTVNTTITSFMYCGRSEG
5738	19639	A	5782	168	432	GMRRQTGLDQSGRGVGNKRWDFPPFSS LSPPFFFGKESYFVLKFIHGLKFGYL EPLSPGLKEFSRLSPKGGHLKCRPPSP LFFF
5739	19640	A	5783	1	423	TDDLNLNLDHSRTFREGGVDENETLLLR RKFFYSQNVDSRPQNLNLYQARD ILNGSHVPSFEKACFCGFQAGQFQPH VEHKKHKGPLDLKEFLPKYIKQGRGAK RIFOEHKNCEKISERSAKV
5740	19641	A	5784	273	400	DSVVLMLSLFGVCFHQVWFISCTLGAT FGYVAGLVISPLWI
5741	19642	A	5785	445	28	DTNRAFNHMEIKSGSGTEAKVNGADSID

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						KEAAGDETMARTMEAEATGAKPTGVEA TGAKVTETKPTGAEVREMEESTEEANME SKPTGAQATDTETTGVAMGVATRTKA EEAEMQAYGVGAGQAEPPVTGTVLRPL
5742	19643	A	5786	380	2	QRQGESPEASSLIHLERQVQLQQLLVE SQEKEKSLGREVESLQSRSLLENERGN TSYDVTTLQDEEGELDLPGAEEVLLSRQ LSPSAQHEHLASLQEQVAVLTRQNELME XVQIMNEHFEKDECI
5743	19644	A	5787	663	2	FGVERRATRTITRLTRTVLDLYSLAGVS ENLRHATODDASRTAPGLSSQHPKPD TVSGDTETQSGPGVFMTRKESGMKDIKE LAEVKDTLKNKSKDLEELDGVKGVYEGQ LRQLQEAAGQPTVTMTTNELYQAYVDSK IDALREELMEGMDRKLADLKNSEYKLT GLQQCCDDYGSYLVGIELIGKETSRLR KEINNLRLRLQEPGSAQANCCSVY
5744	19645	A	5788	398	1	TRCYHSALRYGGSFAGLGPRIKGLQOAO LWNPHFGSCQHRAKVLPPLEQVNNLLEL EYKRNKYGAKRGPPVVKRAAEPVVPQVP PAALSGPFGSGEGLSPGKRRGNCSEQT GLPPGLELPPPPPLPPPPPPV
5745	19646	A	5789	116	371	RHPKIWLGRPPGLTLEKRGKEEPLDP RSWGFKEASTPPRPFRGKKGTPRLKKK PKERKTRERGKKEGKKKKNNGKTNP L
5746	19647	A	5790	406	284	RRGFFHVDAQGLELPTSGDPPTLASQSK PGPLCPALLHTF
5747	19648	A	5791	200	3	GDALIYMEPERQVMSRSSDECVALCDQ MLVSYSKIFLVNLLTFDLKKNISICPL PGTWIMEMY
5748	19649	A	5792	372	278	LQIQSPAGQSCRGGLFVREDPVLTAHC WGR
5749	19650	A	5793	1	167	VAPFKLDPHSGRVRQAQGLELLTCLDPF ASSQKTAATGASHTRQVLGSKYKALS
5750	19651	A	5795	112	3	SSWKVGADHGEYGAELERHFLSPFTT KIYFFHCI
5751	19652	A	5797	356	238	PLFCNNGVYSLHFRCLAENAGDDAFVK DVTVLQNTDGR
5752	19653	A	5798	379	60	VKIRCHTIVVSMSLKNIRLILEEEQVE GMYSFVCVLDNQQLQWMDHRSLLTICA GMVYFAFNRLCVSEIYRMEVETGTRKOR QSKGDINTSRNGERASCE
5753	19654	A	5799	377	3	KVAFPGEGRGESWSAFOGHTRVVSDLK NAVYEPDLMTVSVGTIYIWDIKDTRK LTVALFVVGASQVKNKNKANCLATSH DGDVRIWDRKPKSTAVEYLAHLKSIHG LDWHPDSEHNLY
5754	19655	A	5800	143	316	CPTSPERLPYTEFFGVGSGLTVEQFRKI NGFPNAPFGWGGEDDLNNRYLCRSFGV F
5755	19656	A	5801	390	2	LEFFFFFLLRQSLTLVPGQVWRDLSS LQPPPPGKFRPSCLCV
5756	19657	A	5802	342	465	VIFFFRLKQGLTLSPRECSGTIITHCG LDLLGSSESPTFT
5757	19658	A	5803	1	378	VYSSEFENIKEEYRGRGPPTICYFERK FLIQYDNYGSTAEDIVENLKNPQPQPO VPETPNADEGGSYYHLTDEDFQVKEH

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						SSVLVMIHIAWCGICKMKNPEFEKASEA LHGAEASSGVLAAY
5758	19659	A	5804	152	1	KPETFFFEHSRVTTGTGVQACNFGSLQPP PSCFKLPSCLSLPSSWDYTAHV
5759	19660	A	5805	207	31	LYLQLLQQTASSGNLNTLSSLWPMGGKC FTAAEEQHPGQOQTTLTVLGVHFRFCE NIF
5760	19661	A	5806	199	2	GSECCSLLRGGEMHVSLSSEKVTFFSCD AIIHFSFLFWRQEPFSPVQAGVQWRDLG SLQPPFPGV
5761	19662	A	5807	385	239	QDQGLQKMKVCVCVCVCVCVCVCVCIIC KSCIRLSYMKMPINFGKLN
5762	19663	A	5808	39	184	GRIITKFFGEMRSHHAQTGLLELGGSSD PPTWASQSAITGVSLRIRP
5763	19664	A	5809	376	2	WAEPTSFHVCTISTYOTFFRGTLTAFTVR WKCLVIDEMQVRVKMTERHWEAVFTLQS QORLLIDSPHLNFTLELWTVHFLVPG ISRPLYSSPLRAPSEESQDYHKKVIRL HRVTQPFILRSV
5764	19665	A	5810	271	120	FLCFIGKTSERGSFSLYSRDTGLPGCQV SLMIKXSNEMVFKHINKGSINR
5765	19666	A	5811	367	3	DKSFKEWHKMLEDANAPTEERDERIAGL YEEIERDMLLGLASAVEDKLQEGVETV TSLSLANIKIWVLTDGDKQETAINIGYAC NMLTDDMNDVFIAGNNAVEVREELRKA KQNLFGRCI
5766	19667	A	5812	294	37	FRGENPDDGVGRGSPEDYRLRQVASSLF RGEHHSRGSTGRLASLFSLEPOIQPVY VFVPKVSHWAFPNSSLEPLTYKAIPLP TA
5767	19668	A	5813	184	3	TIISVLKNYLLFSPLQRQNFVLLRLECS GTITAHCNKLVGSGDPPAPASQVART GMRH
5768	19669	A	5814	468	1	DMVEYEGSVSVFTQVPRKSVNKGLOYTL MVAGEPGLKSTLVNLSFVSDLYRDRKL LGAEERIMOTVEISKHADVIEEKGVRLR LTIIVTDPFGGDAVISTECGKRAMY
5769	19670	A	5815	24	314	QAPFGPKCFNVLNLCFSLSLSKGPEPHY IAGAHEVNLGRELLELLLVQVFCQBYLA RNARIHVHVESTRHVLPSLNPDPGYEKA YEGVMAALAHQ
5770	19671	A	5816	474	3	TTLRKGYSRHKGLLHSTRQEVQATPLEG IIVSGQMSTMNLSSTLWPSFKVRRLCI GRTLRLSRIKPKRTPLQTRMPQKMR LYGDPGDSPLRSRAIPASSPGSTGSR ARPPHPLHPPHPLTREGEPLPLVLQPR RGPPPLPHSQAASRPV
5771	19672	A	5817	511	389	GMVCTEGREVVPTFFNEIETEEEDHCGRV SASIIILTHCSNR
5772	19673	A	5818	510	2	PLSCVPPNPLFPVPGVVRMIQHIEACAO VRGMQEIYVLIGFYQDDEPLTQFIERAAQ EFLPVRYLQEFAPLGTGGGLYHFRDQI LAGSPAEFFVLNADVCSGFFLSAMLEAH RRQRHPFLLLGTTANRTQSLNNGCIVEN PQTHEVLHYVEKFSICAAAIEDQASSRQ R
5773	19674	A	5819	282	152	FSLFLFLLQSERHFIMQVQCEATQCPDT RVSVRLYEKSVLHLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5774	19675	A	5820	347	1	EPHPVTPPAVGTSTRYNPLIMMDNRSAVTPPSPHPQQSSMQTGMNPSAMQGPSPPPPPSYMHIPRYSTNPIITVTVSONLPSSGQTVPRALQILPQIPSNLYGSPGSIYIRQTKV
5775	19676	A	5821	482	13	IYEKLTITGCYNILNADHPNPSGLDESIL EECLOYLEKQLESSQARKAMEEFPSSDG ELVOIMWATANENLSAKFCNRVLKFFTK LPOLTEKSPNPSLHLHCLGSLAQACVPEP VRLQAWLTTRMTTS
5776	19677	A	5822	608	7	FRFAEKVVEGMFIIVNSITIKIHSKAPH ASFELWLQGGYSVNPNNQSSDLRLTRIT DPGRGEVLTFKEITWQTLRIEADATONG DODPVTTPLRLITNOGRICIAIKRRTKD CNVISSKLMFLDLLWLVTDSOLKAMM KYAESLSEAMEKSAHQKSLAPEVQIT PPAPSAQQSWAQAQFGSGQNSNSSSPV LRPL
5777	19678	A	5823	328	3	AEEVASEDCSLPCLFVAVNRRITIEPVAAMR KEADMLRLFPPEYLGEELFGLTVHVLRL IAESLPGVESQNYLFRYGRHPLMELPL MINPSSGCARSEKILITHYKRPISLY
5778	19679	A	5824	69	308	TSVPSCVRCRYILIRTSALTNILGTHS NSSFFHASSSALHSCCFFPSWLTQILDI NVKAPALMTKAVVPEMEKRGYRE
5779	19680	A	5825	424	2	LQRAFSEIRIKRQYGGADRQIYHRRCSFANHSVRPSADEKCNNSFFEQRHGGSH QSSKWTVPVGPAPSTSGSQKRSGLQSGH SSQRTSAGSSSGTNSGGQRHRESYNNSS GSSRSKKQGHGSEHSKRSSSPGKPTV
5780	19681	A	5826	107	2	SSLTAGVRMGVPAQSTQGTVNGSSPQMS GTAALTS
5781	19682	A	5827	2	437	FPTTESRTSKESMSADRAQKMDGESEE EQESVDTGEEEGGDESLSSESIKKK FLKRRKMTDSPWIKPARKRRRSRKPKS GALGSESDKSSAGSAEHIGPCDSDTDME VSSGLPGSRRRPNVFLCIWAVVRAICP GFLWS
5782	19683	A	5828	487	22	MPEPVPFPLSHFRQFIAAIKLOFQARLSR CVRDLVRLAAPHNDTLRLMLFOHLRCRVI EHGQNRMSVQSVAVIFGPTLLRPEVEE TSPMPTMVQNRVVELLILQCCADIFPPH
5783	19684	A	5829	2	871	RGICSRQWRREGSQSRGGLVITSPSGS LVTTASSAQTFPISAPMIVSALPPGSAQ LQVVPDLSKKVASTLTDEGGGGGGGGGS VAPKPPRGRKKRMLLESGLPEMNDPVYL SPEDDDHQKDGKTYRCMCSLTFFYSKS EMQIHSKSHETETKPHKCPHCSKTFANSS YLAQHRIHSHGAKPYSCNCFKSFRLS HLQOHTRIHSMHTETIKPHKCPHCSKT FANTSYLAQHILRHSHGAKPYNCYQCKA FRQLSHLQOHTRIHTGDRPYKCAHPGCE KAFQLSNLQ
5784	19685	A	5830	463	1	LESRLFPSPHKREEGSRARVIMTSYPIE PHEHRKGLADVATLKQKLEENTRTE QEDSSCKELLKSDKWEKMERLNTSELL GHTIGTFPSLAERQLSTVITQLSLR EQLLNAHDEQKKLAASQIEKQKQMDLA

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						RQQQEQIARHQQLY
5785	19686	A	5831	462	2	MILFDSSLYFLCGWYLSNLLTGTGVGRK PWYFPFTASYWKSXVGLVEKQRYFLSSS LFFFNENFDNKGSSLQNRGELEGSAPG VTLSVSTKEYBGHKAUVQDLSLTFYRDQ ITALLGTNGAGKTTIISMLTGLHPPTSG TIIINGKNLOTVY
5786	19687	A	5832	396	2	VPSTPASKRRGIVPRCDIFITYDRGGALP KDTHVAGILFASAMNWNVPLLSATEFHS AWAMGMGVNFFVASTHHVLSNMSGSGRY APNGRKVYHYDMKTEMGELLSEVDSDHP LSSLAYPTADNNWATLY
5787	19688	A	5833	384	137	EETCLNFGAGGCGSEPRLWCHTFAWATKR DSSKKKCKNCLSKNKKKEKEMFACVVC CVLFISYAFPSKAQELSNPCKHYGNF
5788	19689	A	5834	171	2	FVGGINISGNFYRNKLYLAFIRKRRMNT NPSRGPYHFAKPRIRFWRTVRGLPMHY
5789	19690	A	5835	278	404	SVLIFKEKTKLYKAIWFGAVAHACNPS TLGGSRGIRTSCE
5790	19691	A	5836	417	3	SKGSGSRCEWYDLFSGTHAVFQFFLKQ QGRVPGILOAVQVAKMSLIDLAGSERAS STHAKGERLREGANINRSLALINVLNA LADAKGRKTHVPYRDSKLTLLKDSLGG NCRVTVMIAAISPSMNTNEDTYSTHV
5791	19692	A	5837	409	230	AGRAYCYNGNCLTYQEOCQWLWFGKAL LGTALPSPPLPSOPPLARVVWNLGFK MHL
5792	19693	A	5838	3	409	LRSVPCKDYLTONHYITSPLSEEEAAPP LAYVMVIHKDFTFERLFRAIYMPQNVY CVHVEKAPAEYKESVRQLLSCFQNAFI ASKTESVYVAGISRLQADLNCLKDLVAS EVPWKYVINTCGQDFPLTTTRPV
5793	19694	A	5839	385	174	GLAVEITGSRRTAEDGLELLASSDPPTSA SQSAGSTGVSHHAWPDVTSVYWCFLCC TKQVVVGALSIVSL
5794	19695	A	5840	260	2	PLPRYTAACSRLLVQYKAAFPQVQGSSEY SSIDEFCRKRFLDCPLAMERIKEDRPIT IKDDKGNLNRCLADVVSFYITVMDKLRO CI
5795	19696	A	5842	299	3	FSGIKYICIFLFCVCFYLLLGIGSPYV AQAGTLTLLGSSDPPPSASQSPGIIGVSH YVQPIHTVAQLSPSSIFRTFSSQTETV PIKHTSHSPSPSLY
5796	19697	A	5843	391	2	APHAPFLRARGEFDQPLSHFRVPVAVSA NCRMMHLLFVHSSPTPLRLPLWLKQARW LLPQLVVLQMGYSLLRPAALISMVLL AREFLYPAKMSVSEVCSGLSPFLLEQH KTNLLFYASGDICSAHV
5797	19698	A	5844	479	59	FVGMPEFGVGHASLAMEHLHTRISLQTKL RKRKCTLPFNTQEKSAARRGHILGENIY LLLPAIALRILNCLLVQTSFVDPDEYQGS LEVSHMVFNYGYLPWENTERLRSVAYP LICASIYKVLHLLKQSVQMLVSGNKS
5798	19699	A	5845	406	548	SVQTKPFFFETESHVPVQAGVQWNLCSL QPLPCRSKQPLCLRLRPSW
5799	19700	A	5846	2	394	TLCHRKADPTVHESGRIMYLNGLCFML GPAQLTQLRSVSRQEC
5800	19701	A	5847	472	201	LSILSDTSLCLGRFPTYENGCAVFREEE

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						REGCLARIICLSIHRSYEDFVVDQGFNVLY NKKPVIIYRSAPARFGLGQSLCNQVMWYQ VAILNK
5801	19702	A	5848	127	3	SSNVKAAWGVKVMHAGRYGAEALERMFL SPPTTKTYPPRCI
5802	19703	A	5849	238	1	MAETHPNPTGLPLAPALPLCLAGSATHTPC LFSPEISLDVDADRDGVVEKNNPKKVP FQGRHHPEFRASEDTADDPAGMY
5803	19704	A	5850	423	2	LSPGLNWSANQKVVFDVSKPSRKDLFA VDTQVGTVPSTLAGECGGFGDGKGRAGE QATQAGDWSNNMGSDGILSHSAPLTV PQPLTGPQGPCLCRPLNQOTSPFALL PFSTQLCSMCPGASARPPPLLLKPTMY
5804	19705	A	5851	326	682	PSYSLLSLQVKNVEKLFPRQKRKESMK QKMEHTQKKQLLVSPWQLGSAGAGAR PGMVTREPPLCLCPAPQIPRSEYLNLA SSFMAPLSPPPCSLHRLSCHLHVNSI SGYPNCI
5805	19706	A	5852	263	30	HEKTDDERGFGQSARSALTTPFGPPPLP IEPHETTPPEHAPSGTIPPEPLPVELHE TTPQHPVPSGTIPPEPYLLSQ
5806	19707	A	5853	389	2	GLFTQREKFGASMRTRMTIQSIIVATTSF VCLVGEENNVQFRAESRCRWYDPRHNR WFOIQSLQEHADLSVVCVVGRIYAVAG RGYHNDLNAVERYDPATNSWAYVAPLKR RCMPTKAKRWGRGCISS
5807	19708	A	5854	379	2	GRSLRYSGSCSGEENSTNNSAGQSRRAVI AAAARRRGNSHMYEYEEAEHERRVRKR RRLVVAVEEAPTHIKKLQEEQKNPRE VMDPREAQAIFASMARAMQKYLRAAKQ QNYNTMESILQIC
5808	19709	A	5855	374	2	SDAGAPVNIYEFRRHRCPCLEDTKPAFVK ADHADEVRFVFGGAFLKGDIVMEGATE EEKLLSRKMMKYNAWTFARAGNPNGNLS LWPAYNLTQYQLQDLNMSLQRLKEPR VEIWNSTIPPCI
5809	19710	A	5856	516	18	PYECKEKGKAFNCGSSLVQHERHHTGEK PYECKEKGKAFSRGCHRTQHKLHRGET PIKCKEKGKAFSGWSSLVKHERVHTNEK SYECKDCGKAFSGYQLSVHQRFTGEK LYQRKEFGKFTTHGSKLVHERTHSNDEK YKNECKGEAFLWTTYSNEKCIASAK
5810	19711	A	5857	392	3	CERGMGSGPRALGHHHTSFLKRLNCSV PGDSTFYFDVLQALTGPVNLHGRSALFG VFTQTNTSIPGSAVCAYLDEIERGFEG KFKBQRSLDGAWTPVSEDRVPSRPGSC AGVGGAAKFTSSRDLLY
5811	19712	A	5858	391	3	ARRTTGMVPKAGGGKGRGAVFRSYIRE IEELRSKLVESEAMNESLRRSLSRASDR SPYSLGASPAAPAFGGSPASSMEDASEV IRRAKQDLERLKKKEVRQRKSPKEGAF KKRAKIQEENSEETNGE
5812	19713	A	5859	409	3	SLPEGGDPHWAGQESLLFVQEGKLSLPV ASRVLLIACRYDPSNSWAEIAPMNC REHFLGAMERYLVAGGRNELQVLT VERVCYCKNNKTVFQSFORSLSCHAGYV ADGLLNTSGGVNTNAGYQNPQCI
5813	19714	A	5860	405	135	NLSRLSLCRQPMTLTVTWLLFYDSEKKA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						FWLLVALVKRMLEFDYINIRVVGECPRVL PRLGLOVPAGSMRVAALPRPSSRLHVGS LGVRG
5814	19715	A	5861	389	2	VYSELEEQLTDEFNAELNRVPLKRLDLTI FVTQDQSRMAKRVKDYKYVQCGVQPOQ SSVTTIVKSYIWRVTMAPHPKDIWKHL SVRRFFWNRFAINTFLFFLFFFLTP AIIIMNTIDMYNVTIRPCI
5815	19716	A	5862	525	0	SHLPESERIHTTVGKQEQVMDTSTKTRP NNDVPEPPMPIADQVSNDDRPEGSVEDE EKKESSLPSKFKRKISVSTKGVPAGNS DTEGGQPGKRKRWRGASTATTOKKPSISI TTESLKLSPIDIKPLAQCAVVDLHADD SRISEDETESKGGDGTDRGLTIC
5816	19717	A	5863	399	2	ATRRNRNRVPSGMRTRTMREMLAAGVG PSPYPLPPPPPEGTSSIEYSNQNTCOGH GNPDFPHGNPGTSMNDFMHGPPQLSHP DQPMFNMAALEKPISEHFMQETMPHAGSS DQPHSPMQQDKARNTPOPHY
5817	19718	A	5864	3	714	KRPFIALCLSNVAFMLFWQFAQFILFTQ IASLFPYVVGVIIEPSKFKQIYYNMNIS VTLSEILMFNGSMYLSSTYSSSLMNTWA ILKRNELQCLGVSKLNCGLQSSARWC GTTILKELTSLKLGWSDHILCSDLIANG ILRYTDFDTLKVTCSPEFFMEKATLLI YTKTLLLPVVMVITCPIFKKTVGDISRV LATNVYLRLKQLLHSELAFHTLQLLAFT ALAILILRLKLV
5818	19719	A	5865	423	1	APFVSTVAQCSNSEEAREVGSQAQEF KYQKSLPPRFQOQQQQOQLYXMQHW QPVPYPPSHPPQRTFYPHHPQMLGDFPRW MMPSYMDPRITPTRTFVDFYPSALHPS GLMKFMPMQESLNGTGRSEDQNCVFP CI
5819		A	5866	497	2	AVGAGQKGRGGGGRELMPFOKIVGGGA FTNNAHVGLPKIMRRLIRTGMLIEIHL PGVVQGLFPVCDLSDIHTFLSQLLER RRQALCPGSTRNFIHRLGDLISQFSG HSAEQMCKTYSEFCSRHSKALKLYKELY ARDKRFQOPIRKVYCGRCRGSGQGR
5820	19721	A	5867	382	74	LALSPLKCSGGITAHCSFLLGSSDPP PSASRVAGTTGARHARLPYSLRHYHFV LRLNFSKHSKLKHFHPIILIRNPGKVG YSFQMSDLLQSRARQSS
5821	19722	A	5869	378	3	SFSRSANLISHQRIHTGEKPPQCAECGK SFSRSPMLIAHQRSHTEKPYSCPEGCK SFGNRSSLNTHQGISGGEKPYECKECGE SFSYNSMLIRHQRLITGEKPYKCTDCGG RFSQSALITV
5822	19723	A	5870	375	3	THVIVFQATGHVNAKRVFDITYSPHED AMVLFELMWAPGRVLCITVKDEGSFHLK DTAKALLRSLGSGRQALGWRDITWAFV RKGEAECHWADTELNRRRRRCFSGEY GSVCSCDKDPTV
5823	19724	A	5871	373	1	QPEEVSGLSPPSASAYKLVLLGLIMC VSLAGNAILSLMWLKERALHKAPYVFL DLCLADGIRSAVCFPFVLASVRHIGSSWT FSALSCKIVAFMAVLFPCFHAAPFLMCIS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
5824	19725	A	5872	382	2	VTRNMAIAHHLY KSPFSQKSQQLIHLRTHGTGERPFCEPCGG KAFREKSTVITHYRTHGTGERPFCEPCGG KAFTQKSNLIVHQKTGTGKTYEACAKCG ESFTQKLDLIHSTHTGKPPHECNECK KTFSDKSTLIPIV
5825	19726	A	5873	370	3	MGRVRAQNISGVMSGPKOKLMOSQFFPTO GQQGFCEGKEPYQAMSQNMGNTOQDFSP DQSGMNTMSNVGATRLSHMPLPPASNPFG TVHSAPNRGLGRRSRLTISINQMGSPPG IGHLNSNTTCI
5826	19727	A	5874	362	2	GGKFLVLGNLPSKLEESMVQYRLVTAA SLVRGQISEYNISIRASDGGSPPLSTET HITLHVIGINDNPPTFFHLSYSACTPEN NPRGASIFSVTAQPPDSNNNARTYALT EDTLQGVY
5827	19728	A	5875	369	1	RIRPRPTARLASARTLHEVLSQESIRYA PGDAVEKWLNDLLCLDCNLIARIVSVCP LPEACDLSYVNRDTLFWCHKASEVFLQR LMALYVASRFKNSPNLQMLSADAPAHRL LNKCLLCPFPV
5828	19729	A	5876	119	39	VTQDYYTPPNEELSRDLNKLKPYMR
5829	19730	A	5877	461	2	RRGWTSSRRPKEDPSGAAVPEMPKSSK IASFI PKGGKLSNAKKEPMAPSHSGIPK PGMKSNPKSPSAPAPSKGERSRSGKL SSGLPQQKPOLDGRHSSSSSSSLASSEK GPGGTLNHSISSOTVSGSVGTQTOTGS NANSVQLPOPLCI
5830	19731	A	5878	503	3	PSPOVPGCECPSPFKKLGAARAFTTFDPAP LSPOQRVASSGSEQTBEQGSRRNSFOED GSGMKDVPWGLKSLRLHKYIAPLSQMSY ESMTWLTQOHLSEONFTGAKRHKIALSI QKLREOSVLKSLKEDVLEGGNLRNALQ ELQOIIITPIKAYSIVLOATVAANTLY
5831	19732	A	5879	421	34	LVHVKLSASNVLDAGQVTKITDYSISK RLADICKEDVFEQTRFRFSUNAHVYRTO NKGDUVRLGLMLLSLSQQQCEAEYVPAI PSGLPGGFQDFLKKCVCLDDKKSMESPA VVETKQNKSPANVLRPL
5832	19733	A	5880	379	3	AQGLLLAWPNLNROHCPSCSNNLSTFI QNNWSPLGLSLKTRAPGGQSVLSSDLP AVLTGTFVAVMSVMGVSVTESLAPQALNG SMINETARDAARVQVASTLSVLVGLFQV WNSQEVVPPTTCI
5833	19734	A	5881	429	1	SLVSYMDTSTAERLKGELGLQAKELSA VHSSHIEIGVNDNLFSLEMRPLESS TKSFHSAVEIKNRQHELPCFOHHGIDT PTSLQKRSACCPSSLRLLEETASSSQDG DPQIWDDLFPSES LNKLFTVLESEIATV QCI
5834	19735	A	5882	436	3	WSLVSYMDKSTAEKLGELGLQAKELS AVHSSHIEIGVNDNLFSLEMRPLESS NAKSFHSAVEIKNRQHELPCFOHHGIDT PTSLQKRSACCPSSLRLLEETASSSQDG DPQIWDDLFPSESLINKFTVLESEIATV TOCI
5835	19736	A	5883	195	353	DSYSYVRSTADAVAYDSKQYQQPTATA AAVAAAQPPQPSVAETYYQIGGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
5836	19737	A	5884	432	1	LSAKVPVASVSDQAAAMHLSQCPRNLATSLAELRTASQIAHKLCSGMEIDSLNLTVCILKNELQDAKMAVESOLKPLPSETLEKCAQDLGSTSKAVGSSMAQLLTCRAQGN EHYTGVAARETAQALKTLQAARGVAAS TTDP
5837	19738	A	5885	313	1	GKSFHLLILQTSPLSKAPQLTLLLLYW SWGVVVSVAASARETEAGIOVSSEEPGRNVS PHSRLQDETNI RLEAENNLAAAYRQ VREVQGRDREGKGLMATLY
5838	19739	A	5886	432	3	GSFGCSPTILCNWVEEAVGITRLHLNLR ELGCHWSFSLPGTYSLEFLSTCTQVLPY SWSGLLFASGNLYLSLYLVPSRAETDSRG SQPLPVARHGVGACKCKPOTRPGLS PQ VCVEKLMPLSSFCSAFQNTYKOPMSR PV
5839	19740	A	5887	417	2	ASLMVAPDYAETISPLAMPAPSSGVVCTP IMSTSSSEAMSTPLMLAPDSGELSPFILM QDMNPGVMSTQVPVAPSPFAMSPLOITD EDTAMSKVLMTALASGEISLLMSGTD SEAISSLIMSASVAGSGTSPQPTSTLY
5840	19741	A	5888	420	3	KFDLIKLLDKTMSYDLDIEASDGGGL SGKCSVSVKVLVDNDFPELSISLTSP IFENSPETEVAFRIRDRDSGENGMIC SIQDDVLFPKLKPSVENFYRLVTEGALDR ETRAENYITITITITDMGTPLRLKTSQSV
5841	19742	A	5889	321	414	FNMRINWPAGAGAHACNFSTLGGRGGRITR SAD
5842	19743	A	5890	415	1	PGLPSTSVKGI PASKQSPHESFRTLHLK TSPITQQLGLYLSHTAIRVHPQETLKEF VQLVCPDAGQAGQVGLPNPSSQDKV HNFPLPTFMLPPPPFPMPAREVPLPVPD TKPPTTSTEGGADYPTSTPTYSTPSLY
5843	19744	A	5891	193	3	KPSSKVNRSRDYFDLSSVEQPIKDAVIT VPVFFNQARRAVLQAARMAGLKEMQLI NNTACI
5844	19745	A	5892	412	2	KHQSVDNKSFFVSLYPDFSSLSRAILD VVOFFKNKTVTVYVDSAGLIRLOELIK APSRYNLRLLKIRQLPVDTKADKPLLEK KRGKEFHVIFDCSEHMAAGILKQALAMG MMTEYHYHIFTTDLFDALDVEPSV
5845	19746	A	5893	413	3	ELLCSNTSCRCRCFCVECLEVLVGITGA AEAKLQCPWSCMYCLPQRCBGVLRRLRRD WNVRLQAFPTSDTGLEEAPKLYPAIPA ARRRPILVLSLFDGIATGYLVVLKELGK VGVYVASEVCEESIAVGTVKHEHR
5846	19747	A	5894	424	3	CSGRREP SVRGVQCQGDGHHHSARMAPS EAPGTRCTSPSHGQNTAABATPAQKTPA KVVYVSTEMANKAAKAVLKGQVETMVS FHIQNISSSKTERSTAPINTQISAIRND PKPLPQPPAPASQDQNTYSONTRLOPCI
5847	19748	A	5895	400	1	ASVQNPALRLVTREEFAIMQTPAGELYD KSI IQSAQQDS IKANKMKNENKAYSFK EKIIELEKEVSTRHRRLKVAEELGGLKL VAFPTAMMLFTWNLKPMHSSDAPDQC LVHHTPPSFLHSHFIDLY
5848	19749	A	5896	421	3	VSSIQGAVNLLGGGLSLLGSDSLGGGI AGSPAVGQSFI PPSVQATCAPSTPAVV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
						SSGLNDLSELSTWIGMAHGGYVAPKAWV LPVAKAGLESSGTFTRRQGHYIMAMDF TNKALQHMTSAIQFTKNSFGVIPSCI
5849	19750	A	5897	384	1	PRASRFIHEAGIVPLPMRTHTFPKFPFC EVAGVQFSRNVKVKNMRKHTGERPYSR QSCSVRFVHSYDLKNHMLHTGDRPYEC HLCHKAFKEDHLQRLHKGQICLEVRTR RRRKDDAPPHYPPPCI
5850	19751	A	5898	429	2	QDIAAQSLSLTVLPESWRKANIMTEPQ KSQERYKGIYVKEKLYRRARHDESINWT SCDHHEQCEKGEDPGRHPNCGKNLGMK STVEQHVVHVLPPQPTFCNCGVAFADD TDPRAHPSHLGKSYKCDYQKILSQS LY
5851	19752	A	5899	424	1	GTMLQALAAHDAGSRAHVLLLSQDQGI EQHMDFDSRYTLLELFAETTSSEHCMA FEGIHLPQIPGKLLFSLVKRYLCVTSLL DQUNSSPELGAGDQSSPCATREKSRGR ELEFSMAVGNLSLSELRSMGARNLSEH V
5852	19753	A	5900	135	459	VFMKAEHVISVCSSENSLMVVVMRPF LIGLTHIQEFYFEMEPHRAIQAGVQWC DLCSLQPPPPGLKRCSCIPFSSSRDYRC APFPY
5853	19754	A	5901	418	10	GRSPKPGDLRWESVHLSFPGADSLSGG SAPASSYEPQSORSFSSNRSORGSTSTR NSSQKGSVLSIKQKGRLEYMEKLEH LIKAKAFTIKKKFSQNLVAQLWYFVKCV YPGLSAYQIPRGYPTRVLGNFLTK
5854	19755	A	5902	402	2	GYRHPLEIKSVDFGQPEKOPVILSLV RSNRKGEVGFVEDRRINVDVTRARRLV TVICDYRTVSSHAFKLPLVEYFTHQGEV RTAFEYLLDDIVPDNYSHEDSQSSQAAT RPQGGTSTRTKQKQRBGGMY
5855	19756	A	5903	346	1	GICPLSHIKMTDARCGIYEMKGGERSPK DTGKEPGHSEAKTQPPQVLAVGVAQPEA POPGNTTAAPVDSGPKAGLAPETTETP AGASETAQATDLSLSPGGESKANCSPED PMY
5856	19757	A	5904	139	212	EVENDDISHHHHHHHHHNSKS
5857	19758	A	5905	2	345	PCGCWGRCALLLISAAKAKSKCGQPTFL PCASGHIICIGRFRSGKFCDCPDGSEEB NCTANFWLCSITARYCKNGLCIDKSFIC DQNNQCDNSDESCSSQGVGVCGFK KA
5858	19759	A	5906	432	17	PQTTFHRTFGGKKAUVLLAVGGQFLC NSPYPSFPHYVALSAQPISTGQVESVT WIGVFCFTSNFFYGCIMRQIRGELSKQ FVCFKPAPEEELRLPSREGSIEENFLQ FLOGTGCPYKSNVSRPLPCIAAALRV
5859	19760	A	5907	407	1	PVACGCEGKSYQSSSLVSHERTHSGVR PHHCDCGEFFSRKVDLLIHQRVHSGER PYKCECGKSFHSCSLIAHQRHITGMR PYECSECGISFIHSCSLITQORVHLGTR PYMCCEGKSFQSCRLIKHRSV
5860	19761	A	5908	419	3	VLAKKTTITKSARDCHFGNLIHLSSTNL VASIQRPDKHESFGNMVDNLDLSFRSS AENKYDNGCAKLFPHITYEKTNPGMKPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						GYKECGGLRRKGLSLHQRIKNGEKKP ECTACRKTFSKSHLIVHWRTHGTGV
5861	19762	A	5909	441	57	KVMGIFKSSLFQALVDIOEFYEVTLINS KQSCQKIEBANQVLQWKEKSLAPCH DRLOKSSSELQSLIGQSSLETDDQOPW LFPRGSSGHRGKTYDCHCSIGLQIADVQ RKMLHVLISKIKIRV
5862	19763	A	5910	3	317	CLLMILRRRWGSGRGRQRRLQATPSWEST KTADQGDRRESGGRQRHCSSPHQKST TTSVPAAREGAQEAAGGPRKQGTSRP QVSTRQCAMPFAHRKLEND
5863	19764	A	5911	183	1	QNSDSKSLNRVASRDHAKPNLTCHVSP AIQGTGSLSESSIPVSDTSTPPRSRQ LPPCI
5864	19765	A	5912	395	1	KTFQFNICVKVHFRFSSNSNKKIRYAGD KTFKCKECGKSFHVLRLTQHKRIHTGE NPYTCEECGKAFNWSSILTKHKRIHARE KFYKCEECGKGFTRSSHLTKHKRIHTGE KPYICEKCGKAFNQSSTPV
5865	19766	A	5913	449	2	FGSHLEKEDEKQELVDKAIKPSIEATL ESIQRKLQYKRAESSRPEDIKDMTKAQI ANEKVALQKALLYESIHGRPVTKNERQ VMKPLYDRYRLVKQILSRANTIPIIEEE EGSEADSNVKPDFVMVKNKCTDFSAVMVKR PLGGSARPD
5866	19767	A	5914	464	23	SAHMTETRSKSFYDGSLSLTGPSAPAPV APPARVAPPERRKCFVLVRQASLSRPET ELEVPAPKRGQSEEPQPPSSKPSAKSSL SQISSAATSHGGPPGGKGGPGQDRPPLGP LVFPYTEALPVFHHPVAGTHKHEKPYLPP LVGCRGG
5867	19768	A	5915	366	1	LVSFNFETTSVLATLVFVAVLGFKANIM NEKCVVENAEKILGYLNTNVLSDRLIPP HVNFSHLTTKDYMEVNMVMTVKEDQFS ALGLDPCLEDELKSVQGTGLAFIAPN EAMTHSPACI
5868	19769	A	5916	246	366	TSVKEQQMPGVAHACNFSTLEGQGGRI TRSGVRDQCOH
5869	19770	A	5917	400	3	NDNAPEFYQSVYKVTULENAFNTGLVIK LNATDPDDGTNGDIVYFRRPVVPAVVY AFTINPNNGEIRTKGLDFEELKLYEIS VEADVKGNI PMAGHCTLLVEVLVDNDNA PEVTITSLSLPIREDTQPCI
5870	19771	A	5918	410	200	CTPPQPPVKCRFLNRDRVSSCCPGWSOIP GIKRSSYSLPPECNDLRPVILLFCFLSH ISSKQPYFLPPSYR
5871	19772	A	5919	214	407	MYFYIDRASLLSPRELICIVVTIAHCSLE LLCSRDLPASASQAGITGIRHHTWLKT HFYSSFKT
5872	19773	A	5920	476	39	VFPYGLFVGSTGRGLGFLYLRGTSHPLRG LHAAALNGRRVLQPLTRNKHGEGCAEF ANDDVALGFCGSHSLAALPAWGTQDEGT LEFTLTTQSQWAPLAFAQAAGWHGDFIHV DIPEGLWSMVEKGGQTLLNLSVPTVD AQPHM
5873	19774	A	5921	430	2	SLRPSSTGSPSGGGLSEEPAAKDLNRM PGLVGQEVGSGEGPRTSSPLFNKAVFLR PSSSTMILFETTKSGPALGKAVSEGAE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						AKLGVSSESRPEVAAKPAALPTQKPAAGTLP RSAPLSQDTKPPVPQEEAGQDHPSPKAS RC
5874	19775	A	5923	411	2	MSLKVDVEALENSAGATYTRKKGGKVTG DSQPKQGGQVGLKKKKKKKKGMVPMKND PKVTPDPERWLPMPRRSSYYGRKKKKKK DQIGKGTQGTAGASSELDAKTVSSPP TSRPGSSAATVSASTSNIPRLRY
5875	19776	A	5924	402	2	LOGGAIMNKFYOPHEAHIPYLLQQLFTDY NLYGMNLINLAALKFRKARRKSNLTHAT GSKNHLISGNSLADTLFRWEQDEIPSSL ILEGVEPQSTCELEVDAAADILNRLDI EAQIGGNPQLQAIWEDEKQRR
5876	19777	A	5925	215	403	AETSTYFFFLERQFPFAPQLGGHGRNL NSLNLLPRGLREFRSLSPGGVIYGGAP PSPTFFC
5877	19778	A	5926	320	1	PGRRDRWINGQGECELYLLASMTQWCER EISSIAPGELCCLLLSLPQEEQCNVVR VLIVAGRKVFMCNTAFSPMCTSRQVGN LSRTTEKINGVARCPYDPRHRV
5878	19779	A	5927	400	1	VVATDGGLLPLASATVSVALQVDNDNE PQFQRTFYNASLPEGTQGTCTGLQVAT DADSGPFGLLSYSLGAGLGS SGPFPFRI DAHSGDVCTTRTLDRQGGSPDFDTVTA VDGGGLKSMVYKVFSLDEMY
5879	19780	A	5928	398	62	INTEVLVGSEVTLCSATGHPHPPRISWT RGDRTPLPVDPRVNIITPSGGLYIQNVVQ GDSGEYACSAATNWDISVATAFIIVQGG YPSVPEPGLSPILTEPLAARAAIPTDAP
5880	19781	A	5929	403	1	LASDGGDFVLGSTRICVKVLDAANDNAP VFTQPEYRISIPENTLVGTRILVTATD ADEGYAAQVVVFLEKSPGETSEVFELKS TSGELTI IKDLDYEDATFHEIDIEAQDG PGLLTRAKVIVTVLDVNDNANV
5881	19782	A	5930	408	3	VASDGGDFVLGSTRICVKVLDAANDNAP VFTQPEYRISIPENTLVGSRILVTATD ADEGYAAQVVVFLEKSPGETSEVFELKS SSGELTI IKDLDYEDATFHEIDIEAQDG PGLLTRAKVIVTVLDVNDNANV
5882	19783	A	5931	126	391	PVLTCMHFHSAGAGGSYFNI SRSLGPE FGAGELCLYLATTATAMAYILGAIQL LVSAQEPWSTLAMI KQFLWTPNRLMVL IPTC
5883	19784	A	5932	436	359	NKEWLPGSKVPEKSIINDVKNTSGLL
5884	19785	A	5933	365	3	LIIGMLTAIIGDLASHGFCITGLKDSVT AVVVFVAGTSPVPTFASKAAALQDVYAD ASIGNVTGSNAVNVLGIGLANVAAIY WALQGOGEFHSAGTILAFSVTLFTIFAIV CISVLLYR
5885	19786	A	5934	394	3	FQYFSRTRDVLKHERMCHENHDKLNRC AIKGGLLTS EEDSVFSTSPKDNSLPKIC KQITERKSSGMDKESALGKCDLKKVQND YSPLYSSTKVKDEYIMVAYAVEMPHSS VGSXLEYAGSEIHCICI
5886	19787	A	5935	393	1	REDLIAGIDFLEDEVTVLPGGWDNPNR IEPPKIVPSADKKKSVGLAELEQMCNS VGGGGGAPGGGNGGGGGGGGGGGGGGG AGGTSOGDDGEMFANHEIGELIWTGRF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
5887	19788	A	5936	410	126	FGGLCLDIKRKLWFFPSCI PICYYKKAGARWLTPVIPSSWDYRHOA QLIFVFLVETGFHRVAQAGPELMTSGDP LAYNFLCSYPNEVFRSQASASDLQFVLR NLEPPFDAGNV
5888	19789	A	5937	426	1	DATFHEIDIEAQDGGPGLLTRAKVIVTVL DVNDNAPEFYMTSATSSVSEDSLPGTII GLFNVDHSDSGQNAFTCSLPEDLPFKL EKSVDNYVRLVTRALDREQFSFYNTL TAKDGNPSSLSTDAHILLQVADINDNAP CI
5889	19790	A	5938	438	3	ADPTKGLLRNGSVCRAPGGVSGQNSVN LKNKQACLPSPGGIPSLNNGTFSPPKKQ SKESKAEQABSKRVPLPEGCPGSAASDL QSKHLPKTAKPASQEHVRCASIGTGESP KESALSGASPESPSRGPAPQENKVV SPVV
5890	19791	A	5939	3	191	YSVCLWSQLLRLRLQEDHLSPGGGGCTE PVVTERLSKNKTKRERERKQGFHSM WYCNLK
5891	19792	A	5940	399	1	QYSDNDMSWKVTRAAAKCLDAVSTRH EMLPEFYKTVSPALIVYRKEEENVKAD VCHAHHSLEKQTSFVQSWLGLDAMDQ GTPLAMLQSQVANIVKAVHKOMKEKSVK TRQCCPTLLTELNVLLGAVY
5892	19793	A	5941	411	3	SPCEGPRRFQCKSGKRVDGGKVCQDVORD CRDWSDELLKVMCGACCLPLAGLSLLPS PSWYLGSRFSSAPCPDTFCSGPLFGFMC RPMASHGAFRPAQSGSLHLYKVLRACPGQ VLKNYVFSHKLGLSSFLFRSDHV
5893	19794	A	5943	431	26	KAVVGIPIGDMGPPGIVTRPGYNGLPGNF GVQQKGEPGVGLPGLKGLPGLPGIPGS PEEKGSIGVPGVPGEHGAIGPPGHGQIR GEPGPPGLPGSVGS PGVPGIGPPGARGP PVGGPPPLSGPLVIKGEVSRVR
5894	19795	A	5944	396	3	PLPVELTRVPAFLDLFMOSLFRKGARTS ODLKHXYIHI LAYAASVETCKKNRVS INKDELKSTS KAVETVHNLCCNENKAS ELVAELSTLYQCIRFPVVMGVLRKWDN TVSEPRYFQLQTDHTPTV
5895	19796	A	5945	465	32	ERVTLADITVCTLLWLYKQVLEPSFRQ AFPNTNRWFLTCINQPOFRAVLGEVKLC EKMAQFDACKFAETQPKDITPRKEKGR EEKQKPAERKEEKAAPAPEEEMDEB EQAPAAEPKAKDPFAHMKSTFVLDDCI AAL
5896	19797	A	5946	414	2	ATPPEVRCIRKEIRNNVVDIQVQEFKAO ACGNGHGIIIIAETSTGCLFAGSSLGKR GVNADKVAIEAAEMLLANLRHGGTVYIE KODQLIVFMALANGVSIKKTGPVTLHTQ TAILYDEQIVKVNCKENHSVDQVY
5897	19798	A	5947	411	1	EPCVVRRIADSSVQTDDEDEGESRYLLSR RRRARRSADCSVQTDDEDSAEWOPVRR RRSRLPRHSDSGSDSKHDATASSSSAAA TVRAMSSVGIQITISDCSVQTEPDOLPRV SPAIIHTAATDPKVEIVRYISAPCI
5898	19799	A	5948	153	409	LEFFFFILLFFISFFRYRVLGLSFLKLC GVIIAHCSELGLSSNPPTSASRVILPY

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						LSLCLFVFEMESCVAQAGEQWRDLGSLQ
5899	19800	A	5949	21	447	RAAMSSSRNFRFLSSHRELYFGVDLPSG NLVVEPADREQLCRKAACVLTIDLV EDPLELHKIRIHVLDTNDNSPLFPAGDV QLHIPEFLTPGARFTLPNAQDDDEGSNG ILSYSLSPSQHFRDLDMGSRVDGSEYPEL VL
5900	19801	A	5950	268	19	QDNWAYCYTVPYCKTKNLINLAWNLVIN YLSGDFYFFFIFFLDGVSLSCHPQWSAVA RSGLTATSSSSVQGRFSCLSHCIAAAL
5901	19802	A	5951	389	3	QOMDLARQQGEIARQQQLLQQQHKIN LQQQIQVQGMPLPIPFPHDORTLA AAAAQQQLFPFGITYPKPDYFVQFL PSTMAAASGLSPLOQLYAAQLASM QVSQGAAMPSTPQPMY
5902	19803	A	5952	2308	307	RRRPARKKTVWRDGGPHQGL/YPOLPSA VLQPTOPGHGPRALGKRELESWQKRP GK/GQTHRRKTRGTASPAVYFVSEWGD SGGCCPMTGKAQKQRAQLGAAPNPELSG EQGTGRGAQDSQGHGGKGRROQHPDG ND/PRGVSGMGQESVHSPEARPTGGGTG /EMLGRTWRHQQLVGQGNLLETGSWS SGSGWGRGVVLRPQGEQVTTMGMLAGR/ YQPARQRAVELSPGAQGLRORRGWGSFP PQETEQSGVPGG*GSWPLESHQGEQ/PA AGQKQSLQMLPGGFP*CW/SGMGGGPQQ LLESEGAGSPSGGGRHHGKRVAVTTTP REGD/RQQSPGGHTLQLFPCCPLWS*ETQ GQGSRTVQHGEWGGEGREGEAGSDQSR ALGIA*ICPHILRPTSMEPQSTAPAPGQ PFGPPSWGRHGHQMGQYGGRCPOQ/IGQ RGRQLGSTVG*RDG/QKG*MQGRDQQG PRSNAGVGSWSHTSQK*TPSSSLCT*H SSHGASGQLWWSPPFHSPETIHF TLTEPHSVPGNCMDTLRRHGAQOQHPO ARSGTGEGG/QRGRY*ERGRERGRQKQ KKQGLKEFG*RAAPTLKGATRLICRLR KVQPKQDGDVGS*LLKVFRAPGALQTK PORTCRGPADFFHALSGLSNVHRSYCS NSGFGACM
5903	19804	A	5953	461	117	HPRDITGPVHOGLPSPQPPFPKQAP TPSS/M*P*TNRHDTGLSGPVQVPGADW KPLNAP*LPELAFGEPCRPVGPDPFV WLPDSAPHCVTWATSPGLSDLLSYPRR KQA
5904	19805	A	5954	845	610	FFETGSY/SVAQGAQWNCNFGSLQSQPF RLKRSCHLSPSSWYDRGAPPRLARFFF FCIFYRNGVSPCCPGWS*TPLEQ
5905	19806	A	5955	1	378	KTPVSDR(ATKCCSESLGNRRFCPSALE AYETYPKEFNAETFTLHADICTLSKKE RQINKHTALAEVLVHKHPKARQQLKAW DDFADFVEKRCMADDKETCFVEEG*TLV AASQAALGLLHRK
5906	19807	A	5956	723	343	GCQGGTCFSPCPVYPATREAEAGESLEL RRRLH*AEIVPLHS\KAQSLCSSDFI RLVIFSGMFLVETLAGALFLHQRKRY SNKGSPVEPAEPCRYSCPREEGSTIP

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5907	19808	A	5957	55	491	IOEDYKPEACSP AQHFNPNHNPVPT*LLPHFTNEGGQVTEA RCLKWQAR\CLVPWQKVENAMPTG**PS AEVTPPVCNQHWPQVEGIPSS/APAFA WPLTMGHPC\WESAPRODASTSRPRGT SHCPSAVAFCQERGSSPCPPHHSDSGLCL LPRLLPAP
5908	19809	A	5958	2	413	KKPDQ\AE\REHLCISL\WSGRNTDKNG BELHGCKRVMERLKKAVKIANQCMDFSL QMOLYIEILNRYIIFYEKEYDAGTIQVL NQLQKIREDLNLESSEPEQIT*HFH NTLEHLRLRRSPESSEGPPIYEGILLYE
5909	19810	A	5959	871	564	WMCHATFGSHLN*ANRLRPVNSG/LLM/ PSEGGAKKESTLMVGVTPND/MGKIRL LLHSDGKDEYVWNAHFDILG\HPLTLQ CPIIKIKKKL**PKSGRTADGPDHSRIK V*VTPLGKEPTTDEVLAEGKENME*VTE TC*IDMN*VLQGGTWNLQR
5910	19811	A	5960	390	271	GINFFSRN/RSLTT*SRLV*NSNAQVIV LPWFSRVLGPOA
5911	19812	A	5961	333	922	GLSCRVFGRTLSCFPICILRHLSVETLQ TLQKKEIEDLYSLRGKQPPPGIGAPAM LSSQRRLSKSGSFPTSRRLSLQREPPG PGIMRRNSLSGSGTSGSQERASKGVTF GDVGRM*IQNRSHVSPHQGPWMSLCSQ NLMLSGQGN*ARKIPTLKG*KA\GGHGE CSSIIIVKSQTYVNCLLCGGVSSAAYHLH L
5912	19813	A	5962	705	387	CVAQTGVQ*HDLGSLQPLPFGPKQSSHL SLPSSWDYRRVTPRLPNF*FVETDFC HIAQVQLQL\ASSNNLPASASQAGVTG VSHRARPTLLDQAEIPDLKPSG
5913	19814	A	5963	425	182	ASNQ*DSVGVGSPPEGAGYNLLVRFLK \LEKHSWVGVTQFSRCHLSPLSLTRKG NSLTPCTSRVRQCLALLWLTHGSRTH
5914	19815	A	5964	388	14	PFMYTOLCSIRSTQACFCVFVFSRDE/SL ALLPRLVLNSWVOALLLPWPVKVQ*QA QWLTVLVIPALWEAMAGGLEPRSSRPAP ATTQDLISTKENKTKSLSASDAELCVH WRLLKI
5915	19816	A	5965	1	373	DDQRVKSVINLLAAYTGDSVALRRFAL SAMDMEQRDYDSRTALHVSAAQHVEVV KFL\LEACKVNPPFKDRWNNTPMDETLLH FGHHDVF\KILQBYQVQYTP*GDSNNGKE HHTVHKNDGLGS
5916	19817	A	5966	3	329	HEETSRYETIELIHVHPYAVKQSFDEE YLSQS\TLEQVGHF*GFVSSMVYVYKTF PGSCROSTALFSSLYFLPPFQVFLSLSK EQELGDFE/EDFPSPVSKWLLPQEEP
5917	19818	A	5967	2	47	MEDRRIVRGIPCPQHNRQCPAVPPGIQ AYGAAPFEDLQVDFTMSKCRONKYLLV LGRTYSG*VEAYTPRTEKAREVTRVLLR DLLPRFELPLRIGSDNRPAPFADLVOKA AKILRTWKHLAAVWPQSGKVERMNGT TIONSLEKVCORTLKNQOLAPVWLFKIR CTTSKRAGYSPEILYHRRPPLRLGLPG TP*ELGEIELQROLQALGKITOTT/YSP SKWPVSLFSPVHPLSPQDRVWIKMNVA

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						SLCFLWKGPGTVVLSPPTAVKVE*IPSW IHSHVKP*TA
5918	19819	A	5968	2	150	KSGST*QSLSLSYFEKLPQPQPSA\TS TSKQDP\PLATRLWLAEQSDH
5919	19820	A	5969	3	371	HEGKSGPNTGVVLVAGEVAMKILLCL CLILLRVNSGRKRAARALGWERADVT D*SPDSRLLD\PPHPVPQSERPCFLC RLCMVCPCLLDSPDPSPFCHPTSPQTLRA KDSAAOLDTHV
5920	19821	A	5970	396	58	YVWLSKGFPVTCMLNLSVFSQASCLSF LINS*AP*PGIFLGMSVFILPFVFGVQ AGLELLTSODLPDSAQ\ARITGVSHCA QPH TALSOYLEQCCLAPSROLISVSLTLR
5921	19822	A	5971	442	120	ICKKQGLALSFRLLSSAFSNTVCPNPP RFKSYGLSLP/RSWDYRCTPPHMRSG NGV*P\FMVETGSW*AAQGGLELLSSN LPP/SAFQSGAGITSGKHCTRAVFLVC
5922	19823	A	5972	459	434	MWPLPWFSSISSPSPPT*VSSNNHPCA VPRAYPGADIPGPGWQRLPPHRLSGSP PESCLLTITLCKHNGCPLTONPRSLP GPRPCLYSTPSPPP*AQL/YAAPSP*L YTVVREALIR
5923	19824	A	5973	681	1758	VANKQCPDIAKATYCICTNTEKRSYLR T*NLHRGF\IKKQIEEFNFKRHLANM GEDPETFTQEDIDRAIAYLFPSGLFEKR ARFVMKHPEOIFPRORAIOWGEDGRPFH YLPYTGKQSYYSIMHDVYGMLLNLEKHQ SHLQAKSLLPEKTVTRDVIKSRWLIKEE LEEMLVKLSLDYMQFIRILLEKLLTSQ CGAAEEFVCFRFRSVLSEKQLIEPV QYDEQGMAFSKSEBGRKRTAKAAEIVVYK GSGRIKVNGLDYQLYFPFITQDRQLMFP FHFVDRILKHDVCTVTSVGGGRSAQAGAI RLANAKALCSFVTEDEVEMRQAGLLTT DPRVREKPKGQEGARRKFTWKIR
5924	19825	A	5974	1232	980	SLSLSPRLCCSGVTAHCSRLFPASSNSC FSASQVAGTIGACHHILWLVFVLEVETGF HHVGTGLELLT*\VICPPWPVKVLGLO A
5925	19826	A	5975	1	259	LTSYDYRRALPCLVN\FCVYFLKREELA LLPKLPWNSWA*ATLLP*PKPIGLQAQ VAMRLKXFPACLPACLPAYLPPLPFSFI PP
5926	19827	A	5976	24	223	PVLTQISTNESSVCSHARAFLDHQNL /WLGTVTYTCNPS/TLGG*GGRIT*GOE FKTSLGNTARPC
5927	19828	A	5977	395	136	GSWDYTHVPPRSANF/LVETGFRHVA*A GLELLGNPPTSASQSAKITAMSHCTWPS SYY*CEYNARFGSLHRSGMTIYIKSYK RON
5928	19829	A	5978	1	785	GTRLSKGTNTKALQAVYSMMSPDPDP PEGWNRTRHVIILMTD/GSEGTSLLSQP PHLLPACQSP*VHL*HYTHGWGPECD* LAVHLSGDS*GILPQPCDQSLSTLCPQ AHPANCIPAFSQFTLIEYHPGVSSAC LHNMGGDPITVIDEIRDLLYIGDKRNP REDYLG*PA*DPAPHFLRAWTLILEFY PSEVYVGVGVLPRVONNINALASKDNE

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						QHVFVKVMENLEDVFYQMIGREIQGNK EPNSPQVPLK
5929	19830	A	5979	2	419	KAIATPDSDDSGSQGNLKT*KEFTIL NAIKSIYDSWEEVKISTLGVNKKLPI LIEDFEVFK/ADLVEIARREREVEGEL /LQSQDKT
5930	19831	A	5981	1	154	KKC*MMLTWMCMPVG/PTFRAEGGSPE TGNLRL*CTMISMVNSHCTPAWAT
5931	19832	A	5982	12	311	RKSLNFVEGCNIRLNKCRHTNFVPTIF FFLLFL*LGQC*VVVFSEFFFFFCFV LFFVFVCVVFVFFCFCF/GCLFVVFLL /YFYLEFCIVIMCYLRL*YV*IVMLF FVCWIFVYLFCFHY*LFLFFVFVLLF ICGVFVVFELFCIVIMCYLRL
5932	19833	A	5983	3	203	IGQKRASEDTT*GSAD/PKSSAGPKRD ARQIYNPSPGKYSNLGNFNYERSLQGK YRNPRLGHTRKS
5933	19834	A	5984	368	138	STVGKMLSGQHPCYRE/IL/REKQSQM *QISLLSYFKLPPQPPSATTALISQ PSASRQNPAPKRL*LAEGSYDH
5934	19835	A	5985	2	155	LANF*ITYPC/RDKCLPVLPLVSNWQ VILPPWPVKVLGLGMSPCAPRHS
5935	19836	A	5986	325	403	FTYYLFLSSLYLITYALFLSSPFR*V VYHMMVLLKVVICHFTPLTFPSFRSLI LHFLFLFM/YLLITFVLFIQPSFYLFF FLFLFYLFNDYCDLFLFLCLITYYHF QSYFIS*FTYYLFLSSLYLITYALF LSSFSI
5936	19837	A	5987	81	651	KLVAGACRTLSQIDVKEFESVHSSLA VRANYPTSQPNVIMQVTLTRCVASHK LGTVSYSWYIKLFPKSHFIFYLILRR SLAPVADPGVQWLDLGLSQPPPGPKRES CLS/LPR*LDYRHPNPRLANF*FLVEK GFCHVGQAGLELLASDLPTSASQNA TGVTAPSPQKATNLILGGGFHI
5937	19838	A	5988	301	341	FCFCFCNKRNSLV*WHAPFCPANF*LF IYLFVETGFSHVGQASLKLLTLDLPA AASQASGIPGMSHHDGLFL
5938	19839	A	5989	71	1252	TREQRSLSQQQVGRQQRSHRLKFGSGG APSARGVGGWSLALRLGPVSTANMSR VRNRKVVDSYQFQSDDADEYGRDSGP PTKKIRSSPREAKNKRSGKNSQEDSED SEDKDVTKKDDSHSAEDSEDEKDHKN VRQQRQAASKAASKQREMLMEDVGESEE QEEDEAPFQEKDSSGDEDFLMEDDDDS DYGSSK/NEKQKDG*EVOT*KKRKENAQ TQTKGYSDAKSSERQSGSP/QASKAS KEKTPSPKEDEEPSPPEKKTSTSPFP EKSDEGSEDEAPSGED*K*WSGERFY *KKKKKKKKKKKK*DRTWFLWL DSWGFQCFPFPEVESNISLSLSPFFFPFK ANHCMCKCLSYLFFVYVSLCQSPFPFMA MSN
5939	19840	A	5990	630	316	RNNVNSVA/QAG/ITQCCLGSGTGNRPFP GF/K*FSCLSLLSSWDYPTHATMSSKFL YF*WRRGFTMLARLVSNVNLVNS*PSDP PASAASGAGITGMSHRAQPIYLS
5940	19841	A	5991	2	182	WQEQKAE/CLRDVWTAMCTAALLTIARK

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						R\NIPCPMMKEWVRKMGPIYTFEYYSAV IMQVILKF*HATTGMNPDVISEVCQS QKDKRILLSCNNAGNS
5941	19842	A	5992	79	278	EAKRVNGCSKPTHTMYTYVTNLHTYV/ IKPAHCAHPV*KLKYKIIITIIK*RWG LTILPRLVNSWAQVILLPWPPKILGLQ A
5942	19843	A	5993	22	274	AGDEHRAWGYQFAMARLEMTGPGDIT/ MPAMASQRAGITGVSH*GCPFFSLNLKI WRSHVAQAGSEQLFES*TPGLSCYCS LPSN*DYTSAPLCPPYDT
5943	19844	A	5994	347	195	YMHKTHHTHTHTHTHTHTHTPEKHLKA PNEV*SKSNV*IKPKQSQCSPS
5944	19845	A	5995	1	122	RYELEDELHQLMTQLHALKENNYOLR/ SSHVSIPT*GYRHPVSPCANF/SSLTM FPSLVSSCAQVHLWPYPYKVLGL*ALK ENNYOLRTIIIDCTLNNNIF
5945	19846	A	5996	365	229	RPPPCPANF*FVETGPHHVGRAGLEL LTSSDLPAPALHQVFYA
5946	19847	A	5997	357	17	ILVDKINNWNLPONNLVVC*RGWYK* DRSFHLKTVAB*WYEGSLY*SLSSY YLF/C*RGGLTMLPRVLVNSWHOAILLP WPFSLLLCILEVFNQRELKKKNGKPMPT GS
5947	19848	A	5998	1	207	PILYNLFQKTEAGTLPNSFYEASVTLL PKPKDKITR/ITTY*FILL*NLNKLVL SNQILYIKRITY
5948	19849	A	5999	603	269	EDRVLLVLPKASAVAFRLTATSASW/ VQSFHPSPSPRWDRHVP/PHSANFCV CL*RGGLSLPGLVLVNSWAQVILPPWF/ PKVLGITSMHARPLSFYGHFKYIQK
5949	19850	A	6000	3	150	DYRHAPLHLATFRK/FFCRD/RGLSVLP GLVNSWQPTVLP*PPKALGLQA
5950	19851	A	6001	365	62	AIATACSLNLLGSNNPTASATRIAGTIG EAMSYF*ISSTLTHFSYT/C*LHHVWL IKKFFVDEVIVQAQSLLELSSDPPAL VSONARFTGVSHCTEP
5951	19852	A	6002	537	236	DRVSLCCPQSAVARFQLTATSAFAVQ *SSCLSPSCDVSAPPANFLSPCR DEGGGLPGLPRVLVNSWAQAIHPQPPS VHITGVINGTWPKIPLS
5952	19853	A	6003	22	368	NFFLQNKENTKRRI*ERKHLMQRTSL LSYFKQLPRPPTTSQQPSTWRQDPPAK R/LRTYKGLDDR
5953	19854	A	6004	327	335	NQSIFFTFNNYPRFF/CKPFKFN/TLHL WADKVAHTCNLSLLEGQGGRIA*GOEFE ATLANMVK*LLCKVK
5954	19855	A	6005	2	367	WQFLKRLNTKLLYGVVF/PYLGIYQEK WKHVAETCTQMFITVLFIIIVPK*QKPK CPSEEE*ID*M*FVHMLEYRAIKENKLI HATWMNLRNTMLSEISQTQITTCMNLH KMFRKVTETES
5955	19856	A	6006	1	176	PGFKQFCLSFWRGFIEMGPHVGA GLGLMSGDPPASASQAGITG/VSHCA WTY
5956	19857	A	6007	1	289	EVLTKRIPR/FFVEIGKLIQDLKDTGPR IA*TMLTCKTMEGRIVHSDLVAYIYAV IKMWVYYN*RRRHINO/WERLEISEIDS

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						QRMFNVFTKQKLP
5957	19858	A	6008	439	223	FFSPGSH/SIT*ARVQW/PHHSSSQPEP PSLKQSSHLSPSSSDYRCAPHPADLC RDWVSPCCPGWSOTLGLK
5958	19859	A	6009	1	252	MVSTIS*PRDFPALASQAGITGMSHHQA LFFLN/CIS/ELISSTVTPGLKESACLG LPKCNHYRREPQHPACTVLYLQFQSDPQ LK
5959	19860	A	6010	131	514	PWPYSLSSSGLSSFFEN/VEKWPETI IH \HSLFLGTITIDLS/EPCITTEKN\KDK YNPLTPQMADMVCDLKVVE*LECSAFM WKRKL/VFDEALWAALEED*RSSCRKET STLLQSTPLLSYALPCTF
5960	19861	A	6011	625	141	ETGSRFVTHAGVKNHNSLHPQPPRLK *FSYFSLSSWDYRHVPPRPANLVVPL *RGGPSPMLQASLEF\LDK*IPPCLO PS/AKVVLGLQVSHRPSPKVTFHQRAKEG DVVSHVVSQKSI PDGNSQCMHRSIPC VFEEQKGGQCYCSIESKEETSRI
5961	19862	A	6012	302	42	GLAMLPLRPGTGLKQSSCLSPSSWDY KHLS*PAVY/C*FLKNIK
5962	19863	A	6013	363	82	VSVLSPLSLKTKVNVAVASFTIARIW KQLKCPMSMDKQK* IWHITMEYISA/I KQKIMSYSTTWMNLEDIMLSEISISQAY KGHHMITYGI
5963	19864	A	6014	329	99	HIFGNTYFFQVASSPIYLFDRDSVSLCRP GWSAVA*SWETATSG\FRESACGLGLEPC /WDYRREPPRPANVLFMSRVTH
5964	19865	A	6015	324	238	LAMLSRLVNSWNPQAILLFLFPKVLGLQ A
5965	19866	A	6016	2	308	FWKAIAGIEGSSDKCKQ/SKLKTIWKK FISLDAMRNHDS*EKVMSIFNMKIPT PRDDF/EGLKTSVEKRTEDVVKTAQ*E LKVDRT*DEELLLLDQQRK
5966	19867	A	6017	2	457	FFFLRWLS/DGVAQAGVQNRDLGSLQAP PRGFTPFPSCLSLPSSWDYRRLPRPANF FYF**RRGFTMLARMVSI*PRDLPALA SQSAGITDVSHRRAERVISKQIVSVVM KPLPEIHIPCILNLSLRFNHRVAGLRN SLIVRMLSILTEG
5967	19868	A	6018	389	142	AHMLFAAQGDSSIFMLVAPLFTVVKMWE QSKLPADDEWSGF*HIVTEY/YAKR REILTHATTSLKALCYVI*ALTGRTL
5968	19869	A	6019	384	232	LNLPSWDYRRAPSHSA/NFSYF*RDGG LTML/PQWPQVQIMPRPLKAL*LQA
5969	19870	A	6020	333	84	GLIDQEFATDTTKSTSLST*T/IPSRC SLCLRGSDDSPASC/SQPPASVAGITDT CHHAHII FVLVETRVHVGGRANTEKPR LH
5970	19871	A	6021	106	366	DTISFFFLFKAPIEPVFIIFIPYFFFI FFFI*FFFLFLFLFIIFYVF/IFFFIL LCLFFFLVLLFYLLFFF/SLFFLFCFV FCFFF*FCYFFYLFFLFFFFFYLALE IFFFGSSFLFVLFVLLFFLFCVFCFF F
5971	19872	A	6022	384	18	REKFGPGCTGPKPKKKGGPKGPKGPKK RSEKKGKGP/NSFFRGGGTPOGNF*R GPPPNQKRRKKFPQGGKRGANPGIP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PLLGPKAEGGFTPGKKKKKKNSNKKSK QTKKALSRSTSH
5972	19873	A	6023	3	191	LVKGKIRSWEEWTWKTW/RFPYGMVAH/ TYNPNPLGGQGRWIA* AQEFKTS LGNVV KPHLYKKKI
5973	19874	A	6024	364	142	TINGLI THLHNFKINGHTLSTWYTFPHIL CVCVYIYICLC\CIYVSVCLVCVYTHI QYTY* INKHIC* RLEAK
5974	19875	A	6026	338	102	WGPTLRLRVSHS*HLVICHLDLDFEWN YRHEPPCLALFLIEVGT* VYI PMGVRR Y/C*YRHAMCNNHIRVNMSVGLNF
5975	19876	A	6027	99	77	REICITFTTEAFSEIAKWK*PKQPLTN EWINTMCMCHMRGK*P/VAKTSMKLED VFHEISKQDKHYI*FLSPTVYKIQ
5976	19877	A	6028	2	328	TITVRGAKIRITSDSSSETMQAREE*SE IF*VLK/EKKKH*PKILYSGKLSFKSK GEIK/YF*GKQN/LKEFVSRRPVLCGML KVVLOREGKLYRSETQTYKKKEKASEKE
5977	19878	A	6029	8	241	GFAPLPRLECSNTMAHSHLSLGSSEDS PASANFSIF\IETRFQHVAAQV*FLSS SNPISPSPSVEITGVSHHARP
5978	19879	A	6030	108	362	CCYLMVTEISAHQNPQKGLA/HTAFF* KIFFLKVSWTGTVAHV*KPSTLGG*GGR TS*SQKFKTS LGIMRPPSLQKKKVFKI YP
5979	19880	A	6031	1520	77	ASSSSSSSSVILSS*INPNYNIYVIFM/ CL*IF*AASSSSYYVPGICYIYH\IL CVCVCIMCIYVICIYSIC*YIVVYSI YYIHY
5980	19881	A	6032	405	100	EGFFLPPRGGGGR/PPGFLTPGGPGNP RPKPPQKWKGPDPGGGPF*WVLLSPS LPPGQVESPGVSGPRQVPSPGSRPFP TAVGTTVTFLSKKKKQV
5981	19882	A	6033	42	309	CDKFFHKASNHIVSYTYIWFQICVCVC VCVCWCIILC*AY/CGLGIMIWFLFVL *CI/CYCCY*SSLFSVILICFLMCFVSY ERRFLIFA
5982	19883	A	6034	397	2	KGGPPP*GGPDPF*PRGGPPQKNPFPPF GCGPPFPKNGVGGPPQKAPFPQKRG A PQKGGPPGGPPRGKSLCPNNENT PRGLKGGPPPPPPPPPPPPPPPPPPVLR STGLRAPFQSVFIVELVEDMS
5983	19884	A	6035	343	2	LWPPQGSFKTAAPFFFFFIFISDITF HFLYM\YVFFIPLPLL*SFCEIK*IFYI VTF*FLQSFSLFFSVL\WLL*SLLY SF*LIRIYFRILT*FQ*DTETLFEYYS IP
5984	19885	A	6036	319	68	SLGEICAPK*FFPPAQKKGFQKFPSPCK FSPSPVFKTRPAK*KGPP*GKFEYVA NPGKI\GPPKGSFKRPLPFFFFFFFFFF F
5985	19886	A	6037	419	191	RIHTIPTALFAVAKR/WQSKYPLVDE/ MDKIWIHTMED*AYGKKEIMSHARTW INLKNIMLSEISQSQDKYFPFI
5986	19887	A	6038	434	401	YGKNFSFSLKV*IFCEGLVLVFPKPKK / /FFKINFRVVFPLYVFF*TRGVVFFK PPFLEKIFFFLTRVNLGPPRGGF*GAPF FFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						NEYFMN IETVL
5987	19888	A	6039	12	346	SFSFVRRSLT VTQAGVQWCNLSIOPP\LPSPFK*FSCLSLQSNWDYRCLPSCLSNFCIF/M*RRGFMSLARLVNS*PQ/CDP PASASQSAGITGVSH/SHLV*NA*SFKE SHF
5988	19889	A	6040	275	45	KDVOHONKIVOPLNKQVGLKASTESPH DPSILLGLSTYPRMKT*IHIX/TCIRMF AEALFLISK*KLKCLLADK
5989	19890	A	6041	355	1	PGTIKNFFFYIFFFKNYF/FFLYIIFFK KKVLF*KKKIFFLFIPNKKLFWVFF FFFFFFFFCPRFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFLVIRHLF EMRKG
5990	19891	A	6042	635	209	PLNIKKTFFFLRQSFVLVAQAGQWHD FGSPQPPPRFK*FSCLSLPSWDHRRPP PRPANLV/DFLVETGFHRVSGQGLDLL T/S/GDLPALASQSAGITGVSHCARPTL EFLKVKEMIFCSTTVKAVLDHANFLILR FSIT
5991	19892	A	6043	12	348	ESRYSSICLDFSSVVCRIISLQLYSYV LLVYLFFF/CFLKREFCFPLQVQGP GLGSLNPPLL*QKPSGLIFPGIGTGL APPSPNPGFRRKGVSPGPNRPAISK F
5992	19893	A	6044	192	1	IFHRFCT/HITLP/TALNN*PWLGTM AYAYNPNTL*G*GRRIV*AAQ*FKSSLGN MTRPCLYKK
5993	19894	A	6045	338	42	WKTAWN/FLKCLD/MNYC*DPAILLGI YPKELKAGT*TDIRTSMTAELFAIAKR WKQNVDLKLNLRQNECRQFIWAKVEGNWL PSWFGEWSIQHRLQAGF
5994	19895	A	6046	300	3	RLDCHYLNSHTHTHTHTNPAGIYTHH/ HCWNLHTNPGGILGVALDL*MQFLNR GWSWGGEQMANPCQGHVWMLGDPGKMI LKPLWVCQLQSSYDG
5995	19896	A	6047	332	3	SLESAGFT*YMYFYIYKIK/YIYKSI FIILFL*IFFFDLFFIFFFIFFFF FFFFFFFFFFFFFFFFFFFFFFLKSP KRVIFYFGGTQNPQMSLTLKYVLC
5996	19897	A	6048	2	152	KNLKSISW*WLMPPVVSAT/WGSSLKEGR LRLQ*AVIAPLHSSLGDRARPYL
5997	19898	A	6049	1	288	PIITYVLLLFETDSHVT/RL*CSGA FSTHCNCLPGPGSSASDS/RVAGVAP ACLF*PYRGFGSPATLAFRALDPGLFLH PGFSLQRPSCSRGG
5998	19899	A	6050	358	1	FSIFSILIDFLGLGFLKFAFFYGNDFL RFFEFYR*PGCKSSFIFFHYV*RAKIW FLLESNWLKWSFDQFFLKFRRFFFF FPKGFYKRVFFFGFFFSNLLSSQG KGVWLI
5999	19900	A	6051	308	45	ADLSAEL*TRRENDDFKVLKEK/NKG QPKILYPSKLSLINE/NEIKSPDPQKL REFTTRVL*ENLKGILHMAEQOYLPS *KHTEV
6000	19901	A	6052	2	124	IFCVLVTGFHVVQAQGL*LLSSGSPFA S/DLNPAGITCVSH*AGITCVSH
6001	19902	A	6053	1	330	LC*PGWSR\FLTS*SACVGLPKCWDRR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EPHLHVFFVFFFT* IYLKGFYLNPRK IFKNFFLLKNPPFGVPPKIQFSPINL PSLVVPMVFFKRVLGEKIFRGFFPP
6002	19903	A	6054	34	293	SPILFLLCLRHSQCHPSWTAVAQSELT AASNSWAQAILPHSWDYRHAPPH/LNLF GWSHAALPRPDSNF*PQAILLPOQVLG LQA
6003	19904	A	6055	319	217	YHFTTGMATSKNKQKTGDNKCC*GCRE IGMLVCC*WQYKMWLL/WKTVMWSLKG IK/L*ELPYDPAIPL*GIQVRWSKPIPH SSEG
6004	19905	A	6056	341	151	VHAGGSPES/REFETNLGNKARLHYKK *ISQMWCIAPVATHAGCSLPHNLVYS PWLPOCDY
6005	19906	A	6057	2	558	FFFLRWSFTLIAQAGVQMCNLSSLOPL PRFKRFSCLSLPSSWDYRHPVPLRIANF FVFLVEMGFLHVQASLELLASGDPPSG DPDLR*LAFQSLGITGVI/HHAGQIFLF /CLETESPSVAQGVQVQCNLGSILQPLPP \GSE*FSCLGLPSSWD\YRHALTHPANF /SIFSRDGVSPWPGWSQMPDLS
6006	19907	A	6058	320	21	ETCMTNHPVSNTIW/SKMTLASVYLT LLPISKTSKTSGLPASKEVNRVLTCAI RYFVFYFIMLFV*RGLTMLPRLVNS WAQVILPPWPKVLGLQA
6007	19908	A	6059	294	50	CYFSLSPGL*QFLSLNQSFVTLSSHCDR DTPE*SWSVI/PGIGVYSS*E*TRGLAM MPRQVYNSWAQAILMPWPKMLVQYT
6008	19909	A	6060	616	354	ERVSPCHPGWSAVALSQPTAALTISW/VK QSSHLSLNSWDYKCMPELLANF/KFFC RNE/SLMLPRLTSNPNWAQVICPP*PPK VLGLHA
6009	19910	A	6061	214	11	AASTRPSAWQPPLLGSEELCPATTFSG RCTQO/LH*ERAMMTMAVLNWRKGGKVG KRLRNRLVAMSV
6010	19911	A	6062	349	54	QSKSAFPKKRINRISDSSEGGYQSKLKT FWKGTFTLDAIKNICNSSEVKIATLMG V/WDDPSGFRTSVKEVAADVCE/ETARQL EVEPESVTG*QOSHVP
6011	19912	A	6063	332	3	SQPSAGTISKVTSTRLCLKMSVQVQKS CYKCTATYLCAKFNSEFRSSGVGCENPV SYFYTHSIRSKIL/WPGMVAHTCNPSAL ESQGGCMT*GHCETSMVNMVTPRVRSRA
6012	19913	A	6064	174	416	NENELFFCFXIFFFXFFXFFXFFXFFX FFXFFXFFXFFXFFXFFXFFXFFXFFX FFXFFXFFXFFXFFXFFXFFXFFXFFX
6013	19914	A	6065	826	571	DGSHSLA/RLECGSVISAHCNLHLPSS DSVASAS*VAGTTGTCHHARLIF/VVFL VETRFHNLGQAGLELLVHPWPPKILG LQA
6014	19915	A	6066	1	284	GTSFFF*NRVLFCFPG*RAVQ/SWTLA ALTSWAQSS*NRHLKP/HMLSFPNFK QGLTMLPKGALNSWAQAILQOPPPM*LG LQACTYANSLGP
6015	19916	A	6067	36	384	VSKNKPILHFLFFFSKTSKSSVST/RLEC SGVTSAHCYLRLPGSREGAASAL*LSAT TWLCKVALPLGEDLGAALCRNPNWAGVKG SSRESPLGEARGELPWGVIRLWGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						GEFAP
6016	19917	A	6068	393	116	PQIFPRY*ONKDPNL*KTFF*HKYMPKC PAK/LIIFIEKGFSRFGQGL*HLSSN LPALASQSAGISGINPGGRARFPLFFFF FFSLILLSF
6017	19918	A	6069	53	280	FFRFCC/LLESESHSA*ARVHWRRLG PG/LKRFACLKLPNSWNYRHTPHANF CIFIRDQGMTL*PSWS*TPDIK
6018	19919	A	6070	3	377	HEEPQGCATVPGEFFKFLWRHGLITYPR LVNSWAQAALPPQ*METHIIFSIQRLLH MVK/RQYNSGAVAHAYNPRLLGS*GGKA A*AQEFETS LGVVMRCLHKNLKNSEGT VAHPCGSSC
6019	19920	A	6071	337	3	RESQAFPSKKKKKGTGMVFEQRCER KGARQSHLRKSIIV*EIASAKALRRHM PGVFQKQPGG/WPGVVAHT*NPRTLGR CGWIT*AQELETSLGNPEKPCLYKKYL V
6020	19921	A	6072	1007	628	FFLLAHSFHSVAQAGVQWGDLSLOALP PGMFPSCLSLPSSWDHRRLPFRLANF/ FPLVATGTFHVSOMVLIS*PCDPPA SQSACTT/GARKPVF*IFVYMGVRKH SILMSPOHDLPGYKI
6021	19922	A	6073	27	364	MDLFSVITFLRLSWADISRATSTLEWL LFSWNCFLHLLSFNLFLSLGK*VCCR* HIQSCVT*QWRY/WSGLVTHACNPSTFG SQGGNVASV*EFETSLCNMAKPCLYKKY E
6022	19923	A	6074	2	68	ARACSHGTVALTASCPFLQDLYKCLQVS FVCFFFETKSNFTVRLKCNIGISVN* NPNLPGLTRSQ*ASREAGTTGTCTYHA* *ILLPSSTRL
6023	19924	A	6075	330	49	KRRFALVQAGVQWRDLRSLQPLFPVFS CLSLPSSRDYRCAP/RPS*FFLELLTS GDLPTSASQSAGIIGMSHCAQPLIYFL FQTKVILFFS
6024	19925	A	6076	2	267	ARGVEVKVGKTKOFLNMIRTLVHCWWK CKLIQPLF/WRILPKVKEELPYHLAII LGIYPKQMKSSISLKYICSYI*IVDFV *AILPLGIYPKQMSISLNIHMFPLYDC RSFCIGTFLLL
6025	19926	A	6077	379	236	PPFPQTRTPPPGHVHKDPPPHHPYP PQEPQRTPVNTHPGBEQNHLEFNSSL LEFW/YYSLLPPEQA*EPHIH
6026	19927	A	6078	2	290	RRSLFSSPLEDGLSLIAGLITWEPSPH PPQ*RSPPPPKKKKKSPPOPKF/HK FKTGPKPKPRVL*RGHNPFFKFF*LKP GLPF*GTPEKV
6027	19928	A	6079	1241	1487	KMYCLFVE*KECLSCAIFIRLLKNS*P TWNSISGGPPHG*IMPSIL*PLET VFHSV/TRVGQWMDHGLQPGPGLK* SSCLTASQSTQIGVSHAWPFSITFEI FKRLAYMSADGW*KSPMKLDLGLALK KLSFARPG
6028	19929	A	6080	333	1	LCHIVOLSKFFVMEVSLCGPGWFFK* FSHLGLPKCWDYRHDPPLHAFFSLS* FFCRDRVSMPLRVLKSNSSQAILLL*PP KVFFLEVCLRRVSFHAEPAVYSSC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6029	19930	A	6081	2	239	ARGKYIYNRDKISFCCPGWNAIT/RSLQ P* TSELKRSSHINRPNWDYRCMPSHLA NF* IFRDGLASLPRLGTGWLKS
6030	19931	A	6082	323	185	SACLGPKC/WDYRREFCLVSR*VLNS *AQACLPWPPKVLGLQA
6031	19932	A	6083	296	2	GERILEECIYARSHRAEITSLHCSLSVS K/HSAVQVVKWDFPCSMQSPPRFK*F SCVSVSSWDYGLPPCAGLHIWRNRVT LALQGLPTTSLALV
6032	19933	A	6084	443	1	QKPK*RTQWSSISLQSRKMKKILSV ITFFKT*GEEEEKEKKR/KEE*EK*K EPSOKKEVEVEVEDERRGRK*KVDMEV KEEEKDKGEESGEEQ*KESAAEAVRE* VDS/SELVFAVLPGDSSEEEQGMVPR A
6033	19934	A	6085	328	1	SNILIFKAQVTKHIVSELTCSPPYEGIS QAIKANFSPCTVG*LPNSWAYRHLPPCL DNF*IFCRG/RSILCRILSNISMLQOVKL QEFFPQGLGCHARFGAGFLSHCLV
6034	19935	A	6086	299	46	LDDLRLSLCLSLFRDRVSLCGLGSSVS A*S*LTVA*TPVILSLRLK*SHNLND SSWDYRVVNS*POGILLPRS PKVHLL
6035	19936	A	6087	266	48	GIEIVRQMRSGTADRVIVVQSPFLRM QKI/WLGTVAHTCNPSNGGSGRIT*G QEFKQSHSLSLPKCWYRL
6036	19937	A	6088	2	185	ARVTMLPRLISNS*GPK*SSHLEGRKCN DYRCEPPCPAEISFISSGYLTRSGIAGS YCNVS
6037	19938	A	6089	520	297	LGYRDFLHLSFFIS/WNYRCLPSCPA/N FFILVETN*FHHVQGAGFEHLTSGDLPT SASQ/SAEITGMTYRAQPAAGS
6038	19939	A	6090	388	187	SOHLGKLSREDCL/RLIVPDQS/GQHSK TPSLKK*F*K*AWW*HMPVVPVIAQEA VGGSLEPRKSLQ
6039	19940	A	6091	188	329	TGLKRRFFCLSLR*FIYFFRDRVLVLY PGWKAIVGHRDRYSMLYSELLASKDS/ SCLSLRSGWDYCVWLIFPGCM*CKRQDL STIPWORSILGO
6040	19941	A	6092	124	342	RFAMP*WQNPISAKNINITWA*AARVAG IP*GTCCRAQVMVFLAEMGFCHVGQAG LYPKIILYKLSHYKCSHLQMRKALET VSGIYSLFTIYLV
6041	19942	A	6093	169	2	SH*PFTSSTIRSITW/GAVAHTCNFSSW GE*GGRMA*DKIETSLVNMTRPHLYPR A
6042	19943	A	6094	2	324	FFFLRNSL/DSVAQGVQWRDLGSLQAP PRGFTFPSCCLSPSSWDYRRPLPRPANE FYF*RRGFTMLARMVIS*PRDLALA SOSAGITGMSHRAFPVYILTSTN
6043	19944	A	6095	76	340	LRKKFCFSVYFFIHRWTFELLFLNDFLM NFYFRIVFRFMKKLQR/WFGAVAHAYNP STLGG*GGRIS*AEFKTSPGNIVRDFI STKNM
6044	19945	A	6096	349	84	FLLSLF*DTISLCHPGOSAVVRTMTSOL KQSSHRSLSSWDRCVPPCPVNFPSFC RDE/SLAMLARLVSNLWDQALVAEAGVS VVARQE
6045	19946	A	6097	346	184	LTMLPRLVSNVGLK*SSHFGLPFCWDY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,512,26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RHEPCLAKTISLYIKPFHILSLPT
6046	19947	A	6098	378	250	FKQFCLSLTISWDYSREFFQMAN*F LVETRFHHVVSVP
6047	19948	A	6099	3	225	GKRFSCSLSLSSWDYR/HAPAYLANF/ *FLVEMGFHHIGQAGLELLTSGDPPTLA SOSAGITGVSHHAQPLIF
6048	19949	A	6100	1129	457	YCVSSKYRRTITFSFLTA*LLTLKLS/V QKVGQVQRDLG* LQPPPG/FKLFSCLS LPSGW/DYGHVDPHPA*FCV*MEMGVS PCWLR/LV/LNS*PSGSGRPPSASQSAGS LQQLI/HRARPEH*F*TS*PLGEGKTL DIYIKTKTFYQFCIVCLKL*RLMEFAL VAQAGMQWHDLSLQPLPPQFKWFSCLS LPSS*DYRYWLLYHPALELKEAPSFES PCTH
6049	19950	A	6101	3	296	EIIQALLTIVLGLYRTLLQAS*YL*SA FTISDGIYGSTFLAA* TGLHGLHVIIGS TFLTICFIRQLIFHTSKHFGFEADA* YWHFVDED* LFLNG
6050	19951	A	6102	1	749	RHEGGLFKTILLI* TSLTIGSLAAGLL FFTGFSKNIIE/TANISYTN* ALSI TLIATSLTSAYSTRILLTGTQPRFPPT LTNFKENN/PALLNP/IIVAAQSFLAG FLITNNISPASPFQTTIPLYLKLALAV FLTLGLTALDNLNTNKLKIKSPCTFY FENILGFYPSITHRTIPY/LGLLTSOHL PILLIGIT*LEKLLPNTISCHQISTSI ITSTKK/GLKFPYPLSFPPPLITLLLI T
6051	19952	A	6103	377	1	SKAFGPPGF*APYGLKAHCFPPGFRRGV WAPSGFWARPPIGYPGALIGAPVWFSP GGPKPGPP/GPGGVKPKGKRLGIGGP FPGSPGFLITTPGSKKKSTKKGPQKKI TPLDTS CSRTIVM
6052	19953	A	6104	1001	531	FFLRKSFLLVAQAGMQWCDLSLQPPPP GFKQFSCFGLSSWDYRHRVPPPTLANFV FLVEM/GFSMLARLVST*PQ/CDPPAP ASQSAGITOMSHCAQLPKPIFNVL* AID SVTTSISLARDWPNSSNRLGLYMGKPS KFKRQOKMECYRDAPS
6053	19954	A	6105	376	117	CSDWSAVSRSLTAAPNS*/VKQSSCHL SLSSCW/YRCQPRHLANFVLCYVLF* RWALAMPILVLNCWEQAVFLPWPPEM GLQA
6054	19955	A	6106	689	433	LCHPGWSAVVQSWLIATSPSLV/KPSSH LSLLSSWDYRCTSPCPANFVFFY* R*G STM* PRLWNSWAQAILPPRPKVLGLQ A
6055	19956	A	6107	2	176	AREYPANFVCLFPLLLCRDG/DFTMLL RLISNSWLKSRDLRLSPK* DDRPEPH QAY
6056	19957	A	6108	328	69	LYTFSFG* EHWLFCHPGWSAVAQSOLTA ASTPRTQVLSLIGRNDNRHVPPIADL/ SPYRDGVSPCCSG* SQTQAILLPWPKV LQFQE
6057	19958	A	6109	777	329	FLEMGSNSVAQGVQVRDLGSLQPPPPG FKRFSCLSFSSWDYRRPRPA/NFFV FLVETGF/TILARLVNS* PRDPPASAS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QSAGITGVTPPALTONFSLNLTGFEEN RKPNDPESCVRYLLLSIRQRSPTALLHV ILFQQMIQLVL
6058	19959	A	6110	345	309	ASLIFV*LVEMRFLHSGISLFSNGKNP TAFSPDPPG/SSVSKAIIIIINKINK* IQHVTVIQIEVQWHNVSLQPLNPELN FSRLSLSSWDHRHMPHSAF*NFKN
6059	19960	A	6111	332	3	RKVLVCPPLSAVAGFQVPARSAFQVHF LFLAEAVVSPGCAPAFKPGQCP*KK KEEEKKKGRKEE/EEEEEEEEEE EEEEEGEEEEEFFFLRACKVKSRA
6060	19961	A	6112	498	191	STDRLVLLCQKARVQWCDPSSKFPFPG K*FLCLSLPKSWNYSHAPCLANF*FL VETGFCVHGKAGLELLASDDPALASQS VEITGVSHHAWPMQEVFQI
6061	19962	A	6113	1381	172	RNIDSKAILSKENKAGGITLPSFKLYK ATVTKTA*YWHK/NH/DVD*WNRLEN MRPHTYNF/LIFDEPDKQWAMDSLFN KSCWDNPAIWRLKMDAFLMPYTKINS RWIK/DLNVKPKTKILEDNPGSTIQDI GTGKDFMTKTPKTATEAKIKHWDLIK KSCTAKETIKRVNRQLEWEKIVANYS EKLKSSIXT*FKQI-KK/NHPIKRWAK DMNRHFSKEDICGQSQS/VKK/CPASLI IREMOIETITRYHLTPVQMAIKMSENN RCW*GCCKNMLIHCWCK/LKLVQPL WKTWV/RIKTEIPFNPAISLGIYPKE* KS/C/CYKDTCTRMFVAA/CPSTVDWIK KMWYIHTREYITALKRNKTDWAWMLMPV LALCAEAVGGSGLEVSRSPAPFTW
6062	19963	A	6114	3	155	HEKKISQVWCMFVVE/TILWLR*EDS LSPKRLQ*SYCDTIVLPWATE
6063	19964	A	6115	47	368	SFFTPSAFLCLAF/YRQVLCWDMGA VAIQHTYSLPT*LSILKQD*PLNLLGT/ WSSRRVACPNQIYRRNGS/WLPLRV LNSWTQVILLPWPKV/LGLQA
6064	19965	A	6116	1	592	RQRIFFLECGGASAHNLHPGSSNSP ASVS*VAGTTGVRHHAQLIFVLVETEF HHVQDGLDLL/NLMTHPPRPKVL*LQ G
6065	19966	A	6117	1	306	LWKTLMQFVLKLNLLFPNPAIVPLGIY PNMKIYVHTKTCTQICIGALPIAKT* KQPTCSSIGEN/LKLNWYIQTMYYSTP ERNERSHENTWKNLCCI
6066	19967	A	6118	2	284	QTGVHHQD/NLL*PETPG/SRDSFGSA SQVAGTGMQHARLNFFSFFLSFPF FFSLGKTLGLGLEFFFRWLQMSGPKIL RLYLQNPKNKG
6067	19968	A	6119	2	315	SRVAGITGVGHARLIFV/CFFFFFLF RDPLFVPRVGFQGNLGLKPLPLGLPL PSGLTLPTKD*GAPLQPRVNFIF*KK G/V*YCGPWFEILDLRGSPPF
6068	19969	A	6120	42	392	LQWRNLCSLQLPFPVFKQFSCRLLSL DYR/HAPPRGL*FCIFSRIVFLHGWVR AGSRNS*PDGSAAPPQASQLAGITG/VS HHHTWAPHLFFKNSGCSCTNR*QVHKV GDKETS
6069	19970	A	6121	2	202	VHLSQDQPKCP*MIWEIKMMWHDITME

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/51,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YAAIKKKKEMSF\ETITLGEETQEWKT KHLLSLRGS
6070	19971	A	6122	355	161	FIXLFFFFFFFLLLLFLSLEFFF XXXXXXXLXVFTGMIS*LWVCLYVM NVVM* IYMF
6071	19972	A	6123	1	133	LC*PGWSR\PLTS*SACVGLPKCDWYRR EPLHLVFFFFFFFTL
6072	19973	A	6124	3	212	HGFLPSSWDYRCT*PCLANF/SCCCC*R LGLTMLPRASNSNTQVILLWLPLKLAQ NTSLINNFYIDQMLK
6073	19974	A	6125	156	2	ALLTHAKNKAL\WLGAVHDCNLSLEG *GSGWIT*G*EFNISLGNIVKHHLY
6074	19975	A	6126	345	34	HPSTIHRVFCSL*S*SSQPARNNGSCLS SEHFGITGVNHTNLLFFKNY/CILIK IETGS*YVAQAGLELLSSNPISGSSES AGFTGMSHGIRFVPSPLKWS
6075	19976	A	6127	2	328	ARAYLPLCFIIFI*VSUYFIWLL*G LI*LNKRYLAHPK*Y*LNVSYSVSFCKT HFFPRHKEKAI IQLGVAHACNPSTLGG QGGWIT*GPEFETILTSMEKPRLYY
6076	19977	A	6128	1	341	GTRKFSVDYGRKPPHPAKNNLLSFIFY FETLSCSVLLCEVTSSQL/CNSHFHFDL PSSNDPPSSASRAAETTGACHAQMIF* FFVETGPDWS*TPG/LLAFLPSPRML ELQA
6077	19978	A	6129	264	2	TAISENKVASRSEHRRHRL*LVQI/LI ALQHSRQDNLSH*KN*KKMLGEVAHA CNPSTMGQGQWIS*GQQFQTSLSNMVK PPRA
6078	19979	A	6130	1392	1157	LSLPKCNYYRREPFCALCCPGWS*TPR LK*SSPLCLPKCDWYR/R*TTAPGLFFI SKSSLRSPAYSCTVCTQLLSHI
6079	19980	A	6131	383	108	MRCLSQPHHHVFSVLETESCCYQGV QWHDLSLOSPPPRPFKRESSLK*LGAIL LLPSSWDYRCTPPHPAN/LCRF*HGPGVC LYMFGEKVT
6080	19981	A	6132	307	1	LKTLPALCLESLSHVSQWRNLSLOPPF LRFKRLSYLSLPSS*DHSHP*AHQANP/ CIFSRDRETGFHHVGQENLIMLIVQSS GLGFSIFATLLAVMQLV
6081	19982	A	6133	351	66	RNSFTMLHRLLLKS*LO/CDPPASASQS AGMTGMSHHTRLHNL*TANNLTQSHTK FYSFISLT\PHFAINVNTNYIFLYTTSINI VCIFLSFKFYARI
6082	19983	A	6134	2118	1392	FFCKGK*IFIQCPDWGG/DLCV*QEKIQ KKTYHTGDKYV*LF*VKPKITKI*ROI HTSGNTDAQLSYKENHDQSH*QAKNFKF FLFFVVYLRRL/NSVTQAGVQWRDLG SLQPPPPGKQF/SCLSLPSSWDYRRPP PRPANFC/IFE*RWGTMALRMVSI*P RNPTASASQSAGITGVSHCTRQEFKVK GYHFLPLPSGCLFLFYVYLYACLLYVS VYVPLRQQRKISKIEMLTTWH
6083	19984	A	6135	383	47	HLFLNFYYLSHYNYLYYLLHLIPSSP KIFFFT*KIIFLILKPKVKP*NLSP*K KLF/ISYVTF*FWP*NEFKDPPPPFF FFFFFFFFFF*OTFLGCGGYNTKLR
6084	19985	A	6136	2	196	TRFSILVTALYYLYIFTTQWG*\LTHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						INNIAPSFTRKENTLMFIHLSPIILLSLN PDIITGVCS
6085	19986	A	6137	700	433	FLRWSSASVTRLE*SGAISAHCLICLLG SSYSYPALAS*VAGTGTGCHHAQLIFVFL VETGFLHVGODGLDLL/NLMICPPRP VLVLQA
6086	19987	A	6138	377	298	QMKWKLILLFRYRVLLC/HPSAVA*LQ LTAASN*FGLK*SSCLSL/MLTMLVLS WPQVILLFPWPKVQEL*AIAYTIKMMV
6087	19988	A	6139	1	199	LYTTYFVTKILLSTLFL*TRTG/YPRF RYEQLIHLL*KNFLPLTLALLI*HVSIP ITISSIPPT
6088	19989	A	6140	381	28	STPNRLIERQEDPPES*NTNPFGLPRKT PSTKNPKINLARWGGPENNPEEKPR KVPESPKRKKP*TKIRPLSPSPDPTKP F\LKKKKKKKSVVPATQEAEMGGPLKA RSLRL
6089	19990	A	6141	1	209	LKLLASSDLSTGQSAGNIVGMSHCTQ PKINMGILLKLVYRFNINPVKTAGLF/ TKKKT*KTEIDRILKFIWCKTEHRIAK QSLKRTKLEDFLNFKTYEATEIKTS* YRFNINPVKT\TAGLFKKKHKEKQLTSG S
6090	19991	A	6142	3	282	QGIFLTRKRVNF*RGKFRTLKKNQGD KKGKNPFGPKIGKNFPGTFFWAKKI*K FNLI\PKKTPPFFQKLKKTGVKFFWAP KGPGLSKK
6091	19992	A	6143	382	158	FFF*DSLAVSAPGVQ\WHDLCSL\RPLF PRFRRFNCLSLLSQWD/YRHVP/QYPAK ICIFSRDRVLPIKASRNVSF
6092	19993	A	6144	185	316	PCLANF*IFFCR/NGGFSMLPTLGLNSW AQGILLPKPLKVLGLSA
6093	19994	A	6145	489	231	SVA*AGVQWHDHS*LOPQ/PLGLKQSSC LSLSNSWDYRHMAHPHTNLFKFFVETG VLSCCPGWSSTPGKGSFCLNLPKF
6094	19995	A	6146	179	1011	GTILNFQSLPFKPFFFSTLIFLKTIVLLC CPGWVNSSGSSCRSLPKCDWY*HEPH SAL*TFWFFP*LVKQTSIHSTQLLKA IFASLDAAPSTPYIRTHPSGLQWNL LDAARSPTPYIRNHPASRLQWCSCTL LPSPSYHTPA*AMTASLISPFPPPLP PAHFSQCRMTFLFVL/CLFEMESRVA QGWECSGAILGSL/QPPPGFK/RGSCF LSLLSRN\DY\GHAPPCPG\NFCIFSRD G\VSLCPGWRSRTDVLVHPPRPKALG LQA
6095	19996	A	6147	348	3	GYHKTINWHCCMSVFANLTCGNAIFPK /IPAKYFVDPDKLVLFKFTWKGKPRRIAG TILKEKKVRLILPNFKTHYKATVIKIG W*W*NNRHNHWQIGSPEIAPHKYSQLI FDKEA
6096	19997	A	6148	22	228	THRVALFVRT*NWKPCKPCTGEWNLTL CYIHTIEY*YYSAIKRNKLSIHVKT\WI DLKGIVLNENNOI
6097	19998	A	6149	406	279	RSIQGSSSHSASA/S*VAGTIGARHHTQ VIIIVLVETGVMAITY
6098	19999	A	6150	406	10	MRYHFTPDERLKSGLKLEYW*GSGETR SLIHCWLEYKMSHPWLK*/TVWLFPFKL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MRNVYPGPAISLLDL*EK*KHMSTKNT YK*MLQALFIITKNWLLSIKRRMTKQIM VYSNRNYSTIKNELPIQTRI
6099	20000	A	6152	367	1	ETPWAEAGGSGFKPR/LQ/CEN*PPMC SCTPANAPGSPPVSKKKWQFHRMGHV SSAWNFCGADVRLRAGGYVHRERFP LPWAAGGRDEVIRCLTVCTACGEDHPS HLAGPRGGFP
6100	20001	A	6153	441	38	ILNPGEAITSEKYQ*FNEMYQAKRL/ QVNRKGPVLLSYNA*POVAPQVSKLNLK LGHEVLGHRPYSLSLSPDTYHFFKCINI FLKEKRFYNQODAEANAPOEFTE*SA/D FCTTRINTFISHWEKYVDYNSYFD
6101	20002	A	6154	308	121	GESFPAEKTFPKENDYRWPSFFQWSSVL /CKINGLLMLPRLV*NSWQAILLPWP KVLGLQA
6102	20003	A	6155	1	420	QNLQPHWKTLRQF/LYKVRHMLSPAIP LLDIT*GRCKPCPVK/ESIC/RMFIEAL FIIAKKLKLKSCGSAGE*INKV*DIYTT EYSAIKSNKQLTHTTTWIKLSITPSE *SQT*ETACFTMLLIWHSRKNIIVTEN RSMF
6103	20004	A	6156	77	415	TLGLKPTSSSHLSLSKCDYRQEPFCPT SEANFFFFFGGFFPFWSPS*LKQFFVE MG/FTMLPRLVLNSWQAHLLP/ASAS QSVGTTGKSHRAPQKLTFFFFLGGNPF FGPQAGCPGAESNYPE*TPGLKAFGL NLKCLKYGDSPTAPGKLEIFFFKGGV SPSCASRVLANOPR
6104	20005	A	6157	436	206	LWYTHMEYYSALKKNAILTHTTSTM SLENMLNEIKQENIKRANI*PHLYEIPR KESRMENQCLGRRGIEFTVY
6105	20006	A	6158	416	50	RFFTHPPAGEFFSPFPKNIFFPPPP*K FWGGGGKASPPQKKFPLPPPNQVLCF DPHKKK*FPDPPEKTVEPGLPHVQRDP QS/PFLCYPLSFLYFCYFFFPFVFF HFLPFFFFFIR
6106	20007	A	6159	443	145	FFFFSIRFLVUVVLYQG*EYLCFMT* *IGVLLFLFEICEFFFLVLGILFGMFL /YFATASDGLFFCFFIFFFFFFF FFFFFFFFFFFFFFFFCCKS
6107	20008	A	6160	322	2	TODKNRHRARHIYKARKSARD*RLV HR*K*KVQKKNRY*PEGLTHTCALSGG NNI*DA/HSQE*WITPVI*TLWEAAGA SRGQEFKTSLANIVKPDANAN
6108	20009	A	6161	421	57	FCEMKFTPGNNVAVNIV*PTTKLEY/WI NI/DKTVAGCEKTDNYSRSTMGKML/ SNSIAWYTEIFRGRKSQLMWQILSFSK KL*QPLQYSATIALIRQQPTTSRQDPS AKRLRLPEGSGDH
6109			6162	333	41	GAWACHLVHGAALNAPTGLSRFHEEPG WSCRTAGGSRLELSVFFVQMGSCHVQG VGFPFCIFCR/DRGLAMPSRLVSNS*TGQ ICFPWPKVLGLQA
6110	20011	A	6163	2	423	KINVTSGCFENILKIEKTLNSLTKKE REDTMY*YME*NMIDTVESTDIKRIIRN TT*ETLHKFDNL
6111	20012	A	6164	434	5	ICHIFFSISKLLNLRPVSKLFFSINFI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						PGPELYYL*THFN* *GKLSFLFLQNI CIGFFNFSFMQI*SYFLRISLFIPIVSPIL LLG\FVQIFIVSINILYLSI*LRLFFSF FLSLFLFFYYTSLSRFHVHIVQVSYI RIHF
6112	20013	A	6165	1238	1017	ETGSHSVTQAGVLHNSSSLQAPPPRLK *SSYLSLSSWDYRRTPPQAN\FCI RDVSPCCPGWSRTPEF
6113	20014	A	6166	504	210	EFKTRSHDQGSLOP*ELGLKSSCLSR TLPHSD/YRV/PFHPAKKYKNIFF VETEFHVAQAGLKVLDSSNPFVSAQS VGITSISHCAPILCOF
6114	20015	A	6167	258	65	YKTKNTTISLPSFSF*TGILTF*NTFY YVY/CRDE/SLAMLRLVNSNSWQVILL PWPKVVELQV
6115	20016	A	6168	1	156	LARMVIS*PHDPAPASQAGITGVSH CAQLFFFFFWQPRFLRAGGGRDLGX VKPLLSGVRFFLS*TLPTGRKSGPPTH FG*VLRE*FGGSH\PVSSLW*QSAGITG VSHCAQLFFFFFWQPRFLRAGGQGR
6116	20017	A	6169	3	285	HASAHASGNILSYVGSFISLTAI\LI IMI*EAFASKRNVLIVEEPSINLE*LYG CPPPYHTFEEPVIKSRIRRLSDQDA ARKETOQGAAD
6117	20018	A	6170	645	15	LPFTYCSPCRNFSNLFWRDERSNNPLG/ ISLPHSDKITFNP\YYT\IKDALGLTSL HSLKDLHLSFPHTS*GQAYYSL/OPT PLANNSPHARPEWIFPYCAYHNFSGSGP LTNLGGVL\ALLSILHFKQ*FPHPPS YPNKRH*YFGPLRPITFIDFLGRPPSF ISNRESGQPVSYPTIIGQVASVLYFT TILLIPTISLIENKILKWA
6118	20019	A	6171	409	25	YTPGOKIFFKSNFGSKLFFPPFF/P FSFSP*KFFSPKLNFFGQFFFP PKGRFESKNDPLVFFSPPFKEKVFPP PLAFAPPRVFLKAPPPFFFFFFFKGG EVKWLSEALDCKSKDRG
6119	20020	A	6172	73	52	VOLLKRIHF*DRVLLCHPGWSTVARS *LTATSRSSCLSPSSWDYRRVPCPLAS F/SP*YIALNN*A*AILPQPSKVLGL* AVAHAYSPSTLEG
6120	20021	A	6173	325	470	IPTEFFFLAFT*FFCNRN/SLALLPRV LNSWLQAVLPFWPFLGLQT
6121	20022	A	6174	2	228	TLEDNSTIPCKTIQSSSCTPWYTQAA CITLLSM*PKKLWVYTKSCTQMFVAI FIAGNWKQPRCLSVSE*INKLWYI*TM E*YPLVLRNELSSHEKTH/MEM*IQLLI ERSQS*KAVVCLHKKLHTDVYSSYIHC OKLEATKMSFSKRMNK
6122	20023	A	6175	3	408	RYLTALIRDMQITPVSYHVFSGDYQ KDNKNCW*RG*KMGSLMHC*W*CMVQ LWKAQWQFLK/DVKRRALLFLGIYPRM KTYVHAKTCMHIFTLALFLVYVHNLALS VMDKMLGHPITEISRDYSYCVCLL
6123	20024	A	6176	2	237	WWWLIPVVLAAEAEAGLLELGGSSRL *WTMPLHYSIGNRARLCLKKKKKKPK VFPQKKKKKKKKKKKKGGAL
6124	20025	A	6177	387	154	AVVQWRDLSSLGAPPDGE*FSLCLSLW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						DYRHKLLTSGDLPASASQSAGITGVSHCAQPLSLVFVFFLTNQRFVAALS
6125	20026	A	6178	1	239	FFFFEMECLTVSQAGVQWYNLHSLQPLP PGPKQFSC/LSLPSSWD*RVPTSRPAKF /CVIF*DGVSHQCPGWSAVVQPLH
6126	20027	A	6179	325	50	RKFPLTWRRVSFFSLRSSTDWMPFTHR HIGGIIICVTQSTDNSIGLIQKPHRHTQ KNV*PNV/WHPMKSS*HPKLTITVYPL STWHTYTSL
6127	20028	A	6180	157	338	SOHFGRPRQACSSSEVRDQPGQOREFF HLYKN*KEITQVWHMPPAQDY/LEPG RSRLQ
6128	20029	A	6181	3	273	HREGQSKLETFWKGFTI*EVIKNIDDL/W RGVKIPILTGWNEKLPTLINNFEVFKT SLEEITEYVVEIGRELELEVEPKDVTCL LQSHKLT
6129	20030	A	6182	2	359	YYPATPLLGIHPK*KNSTYQMHTCTHWF TAVLFTIAKIWNQL*CSSMGWKKM/W MHTHTHTHTHTMEYYVPIK/NEIISFAA TWMLGVIILTEITQAQKTKGIFSHLY VGAKIFDYM
6130	20031	A	6183	3	211	NGKLSVSVINQDCFPATPCPFQMGRCPT LFL*SFGGGAIPLITPSVGTQIFRLKM /FEVTHHSHF*EPLTAAALNQSLPL SLLVDF/RDRGLFCHLGMSAVD*SHLTA ALNS\LVTLQSCPSFLSSWDYRMLPCL GNF*IFRLKMLKSLTIFILFHESH
6131	20032	A	6184	707	384	LQTFYFNKVKCKVKNKSTQNFYIFSRYY MHANRHGKYEI/WIKKMPREMG*AVQL RMKVVKIKKNTIKLGVVHGYNLSTLG GGGGRIT*AOEFKTSGLNIARLHLTY
6132	20033	A	6185	720	363	FFFWGRSL*TLF*/QTGSHSVAQSGVQ WHHSHLQPP*TSGLKQSSHLFQSSWDH RCAPPRVANFLLDFCRDRVCVAQAGLEL LASSNPPTVASQSAGITGGSHTWPFWD ILGIMYWG
6133	20034	A	6186	439	66	KPKTLGSKKVNENRVPFGK/PWGVSPL GPGP*MGGSKP/S*NPSPPPPLFKTRFG FFPPG*ROGHYSGLQPPPGGKTFFPP SPPKKGWHKKIIPQKKKKKKRKNII GSWTTSETVGNPAW
6134	20035	A	6187	83	287	NKMFKIFRRF/CGFLGQSHSVTQGGVQ WHDHSSLQPP*TPGLKRSSLPTCWDNRHK PPHLVLFCFYRL
6135	20036	A	6188	290	609	RRMDDPFFKFFERRVLVCHQGS*V/ K*SSHFSFPCSWDHRCV/PMHPAN\FN PFHTDXSLTMLPRLVNSNSWAQVILWPLP P*VLGFMGSPCPQPPSFCIEAV
6136	20037	A	6189	2	371	RYIFERKVFAYSELTDNSLSLISGKSGI LWKKRLSLFS*Q*SYKWSLGAICYGMH *KRLGTSIL/FT*VETGFHVDQGL ELLTSCETLASAY*SAGITGISHCAESQ STLKKYIPGSTI
6137	20038	A	6190	531	205	RNRPALVAQGVQ/HDLGSLQLPLP*F K*FICLRLQRSWDYRCAPLRPA/NFFVF LVETGFHFGQT/NLQLTSTGDPAPAS QSAGITGVSH*ARVPVFIITDALYK
6138	20039	A	6191	52	375	NRCETSLFFFFEKKNFPCPPGGGEWRN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LK*MEP/LPFGLEKFSCLTLRRGGN*GP FPPLQENFGVFRKKGVPHCNPG*FQTPD PRELARLTSPRGDOGGRPVPRVK
6139	20040	A	6192	3	158	FFFLLLNGLKKETG/WLGVAHACNES TLGGRGGWITR*ELKTSLANMAEPY
6140	20041	A	6193	2	54	FFPETESHVAQAGVQCVDLGLSQPPPL GLKEFSCLSLLSSWDYRHTPPHPANLFV F/SFLVETGFRHVQAGLELLTSGGPPA SASQSAITGVNHRAMPVEVKK*RVSF RFGWAVV
6141	20042	A	6194	1	323	FTLPSSNCKCAPF/RPDWVLYELVETG FHRVGRAGLQLITASDLPASAS*GAGIA DGVSITQCSNMLPMLPCRQVILARYNLHL PAACLGLEKCRDCSLCPAATPSRK
6142	20043	A	6195	619	243	SPETGSCSAQAQAGVQWHDGLGSLQ* LGLK*SSYLSLLSNWDYRCA/PPRLANLFF VQAGSCHLAQAGLELMSSCHLPALVSQ AGITGVSHHARLAVAMKRTPLYGLPSRI SNLCVLLKFLFFLYL
6143	20044	A	6196	385	19	GGHFGAQETSPFGVQLFRLHFLSNWGF KRPPWPPG*FF/VPL*KRGFPPGRVVP PSLFP/SDLPPAPPKGVWSGLRCPERT FFFFFFFDKEC/RLSCPANFCIFSRDGV SPCWPPNSRTDLO
6144	20045	A	6197	498	437	ENLQSSINLVDKANAWFERIDSNFDRSF TTVKMPSNLTSIINACCGEIPHERKS*S IWQTSLLSYF*KLLQLAPPLATTILIS KEP*TSR/QDRLLAEG*D
6145	20046	A	6198	79	394	SVKLLALFFFFFGENFCFAPQVELKGP LG*LNPPPPGLKNFSGLT/LPKKMWLGG HPPPPSKFFFLFF*KKGMAPFSQGWFKT LGLNQFACLTLPKGGNLRREG
6146	20047	A	6199	2	313	SASHSGAGTIGESHCAFPIMPVYSVLNPF FFLEKKPDPFTQLQEQCGNIG/SMEPS PSOLRGIFCLGPKKWEARAPPCCGYF WFF*KKGGLPIDPGRFWKSVF
6147	20048	A	6200	62	732	AFOQARKGTO\GRLLSPFAGALP/VVLA PSGPPPLPA*\GSSS/PASVAPYFPQAT G/SPTTPPGLRRGWSKGLDHPHNTF YCWESSEF/PPN*QGS*APGGVNSEGRG Q/LPFSIARCVPTPSHVPPHPLAFPP SLPHFGPASRAP/ TGSSDLSASAVSAP GREHP*GTRMVPQAGROKPGHGRAS* GSSCSKRTLSPLSPRDSGFQSRCCFHP RQNH SRC
6148	20049	A	6201	424	7	KNMKRSPISCVTRDPQIKITMR*HYTGI KMANV/RLTGNTKC*YGAGKPLIQ* NECKIV*PLRKTAQFSQS/LKIV*/PY DPAIALPGIQLC*KCTS\KKNCM*IFIT ALFIMAKKKQKPRYPSIGEWYKLLHL
6149	20050	A	6202	371	144	RWALPRRTNF*\FFVETRSLHVAQGVK LLGSVSPFISPSAVITGVSYCAQVYG HPFELSFLIEYIYLDFF
6150	20051	A	6203	409	110	LRSS*LCHLGWSAMVQSWFT*FKP*LL GLSDPLTSASRVDIRGMPCCPRNFIFD WF*CVVC/RTWGLIULPRLVSNFWP EVLHFGPSKLELOV
6151	20052	A	6204	15	221	KASRKQIETTLRYLLSPMLAKMQLI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						NTSCW/RKSGERTLIC*W*BGKMOVQLSKGIWYLIQAEY
6152	20053	A	6205	23	371	KVACTCHETITVLFTIVKL*NGSRCPETD DWIKKM/VLCVCIIYSSVCVLCVCDPR* IERHDIYVYIMEYLLAL*/DEIMFSA TRVKLDIAI*S*ITQNVKCCIVSTHSGN LIMVST
6153	20054	A	6206	113	417	SAVTLLVIVLYNLDKTYVHTTKTCOMETA ALFIIAKI*KQLRCP/S*LIWIN* [*] C* [*] KEM SYQAMKRSYARNLWSSSKLWRNLKCLLL RSEQSEKSAYCVIPTI
6154	20055	A	6207	510	167	GLGOAISPLSPKSGQIGAYGPGFFFFFK R*DLVCCPG/S*LNILVASSQSCSLSPKH WDHECEPPLCAFFFFLL*ROGLAMLPR LPLKALASGGGMAKKCRIFYFSMKIHL QAQ
6155	20056	A	6208	418	40	SYTHTHTHTHTHTHTHIP* [*] LTGS/RLQ GICRKGSKHPRGLSOLL
6156	20057	A	6209	1	258	SGFLS*VPSVRDPTGNRTV*LTWQPLP APLEF/CPRLSD
6157	20058	A	6210	229	310	DFSEAKSRQCGGGISNVNPGVVLKPV IQHF* [*] DGVLLCCPGWSAVV* [*] SQLP* [*] LPR LK* [*] SSQLSLPR/SWDYRHVLQ/HPANCF VFFVEMSLMLPRVLSNSWALAILLPO PKVLDDWLEHHTWMIYITVATTLP
6158	20059	A	6211	496	1	CCQESFEILGSGINSFGPLKKGGVKNMR PGAGPTLNKRFPSSDNPLQGRRGCGFPF VSGRGSQKDRVPPKWWFFFFFSF* [*] DRVSL WPPGPSARKPSWLPVASTSR/V* [*] QSSCP PLWFGPPTVSVYFFF/KRODPLMLPR LV* [*] NFWPOVILLSQPKVLRLLQARA
6159	20060	A	6212	3	340	VTAGITITIFNI*EAFASNRKVLIV* [*] BFS I* [*] SLQV/* [*] WRGLLLGSPPPVHTLEZPG YVTSKRKRKESNPPLKASSQPHLHDF KKKKRGPFPRILECAPFGGWHGREFF P
6160	20061	A	6213	60	493	KSQONFFCFETESRSTVQAGQWHHFS LQPPFPGFKVISYL/SLKSNFSGYP* [*] DF FCNGPPCS* [*] GPIRFTYIYICVPSWDYR RLPFPANFCVF/KTVSPGWSQTPDLR
6161	20062	A	6214	414	1	LCNGRPGLLVSLFLPGEELIPLCPFR* [*] KL GPFRVL* [*] KGGPFL* [*] SSFAPFF* [*] EMESH SVT/RLCSRAILVHCNCLPGPSDPPP SAS* [*] VAGRIARAQVEAAVSHDHDALQ PEQHSSETPSQQTNNNQTKLTKQYYP
6162	20063	A	6215	2	403	SLLLPLVOLPLRLCFFFLKRGFNPGAP DKREWGFG/* [*] LKPWLP* [*] NNFSGQTLR RSOD* [*] RKTPHGGVNLV* [*] EXTGFSNLGR GGLKPPSGONTPAWPKGVGTGGTPPP PPVFCFLGFCENTNLRAKKFI
6163	20064	A	6216	2	388	KMEQTLWKTDFEFLTKLNLYPSPAPFA DLGIYPNELKT/C/YTNTICI* [*] KSIAPL FIVARTWKQPGCPLRDGWLNLKGLCIQAL EYISF* [*] KREL* [*] NNHAYKKLKLIFLGR QEDRFSLGWCEQKRGEM
6164	20065	A	6217	363	302	NKEFKTLLAWGEPDEL* [*] KRGFS/WLAR VLNLSLHDSPPASQKAGIPGVSPPR PLFFFFFLETVSHYVAQAGQLISNYDL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						KLPSCLSLDTWDYRH*PFYPVFKLLNS TYKAC
6165	20066	A	6218	576	6	RAVLRLGLLVLLTKHTFFLFFPFRQSLAL LPRVGQV\HDL\GSL\QPL\PPG\FKQ FS\CLISPSWDYRYPFRPANF*FSV ETGFHHVAQVLELLTSSDLPALASQSA GITDLGQSETTHGGSGLDKPPDHKVDKG PTERRACLLSYSAGRKRYKEYH\LPQGS EPFHHGDLISISFQAASHIAGTTPPAHT
6166	20067	A	6219	44	496	GRFVDPRVRPRVLNS*PRDPPTSSGAG ITGV/SSHAR*NIET*KLCISFLGVFW GFLFLFPVCF*FWKGSGLLVAQVEGK /WKFGFLIEFSPSGVKKEFFFNPEGND /YGLAPPQGVIFWVLIKNGVSFPCRAMV QTSGLSNINRLNP
6167	20068	A	6220	1	421	QRGLTATISRETSFTLVAQAGVQWHDLE SLQHLPPGQFGPCLLSLT\TGNCSTV QAGVQWCHLGLS*PLPPGLKPSHLSPS SSWDYRL*KPHOGSD*VCVT\GAASPEP NTMTAMNKPDIRMKETLLLPSSSEKML
6168	20069	A	6221	3	36	AYCIVKPS*PLTGALSALLMTSGLAM* FDFHSITLLILGLLANTLIYQ*WRDVT RETYQGHHTFPVQVGLRGIMLFTITSE AFFLAGFF*AFYHSRLGPTPOLGGDWPP TGITPLNPL*VPLLN\TNE*LA*GVSIIT *AHPD
6169	20070	A	6222	895	13	ANSWANN*FELATQIAFSGRIPLTDSHL GLLKARVEAPT\AGLIVLAAVLKTGGL MLYTASHFSNPLTK\HAYFPFVLSLI EA*FITSSHLPSDKQDLKS\LMAYSS\I SPHSPS*LTPILIQTP\W\SFNGAQGPS IAHGTTHAYITISA*ANFKLTERTSQC ACINPAQGLSNS*LOLIGLFE*LRQA /SLTMGLTPPLINPTGEMCSVASNGRFS /WTQISILLPYRDSITLGSCALYSIYF TTTQWGS\THHINNKLPSFTRENTLMFI HLSPIILLSLNPDITGFSS
6170	20071	A	6223	68	405	HSYALVYNFVGIRVVKHLSKCLITYTWHI SNSQOEVCMPNLLNKRVP*TLAPF*N IS*GISQLGAVAHTCNPSITGG*GRW/I QQLKTS\LANMAKPHLLKKKKNF*PFK RG
6171	20072	A	6224	591	283	GTSTQAGVQWNCGSLQPPPPGFKRFS LNLPCSWDYRRVPPHLLANF*FLVEMGF HHVN/QAGLELLTSSDPPALASQAGIT GMSHCARPRVAF*GEKNHSL
6172	20073	A	6225	302	173	GFFSFFLRK*DR/SLTMLRLVLNSWAQ VILPLWPPKVLGLQA
6173	20074	A	6226	417	81	TQTRGPPPPFPLGGPPSPGPRTVPPFPRG GVPGTGRSFFLFRQNPGLAFPKN/EGG F*KKFGPPLPPF*KTPFFFTNRGNPCPF FVGENPQAPPVFGGNPFPKKKKRND LS
6174	20075	A	6227	41	474	TDATETPHFTSKH\HFGF*AAA*YHNFV DVV*FLFYVSIY**GSCVPHPA
6175	20076	A	6228	503	28	AAHAPPRVKKVGH*AFFTURCTNSRH* IKFKPKDKKARILKGAREK/RTTYNGA

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						FINLAVNFSVETLQ/A/RREWHDMFOMP KKTTFYLRILYPMKISFKHEREIKTFPD KQKPRDFISSRPVLQEMLSWPGARVHT GNFTLLGG
6176	20077	A	6229	418	175	VSPLSPLKILFFPFGKLFKFRREGGPKCPP PKKRVLPKK/PPAMF*IPPPKRRKSKLP PPRKIWPQGIKFKSPPPQYFFFF
6177	20078	A	6230	45	308	ACVRLKH*TDN*QNTYNYQ/HKSLLP* KKKKKKKKKKKKKKKKKKKKKKGGGG FKKPGGGPISWGGEKIIFFFGGKKK TLGIF
6178	20079	A	6231	440	209	IQHFRGFSRRGLLGPPEARASPGQHRESR SFLKNQP/NKKFS*VWVCPTAIPASPKV EARESLEPGRRRLHLTEALQGG
6179	20080	A	6232	419	2	SSPPFPFGGKFF*KKPGKKKFSPPKKRV FSPP\PPKKFFFS*KA*NFWGGGGQKFP PPKKGVSFKKPKGVFKTPPKKKKKFFFP PGENMGPPRVF*KGPPPPPPPPPPPPFF FLSNVNLFKPKVQAPCLT
6180	20081	A	6233	448	112	QSARITGVSHRTPEMLRSTFPLSATDRN AGQKISKDIADLNNEQDHRDIRNSTQ *QONTHSFQAAIRNKKIDPILGHKKMLTH /CKQSDQTNKLEISNKYAKPQRIKHTI K
6181	20082	A	6234	2	351	MDOGIT/SOFESYLLRNTFCQAIIVARDG DSSDGSQQRKLKT*PWGFSLLDAIKHTE DSW/EEKISTGVWKLIPILVDDFEGFK TSVEE/VADVMDLSRELE*VEPEDGTE LQSHSQT
6182	20083	A	6235	3	252	FHTYNSLLVCHSNLCYQNSLLFFIITH* CI/HFHS*AKVSIWKTHYTHHTHHTH MHTHFQATDRKICVNVYMSVAYIHKG LQ
6183	20084	A	6236	3	294	IITF*LPQLSGYIEKSTPYECGDPDTP ARVPFSIKFFVVAIT*FLLLDLEIA\LLL PLP*ALQTTNLPLVMSLL*IIILALS LAYEGLQGLD*AE
6184	20085	A	6237	381	121	PVPASF*FFFFYRDR/VSLCYPGWSQTP GLKQSSCLGLLSHWDYKYDPPHAFISF LLSSLLNLVL*RPVLLLCATVPAFLDIR EQ
6185	20086	A	6238	395	62	PPFFPIPKFFPWGPNFF/PLGPPFPLGF FPGSFAPPSHFSPD*NFPPPPPNFPPG GDLFPQKGDWFFPKRGVFFFLGGFSK FSGGPPFSLGQKKRFRKIGPKKPCF
6186	20087	A	6239	1066	761	SFFLRWSFILTQAGVQNCDLSSQLPP PGFK*FSCSLSPSSWDHRRPPRLANFC IF/M*RWGFSMLARPVNS*P/CSDPT PASQAGITGLSHRNLVFL
6187	20088	A	6240	390	27	GELPTPIYLAPPASPKGVSGGSPSPSRV KFFPLEVPPPPPPGC*PGFFFYIWQGG ARVP*QIIRFSLRW\PPRTPRPKNPHL QVGLRLICLSPETGGGVKVFSGLLKK KKRAASRSN
6188	20089	A	6241	366	1	KIKNDRPT/*SKGA*SV/RNLPTKKS PEPNGFPVGVCPTFKKKLTPV/SKLP KF*KEGILNSFF*SSALIPNFFVPSK KKKTKKNYRAISLWNIDEKIHXY*QT

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6189	20090	A	6242	23	439	EFRSTLKVLYTITK IASGRPPFFFFFFFFFFCLPPPPGGNPSFS FLKKKKKGGGGGNNPNPPGKAPNPQGV GVPPPPPPPVFQKNPPPPPPF*KNPPPS PKGPGGPPPPPPPPGGGGPPPT/PYFL KKKGWGGPPF*KTNPXGGETTLVG 6190 20091 A 6243 20 261 WQGEILKKFSCI.SLLSSWNYCAAPFVA N*PVFVFVETGSHVWQSGLELLSDRDPH TGESHQAQPHFC*ILYTGESQRIIL 6191 20092 A 6244 376 76 LLFRLECSGVIKPSSHLS.PSSRDYRCV /PTMPNF*KFFVELKFNLSL*R*GLTMLP RLVSNWCQVILPWPPKVLOGCATTPG LTDFTITTFKGYRHGDUTY 6192 20093 A 6245 222 233 KSPFYFALIFEKNFCYVKKSQGVLFVFSK VKVLVRPPFFMVIKQNQP/FNPL/RKFF FFFQDRVLLCHPGNSAVV*SKTLS 6193 20094 A 6246 2 358 EIIILTFQSY*ENTFNEAITAIDSDD GSGQSKWKSFWKRTILGAIKNICDL*D *V/KISTLSGVWKKVPSLMDDFEGF\X TSVEEVIADVVEIAR*LELEVEPEDVIE LLQSHDKT 6194 20095 A 6247 3 322 PDSLLQTPPTGFRSSHLGFSSSWDYR LEPHSVVCVCV/FCVYIYFFFFLEKT GPGFVPAQGLNLGVKRIKA*PPGVVEI PGLTHTPGWGGPIKGGKANPAP 6195 20096 A 6248 1425 1280 SLDFQGLALPGWSAVV*SCLEASTSR\ VKRTSHPSLPNTWYRHLPRLANSVYF L*RWGLTMLPRLGNS*TAQILQWPWP VLAL*ADEEMKAKGHISTKGGQTLNPQ PDCGATSVYSLPIRKFO 6196 20097 A 6249 189 336 HAPFFSVISLSQKRRR\WLMVARTS NPSTLGG*WGMIA*GEETFSTQ 6197 20098 A 6250 2 300 PPSFPGFNPVLHGKASTVTFSEPLSL PFLLPAPLFFPFLPKRESIPGA/P QGLEGGQNFLEPSPGKIEIFWNPBR GNEKINPPPPINFCDF*EKGFTVVAR AGLKL*TGGLEGGQNFLEPSPGKIEI FNPNPFRGNEKINPPPPINFCDF 6198 20099 A 6251 1 198 LTGRL/SKECVVSRFVOLKDLKRWQ HLLSQQLACIVLTSAGIMDHKMR*KH TGGKSLGFFF 6199 20100 A 6252 11 214 SLRLKSSSHLSLPSWDRLCEPLHLAN* KKKKKL/CKN/RLTLGPKLVNSNV*T ILPRPPRALGLRA 6200 20101 A 6253 402 3 KKGVLSPQVEDKDAISGSFNPPGPK IPPPQPEVGPPGGPPQTRNLGI/LG N*GGGGF*PPGAGKSPAPGPKQ/PFG KDKREKPYGPPKLPFFFLRQSLCFAQA GVQWCDLGPQQPPPRFQKQCL 6201 20102 A 6254 362 78 VGVN/MTFFQHFGLGSGIPRRYSBYP AYTT*NTVSSIGSFISLTAVLIMIFI EAFASKREVISVSYSTINLE*LHGCPP YHTFEPTYVVKV 6202 20103 A 6255 337 2 DLSCHSHGEATQKHEKCRASCTHMFIT ALFLIAKHWNQPTC/PHMEYNSV/K/N EQITDTTWTMDLKCIMRHEQRQS*KNS VLVCFHAADKIDPETGQPTKERGLMDLQ FHVAGEASH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
6203	20104	A	6256	2	305	QWCHNSSLSHNPGERETVSSSLKLPKAWN PRHMLLCPTTSLFLRWGFIYVAQAGEDT RGHASL/LA*ASPSVGITSKSQVRPVH DIACFHRESTMFSAEFN
6204	20105	A	6257	335	3	GPFOSSPPGVTPISCFTPPKKGGNGRPP PRRGKFWIFKKNNGSPG*KRRVLFPDGP VPPRPLKKGGLKGGAWAKIFFFFLRQ SHSFTQAGMQWNCNLGSLQPPPGFK*F
6205	20106	A	6258	219	2	PTLSSQKDTKAQRLYSFPLTTTKDERLV TLVS/WPGVVAYTFIPSTLGGQGRWVT* AQKFETSLNTVKPPSC
6206	20107	A	6259	306	117	SFELLGSSDPLISALSSWDYRCAPSRLA NF*FFVCVEMGSSYIVQ/SWPQ*ILLSW PPKVLRLQT
6207	20108	A	6260	572	269	ETDILSVAQARVGGGLHLGLSPAPPPGFT PFSCLSCSS*DYRLRPFRPA/NFFVFSV EMGF\TVLARIVSIS*PRDPPSGLP*G ALGLPGVSLRPLALCLLK
6208	20109	A	6261	357	116	FAQAGLELGGSSPLASASQSVGTTGMS HCA\RLLLFFCGGRW*GG/LK*FSCLSL LSSWNYRHEPPHPANLCIFSNITISY
6209	20110	A	6262	3	337	HERHERHERHEQSAEITGVSHHAGGGIG LLNFFLFFFEAGSCTVT*/GV*WHDH GPQ*PQIPRK*SSHLSLHSSWDYRHVP P*LGJQACATWPG*PFPCRPDIENK
6210	20111	A	6263	515	150	FLRWSEFLVQKQGLQWCGVSLQGLPFG FKQFFCLSLPSSWDYRCPPCPNFA*L LVEMGFHHVQAGLELLTSGDLPASASQ SAGITGISHHARPFTLFF*AANGGKQV FLLRLVLNGL
6211	20112	A	6264	1	296	GTSFLPSFLF/LLSFLKFLNFQIVSHC RPGWSAVA*SOLTAPSI\FGLKPSSOLS RLSSWDYRCPIINF\SLPMLRRLVNSN* PQAILPTOPP*FGLGLOA
6212	20113	A	6266	298	182	LHFFVESKIIKILRAEAKWCL*VLPTIA KIWKHL**ICKYLSIDEWIKMWTIHTV EYSAIGNKEI/PIVITWIMYENIMLS EIN**QDKCKMIALL*GIYIQ
6213	20114	A	6267	402	234	PPPLFLKNPPPPPPKNNPPKKKKTIFP/ SPPVNLAPPKEF*KGPPPPPPPPPPFF FF
6214	20115	A	6268	125	17	KGQAOWLTPVIALRREA/EEAGG*LEPR SSRPAAWI
6215	20116	A	6269	1109	454	GDSAGAEGTMENFTALFGAQAQDFPPPT ALGPGPGKPPPPPPPPAGGPGTATPPT AATAPPGADKSGAGCGPFYLMRELPGST ELTGSTNLITHYNLEQAYNFCGKKVKE KLSNFLDPLPGMIDLPESHNSLSRLSI EKPPILSSSNFPIGTML/VRLPPPHWP VAGAVSSSDAYSASQEE*AAQQTPEYPG SCPPRNTI*FRSQEEKEKRRGS
6216	20117	A	6270	111	86	VVGITGVSHCAWSRNGSTLHCWCEKVV /OPKRTV*QFLMLKI\PYQMI*PLLGI YLKKNKAYIHWKTLK*WESLFLFEIAK/ TWKQPKYPSASEWIN*LDSFSLYLWGS RTPDLK
6217	20118	A	6271	2	222	RSCESSQTSACYKSYLYLPLKS/GGPK ILERM*PIYFLPIPVVVTINQRYVYFYL

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6218	20119	A	6272	787	470	NLKKTGRTGIVTLVYKMYKSF LPFFFFFETGSHCWRWERESLGVAQVG VQ*CDLRSLQPP*PRLKQSSHLSLPSW DYRCAPP*LDKFFFCIFCRDGFHVAQA GLKLLSSG\NLPASVSPAGTTL
6219	20120	A	6273	2	322	FCMAIAIDSSSSHGSRKSLKLTWKRF SILDAIKNTCDSEWEV/KVST*TEVWKK LIPTLTDDFQRFKTSVEEVTA\ELLVVE ITREIELEVELDDVTELLQPHDQT
6220	20121	A	6274	175	406	KNSLGGPNLTGEGKKITFSL\NFFFSLE ALI FVGRLSFVPPKIRFFSKNSRNLF /CPVGEFFKTRPPVNVFFSLP*RKSYFF SFG*INP*GIFLKAPPPFFFFFLRE RREVSMLDRLMSNSWQVTPFPWPKVR VLLGIVDQV
6221	20122	A	6275	2	181	PRVGRVGRHKRKKSEVHCWQWKL*P LWKTWVRVLKTLK\IELPYYP/ATKL* SYPLE
6222	20123	A	6276	397	47	PPFSKNFFFPQKDPFLGGLPKKSPFK K\FFPKTKPKKNPPPSFFKPPPPAPI KTPLKKKKKFFPPPKQKGFPPKFKKPP PLFFFFFFFFFFTAP*KITKSIYFYFF TKTFYL
6223	20124	A	6277	2	264	ETESHTVAQSGCSGAI\IAHRSMLNGST NPPTTAS*VAGTTDACDHAWLM*FL\V EMGSHVVAQAELELLSSSDPP\QSPKI LGLQA
6224	20125	A	6278	3	204	IRCYRKIFYERKHQWLQQLSLLSYFKKL POP\PL*ATITLISQSLISRQDPPPV KR*LTEG*DDC
6225	20126	A	6279	57	306	INKANRDL/GTIDFLFLEFLTIKVRKMN TKTESKRN*ESILHVE*EDTGHVRAAA VCRDMTYLGEKLTDEVDK\IIREAKYW
6226	20127	A	6280	419	18	SSSSPKACMFVYEWCTQKCVIYEYMC VFVYV*LVMCCMNVCAM\C*SACV*M CIVCEVCVM*GLSVICEGVCVM
6227	20128	A	6281	459	235	FLRNGVSCCHPGWSAVQVS*LTAAANS* AQVILPSSWDYRPTVTHPAKTHNFYMQ/ CQNKMKCVTHSIVIFSLQ
6228	20129	A	6282	505	470	GVP*GQEFPSLSHGRPCFFLKCKINP AWWQKLF*DRQKFLRTOI/LALAPQGG QQKNFFS/NKKKKKPNM*IALR
6229	20130	A	6283	206	374	GGGGKKKNWGGKKGKGGKIIFF*SP PRFFSFSPVKKKKFFPPPPFFPPNFF FYPPPPPPFFFFFFFVFVFVFVFVF FFFFFFFVFVFVFVFVFVFVFVFVFVF LFVGHSDILMHVINV
6230	20131	A	6284	431	269	YIKGGPPPEIETLFIFFVYIYLIIFIF FFFFFFFVFVFVFVFVFVFVFVFVFVF QRF*TYISIPHFMLM\YTLHLFTFCIC SLFTIIVVFYIFV*L*YCCTVKALCNSL LVSELDKYLKNNYCKQ
6231	20132	A	6285	298	44	YLFFFFFF*VELVFFLCMFFFFFFFVF FFFFFFFVFVFVFVFVFVFVFVFVFVF CFLSLFLKLYLKYNFVQLQGNLHFNNI I
6232	20133	A	6286	386	1	ANLHIKVNPFVNFTLLNFSFLPVWFGFH FLVV*RVYLSHRGTFVFQNFRLRIFPF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SF*VG\VFLEFLFPFPPFFPPFFPPFF FFFFFPPFLCIAIVFY*TWYISYFTKY IEEPTRCGRTRGRTRG
6233	20134	A	6287	190	134	LEFGRRNRFQSRNMLRGSGLQWRNYADM VKIAKT*VLNRTFHKVIAIIGGDSCDGS GQNKIKTFWKGFS\LDAINIHNSEEI KMATLTGVWKK*IPVLKDDFEGFRTSVE E/V/TADMVKIAKT\LELEVEP\EDVT* LLERILF
6234	20135	A	6288	394	2	RROASLSCGGLHPVRSSRLCLCPQAWA MAGAPPASLPPLCSLISDCCASNQ*DSV GVGPSKPGVGYHLLVHRFLSPLEKRSIR VGVARFSRCRLSPSLTRKGN*LP\TPC ASRVRCQLTLLQLAHQALHP
6235	20136	A	6289	233	58	DRVSLCRPRHWVSRTRLTVASTER/LQ AILPPQPF*LGQASANRSPRSPKLTG LRG
6236	20137	A	6290	385	48	TLQVLCPTFTSV*KKKKPENIKYW*QCG ANRTLQ*WQVCKVAQTLWKPVWHYTVL NLNTRIVYDPMPLLGNNNAYMCCIC\ YQKTFTRMFIAALFEITPK*RMHKYLT VVG
6237	20138	A	6291	273	36	RNGRWTPCGGR*IHPS*GTDPVYLPVPG TLSSSQASNSHPLKAPGSRP\PWPTDL GYKDPGRPPSPNACRRRPSLFHSD
6238	20139	A	6292	394	5	AKIYFSINPLVFSRQ*FLKNVFPNILL QFFSNINSLMLKV*ALLQDPFLVHNVY NKICDTSKDTTLFMVLMFVKMKTFPS LKAYI/WSGTVTHYTPSLTGGRMKIT *GQEFKISLANMVIASLY
6239	20140	A	6293	536	190	RRSFALAVQAGVQWRDLGSLQPPPFK RPSCLSLPSSWNYRHAPPRANFVFLVE TGFLHVQAGLELLTSGDPVVLASQ\A GMTGVSHRVQPD*GHGGSRLSQPFWEA KTGGSPEVRSRPA
6240	20141	A	6294	2	238	HEADLGTQVLTHTPSTTAMYVHYCCPP *ILYGTINT*PPVHKNPIHITK/SPC LQASTAINPOLSHINC\NPKDTPH
6241	20142	A	6295	2	447	FFFLMGVSLFCPGL/WSAGAILGLSLT SCLLGQVILLCLSPSSGKLQVCAYPH LG*FLYF*AEDGGSPCWPG*VSN*PQ VIHLWPAPKALGITSMSHCCPACFHCTF FRHFRQNPHLNFFLEGLGLSPPPPSQ PLEGGKPGN
6242	20143	A	6296	2	133	AERERERERERERE\ERERERERERE R*VERERGGVPLRTYR
6243	20144	A	6297	3	244	HDYSSFLAPPALGYMRMLHPAYFILFY FIS/FYLFFSQDEVLLC*LGWSTPELN QASCLGLQKWWDYRCEPQCLAECD
6244	20145	A	6298	1	361	GTRRSAMLARLVLSNGP/CYLPALASQ RAGITGVSH*GCPFFSLLKKRWSHCVA QAGVQVFFRG*TPGLSCFSCSLSPN*DY KCAPLCPP*DTVF*VRVSVSEVPLTIITY RGEAGVWA
6245	20146	A	6299	3	348	HERHELEELIKNLEFFFFFGKIFFFFFF GKNGGPF*FIQASPPGFIFFVPP* KWDGWPPCRGDWFF*KKTFPSILA RVVLNSPPWGLSPYPKGVRFPGGTPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6246	20147	A	6300	1	436	FGPV VDGEFSCLSLPSSGDCRRASPCPANF/S VFLVGI GFRVYGAGLELLTSGDLLASA SQSPGITGMSHCTPRKHH*IANSSSVL GDFRIDYFQISRKAQWITLGVNPAWESH LLMGAGLRVLPAPRLMISQVDLLPATHP SSGRG
6247	20148	A	6301	370	70	PKG*STLPASASRSAGITAVIL*SHCTS PPM*LRKHFHTSSSTSP/CEFFGKK LLIFVDPQGGKGNLS*LKPLLSLRL PCLTL*RGGDYPGFPPPP\SYCFEIKK GV*FCGPGGNS*PASASRSAGITAVIL
6248	20149	A	6302	1	285	KHFFLTFTLFRDRVSVCPYSWSTVVE/S L*SWLIAASN/CLGSK*FSHLSLLCHHA LLVDNF*RRRLRQPRLVNSNWAQAI LSSQPPKALELKT
6249	20150	A	6303	194	351	GTFCIKKPVQ/WLDTVAYTCTPSTLGG RDGRVT*AEFFETSLGNIVRPHVKK
6250	20151	A	6304	354	211	YRHNPS*LADEFFIFCRDSLPMELVL NL*QAAILLPQPPKVLGLQE
6251	20152	A	6305	1	346	GTSSQLISLHSSPTASYPKKHLHRLT ELLSVSLMAHVLVSVPATSS/PILOPH IYPTWIMFTSSSGSGKPSQCTHTHTYT HTHTRMCAHGSGHATLPP*HPLHPRHSA YLLW
6252	20153	A	6306	395	177	WLNTLWYIHTVDYFLAMKRSDDLHSPW MNLOGIMLSEKQ/SOR*HVV*FYLYNN VENKKSQKWRTVLWLP
6253	20154	A	6307	2	718	GVLPHYWGSRTPDV/HPPTSASQIAG ITGKSHRALP/KFAFLTSSQVMLTLLAH GTIAVVSFKLS*F*EPPMTCAVFSVVTG SCHINSFRIOCTCL*YYSVFTSCFYCSMI EKLTGTGS*CKEHELEFSCSDI PKLAY LIFFW/CVMEHSHSVSQAGVQWHLNS LQPLPFRFK*FSCLSLPSGGIYRCPDPH MANFCIFSRDGVLP*FGW/S*TPDLRM DPPGLRPFQSGADLTGMEA
6254	20155	A	6308	377	67	PPFPKIFFSQTLFFWGGCQPIAPPK KFFF*KNPQGFFFPKPKKIFFPDPK FLPPQKFF*KPP/LSFFFFFFFFFFFPF FFFFFFFFPTI*IFYSMSFLP
6255	20156	A	6309	1	362	QTYAKMHVTIIFFGVK/LTFLPQRLGL SGMPRYSIDYPAVYT*NLSCVGSFIS LTALILIFMIREAFASIRQELIVEEPS INLE*LLGCPPIYHT*EPGYLKPKRKR KESSPKLV
6256	20157	A	6310	2	411	VLFTLWEAGARGSLRARSRLQ*AMIT HCTPPWAT
6257	20158	A	6311	59	334	THACGNMLSYAGSFISLTAVLLITFMI* EA\FASKRKVLIVKEPSINLE*LYGCPP PYHTFEPPYIKSRQRKESNP PKLVSS QPHGLHDL
6258	20159	A	6312	3	22	KPSP*PLTGALLDLLMTSGLSM*FNHFS ITLLLCLLTNTLSIYQ*WRDVTRESTY QGHHTFPVQGLRGILFITSEVF*FF AGYFWFFTHSSSLTPPQI*GHWPTGI TPLNPL*VPLINTFVLLALGVST*AH D

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6259	20160	A	6313	11	182	INKM* I*VG*TSVIKK\DELSFMAT WMEVEDILLSKIREAQKVTHVPFSFIG S
6260	20161	A	6314	3	421	IQASTMAGAPPQASLLPCSLIDCCASN S/RGSGVGVSEPCTGYNLVCLLLRPS EKCSIRGV*FSRCRSP/TRKGHSPT PCTSRMR
6261	20162	A	6315	1	111	DKGNVFMFPANTASVLWPMQGVILNFK SFYLRN\TFSKYISAIDS SVSGGQSK FKTF*KGFTNLDAIHDSWEERIKIST*TG VGKLL\PTFRDDFKGSTSVAEVSADV VEIGREL*LEVKPGDRTELL*SVLWPMQ QGVILNFKSFYLRNNIF
6262	20163	A	6316	440	312	TSSFSLSF/QCDG/SLTMLFLVLSNS* PQAILPSPWPKVLGLQL
6263	20164	A	6317	5	404	PRYIMVKLLKI/ERNKILEAAREK*HFT SKGKAIWII VDLSSSEMEVRKNLNFQV LKEK/NKTWEVRILYSAKISPOKKGKIK IFSDGKLR*STFSRPTLRE*RKFSK* K*NDRRRLMLTKGRKKEYPKELK
6264	20165	A	6318	394	182	MFIVA/VFSKAKEWOPKCLSTDEWV/Q YM*YIHTMKYSAIKSNELVHVAA*IL FENTVLSERSHIWHGSHI
6265	20166	A	6319	1	378	AFSDFFLFQSLNKLNLCTHFSVVHNKVK TSLT*LNQWQFRLRDEPNWGHCL/QK YLELQGVKK
6266	20167	A	6320	286	314	NRCCEFLPTQVKCNFLVIGICCVCDNGY YRWLNF*NPIF*FILLRPHSVAQGVQW RDLGLSLQPLTPRPANFYILVEMGF/TP LRLVLS*PSLLKVKYK
6267	20168	A	6321	23	397	OKTLNMEKEMNIYTHKM*ITPNRSNIKR SSLRHITVFKSVKDKQRI/MKLAIEKQ PITYKETTRILSSEDFSAETL/NARR*WD DIVRYWLKSKKKKKKKKKRGGLKN SLGGPILTGGGKEIF
6268	20169	A	6322	411	2	TEFPFPGGNF/L*TKGKKNFLPPKNLG FFSPSPPLKFFFSK\P*ILGGGAPFC PPQKGFFPKIPRGVFFSP/YKGNLI FPPPVILGPPKVFVKGPPPPPPPPFFG QSQQVKLSPCK
6269	20170	A	6323	395	280	MLARLVNS*P/CDPPGLASQASAGITGM SHHVPOVNH
6270	20171	A	6324	3	359	QHYLVFRETIQIAAARVCHYIPTGMAKII KTGSK*Q*CGAAGTLHCWEECR/LK QPLMKTAW*FLI*MLCD*TVPLFIQIYPT EMKMCVCRMT\RVFLSVLFIASSWVK PKYKHLVN
6271	20172	A	6325	3	174	FFFTGPNFVNQAGGQGDHLG/LQPPPP \GSRIFPA*TSRVAGITGLNHHPLG IF
6272	20173	A	6326	265	13	TASPIRIITSDVLHS*AVPSGLKTD AIPVKLA/GTTSSTDRGV*VGCSEIC GANHSFMPIVLELIPKFIETGVPFTL
6273	20174	A	6327	32	259	CYYEHLCTSLCVWYHEFF*VY*EWQW PKYLSADEWINKM*YIWTVEYLLTIKIS EVL/SATTWLGLENIMLSKRS
6274	20175	A	6328	1	228	PGLNHCSSLSDHRLALQCFANPGYVF ETRTVLPGLVSNDDPALASQSAETIGV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
6275	20176	A	6329	346	1	SHCAQPFVCFHYCLTFPSLQ LPKKKKKISRGLFPFQPLPKKKKDKNEKS LTFSSSTMPGRRQWNSKIFKVLGRGKQPO QPRIISLAKLFLKSEDFL/ETQKLREFV ASRPALQAMLKEVL*REGK*YRSLFEKG RALK
6276	20177	A	6330	349	77	HTTPKKNKH/NRKKIKLVDLRYNKVDDN SKMSGLH*QCPDCECAGVFMASHQO/F DRHYCGKYCLTYCPNKFEDKAQCHGSLB FRSLRPANAT
6277	20178	A	6331	319	46	KPRRPFETK*ALNK*KDI/PMCSQWRKH TVMKLILSKLINRNPAITIKISTE\FHR NKLILATIKWCKGPRIAKTT*KGILKE LLVLISRP
6278	20179	A	6332	496	309	DRATAF*RGSPFTSL/RAGMQWHDLSL QPPPPGPK*YSCPSLQSSWDYRCPSPRT G*F\C\F\VEMGFHHGGQAGLELLTSGD LPASASQAGITGVSHCTWPNILNWK
6279	20180	A	6333	3	173	HHHSRL/IFFCVSLGTSSHYVA*AGLEL LGSSNPDLASQNGPITYGSHYAWPDIP VF
6280	20181	A	6334	339	153	FSPFPFPFGFFGFFPPPPPPF/SE*PLRG GGPFPFPFGPPVRPPSPVWCSPFPV VLASFFFS
6281	20182	A	6335	32	331	QLLNHSVIVFLLSFDHSYFLENLSLFLA FKLIGVKNS*YIILSFRYLLHP*HLNLF FFF/CKRQGLFVLRVNSNAQGCQFP WPPKVRGLRAWSPGLSL
6282	20183	A	6336	226	177	DGVSLLLPRL\GGAI SAHCHDLPGSGD SPVSA*VTQLQYVFCICLGLFTFTTRL SAYLGTGKLTALPNTPGLLDS
6283	20184	A	6337	302	59	KMLNTIMCNREIL/RKRKSFRVHOTSS VSYFKLPQPPQHSAASTLISQPPSSSK QDPFAAK*L*FVEGRLIAFPSSNVF
6284	20185	A	6338	197	28	AEKRVFSASVTHLWLGSHSL**SKKNL/W LGMVDHNCNPSTLGGRGRIA*AQAFET G
6285	20186	A	6339	46	317	EVPSSISSQISLFSQDFSSVPLEELSNI FPMFCPEHIVTCERVTNSYS/YKWKPF EFSY*IF/CFKMSLTMPLGLSINSWAQ VIIIPPOPEK
6286	20187	A	6340	4	276	QTTLRGTTVOITKMLSSSTMASRCEKK NL*SAWGWMNNYQPILYSAKISFKN GVEIKTFTN/KQKIKI/FITSITLV*EI LKEVLQAG
6287	20188	A	6341	485	2	GWVEFLETESRSVAQGVQWCDLGLSLQ PP\PGFTFPSRLSLLSSNDGSPPHPA NFFVFVFVETGFRHVSQGLDLMVSI* PREPPASASQAGITGVSHRAPKHSKI LIAGRRSIQMPFVKFQKLAVVENFQNI TKDFLPYSEILLHTSQIHSSC
6288	20189	A	6342	2	339	EDLRVKLKEGYENTSIYVNVHQDPMNL SNGSVTVVALLQAS*YLCILOAS*ASSQ SWTS/VTLAAVSFORISNOEHIPVYQQE ENQTVMTLLNGSKDDFLIYDRCCGLVY HL
6289	20190	A	6343	181	12	RWGLPSGWDYRSMPHFVNF*II/CNRQ DFTVLPRLLNSQPPVILLRWPPKVLGL

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6290	20191	A	6344	3	295	YVHLSCE*FLAITNKAANNIRLLWTCAS IFPR*RSRKEMAGS*GS/SLFNVRNCL TIFSHDCTTL/HS/HQQGGV/PVLFPF HQHLL*SIPLVFDLILIGI
6291	20192	A	6345	334	8	KPSNPGGEGFP*KKGPKVFSWGGKRENF SPKXXXXI*CPQKPKGPPWGAAPAKKKK NF*NPRGSPQL*KKRGIIQGPPTLIPSS QRPPPKKKKKK/GPPKGALLAFGGIKFF FFFLKKNLFFPKGKGTLLAPFFKGLPL PG
6292	20193	A	6346	68	256	WVA\PVTHTCNFTLGGRRGRIT*AQEF KTSIGNIVGPHLYLNKKKKKKKGEKPP GGGFSPL
6293	20194	A	6347	385	60	KKKKKGNRTPYDAAI/PSLGTSSKEFKSG SSRDICTPMFIA/AITKRWK*LKCPSMV NI/VCKMWFHMMQY*SAKKKEILS*MH LKDVMLSERMLSQSQKNFCMILLINGI
6294	20195	A	6348	234	61	CHRIEHTKMNVL/WLDVVVH*CNFSTLG GQDTWIA*AEQFKMSLSNTAKPCLYKKY KN
6295	20196	A	6349	2	358	FLSLGIHFNYCLVTTSKLSKLRLTYFF FFLETEFFPCSPA*RPW/PNLG*LKFP PPGSRTPALTLPTNNRRAPPHPANF GFLRKNV*FPFGGEGKTLDLGGPTRLW FGKGGNN
6296	20197	A	6350	346	27	KMV*SLNKAVWQFLIKLNIH*PYDSAVP LIG/IYPT*MTT*ITYKE*TMQLAAVSF IMAKNTNESNI*FNWIDKLWYIHMEY **AFKRN*LLINTKT*MKLK*LF
6297	20198	A	6351	36	158	KNSVFSQE*LYLL*ROENRLNSGGIGCR EPIWCHYTPAWAT
6298	20199	A	6352	2	146	RSSHLSLFPSSWDYRAPP/H/LANCCIF CRDR/SFTPLSLVLNS*IQTILL
6299	20200	A	6353	74	303	EPSCGGIYLSFSYTIKQK*/WFGAVAG ACKTSTLEG*GGWIT*AOFTSLGNMMK PCVFSKKKKKKKPHPGGGGRKK
6300	20201	A	6354	3	210	NNKIWTLNKLFRRDRVLCCFFDNSTA VHSRLTAAS/TLGLKQTSCLSLVSS*DH RCMPFCLALKRKT
6301	20202	A	6355	2	627	GRVGGFLVPMWRDLAASRGQGGQVKLGE MKPSVSCVCGGV*CSKFKLN*LWPG TVHTCSPSTLGGGGGWIA*AEFETSL DNMVK*PCLY
6302	20203	A	6356	584	166	RQGNHVAQAQVQWRDLGSLGPPFPFGK* PFHLSLFPSSWDYTRVPPLANF*FLVE TGFFHHVGOAGLEPLTSLDPAWASQAG ITGVT/HQARQLL*KELINPSTLGPTW ELLEAWGRCPVVMGDDLALNCFHIFSV S
6303	20204	A	6357	448	202	FTTLVSECI*DIHDSKRDV*ISTLTGAW KIWLIPTLVNGFEG\FKT*VEEVTDVV EIARESELEVEPEDVTLLKSHDKS
6304	20205	A	6358	3	237	DRSSL*P*PPGLK*SYLSLPSGWDHHR A*PHANFCLFTF/V*ORGLDLA*HDP PASASQGN*ITGMSHRAGPLTF
6305	20206	A	6359	49	242	SSYLSL*P*PPGLK*SSYLSLPSWDHK HA*PHANFCLFTF/V*ORGLDLASHD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6306	20207	A	6360	508	223	PPASASQSTSI TGM SHRVW PPLTF FVTQAGAR*LDLSSQLPFPFGKQFSCL SLPSSGWYRHVP/STPIVF/CIFSRDGF HHVQAGLELLTT*STCLGLRSAGITGL SHRAQOERGFEF
6307	20208	A	6361	2	595	ATVVG*GTHFLPFWVKPIIFDHRSPQH NVPVITGSKDLQNVNII PCILFQPVTSQ LPRI FTRIGEDYDERVLPSITTEILKSV VARFDAGELITORELVSQVSDDL MERA ATFGLILDVSLTHLTFRKEFTEAVEAK QVAQDAERA/RNSLATAGDGLMELCKL EAEADITYQLSRSNITNL PAGQSVLLQ LPQ
6308	20209	A	6362	1	259	LESFVFLYYK*SS*ELRLKRLITLFTF ETECPPVA\QLECSGTISAACHLCLOQS GNSPAPAYRVVGITDSFRITHCILTCIP SE
6309	20210	A	6363	60	221	NTTKLGMVAHTCNPSILGARGGRIT*V* EFKTSLDNIVK\ PCTPPKSLKIKLN
6310	20211	A	6364	1	393	RPRRPQTGQVQVQNGSLQPPHGFRRFS CLDLPSSGDYRHTPPCPANFSGFS/HHV GLKLFDSDDLWPWPKFVGIAHSHSKC T*RSRRGRRIADPLR
6311	20212	A	6365	19	85	CINSKIMQSSRITTLCKMVQPL*RALWQ CLIKNIPHPYDSAILPLHFYQCK*RH NPHN\TFTSMFITALFITAK*KQSKCL SIGQWKK*CIHTVQ*NSGI**HE*IN SKIMQSSRITTLCKMVQPL
6312	20213	A	6366	2	298	PPRLAKVQKFLFFVYLVF*DRVLTCHFG WTAVV*SQLVTLAHRNRLPSGWDYRH VPORLADFVFL/CR/DRGFSMLVGLVSN SRPQEV*ATSPSQSLLS
6313	20214	A	6367	67	636	QDNKKGIRYLFVYFQSFALVAQAGVQW HDLGSLQLPSP*FKQPSCLSPSS*DYR HAPPRPANFL/QFLVETEFHHVQAGLE LLTSGD*PASTSQAGITGVSHCTGPRI RFLKTFSHLEAPGGFFERKQPLRSERLQ FRAPQTPQCAHAYLLCGVSHLEMGCRN IDIPELSFELCPQCLTYRQSP
6314	20215	A	6368	3	251	RSRHCTAWAFLSTQHFYFVYFFFLHFL IGSLFIFACFVSSYFTEFSYCLA\VFVD SFGFYRYTMK*NLNSNYFKLSAAILPO
6315	20216	A	6369	333	193	FKKLVLMAKAKYCKANFFFGVFPVASKN /TGDLMREPPGWSQTPDLR*SALLGLPKS WDYRHEPPRLANFCI/FLVETGPHQIG QAGLALLT/S/GDPPASASGALE*LGCG SCL
6316	20217	A	6370	36	369	RPTRPEMRFHPVGOAG/PRSPGLK*SAC LSLSKCDYRHEPP/*PG*FSFFTYIYI YFFFLFSSFSLEEMGFHHVVKAGLELL C*NDPPASAYS DRIIGVSHQARPPFF FF
6317	20218	A	6371	2	375	DIQMDIRNIN/K/CSTSQSRKLIQIKRM *YHLTSVRMAITKKTHKC*ROGK\ LH C*WQCKLVOPL*KTQRVQKTENNINI *PSNSKN/WKSAC*RDICTAMCITT*FI RAEHGGS\PCNPSTIG
6318	20219	A	6372	75	372	NGNSQKKKKKKKKGGPPLKPSGGPNL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						PEGAKKSFPLKGGOKPPGGFLEKNPP LGGAPL\GPPPPPKRPRGKTKP*GG*R GKNFAPWLGSKKILKP
6319	20220	A	6373	605	350	ISTGICLGMETAALEFTIAKL\WKAT*PS FNR*KKMKCYTYASYSARK\DAILSFA ITWMNLENIMLSEISQTHKDKCCMISLI CAT
6320	20221	A	6374	167	378	KKSQGGTNIKPPAATKVLQSQWG*KKLL TGPLKKSLGGGACQVTILLT\NRFTST KINDPDGGGDHLLSQ
6321	20222	A	6375	994	747	VSLALSPLRLECNVYSAHCNLRFPGSNN SPASAS*VAGAHHTTQLTTFVLEVTGPH HVQGAGLELL\NLVIRPPWPKVLGLQA
6322	20223	A	6376	1956	1592	HEFENESYSVTOAGV*HDLGLQLPFP RFKQLSCLSLP\RWYDCLAPCLANF* YLVKMGFRHVQAGLKLASSDAPASA FQSAGITGMSHRARPKSAFKIAIIGEG GVSELHRKINI
6323	20224	A	6377	94	402	KTQELQNKISHCLIRRVDRKM\WLCTVA HTYYP\SNLGGQDGR\IA*GLEFETSLNI TRPRLYRKKKKKNVQAWPLWSNPLRR LRREIRAESKF
6324	20225	A	6378	463	146	GKLGPPKGLKPPPPPPFFFL*R/P/HPP PRGETPFFFKPKKSPRGGSAPPPFP GRVRPENFPFPRGGSP*PKRGPTPALP PGGQKETLPKKKKKKKKYMRLI
6325	20226	A	6379	3	207	LEYQVATQMTCTISRTQLVAEKASVPFV DKTVLS\TMGQL*EKAEDGFFVPG*YG LAVSPLKFQSTRP
6326	20227	A	6380	328	70	RPRRRLGLPRSDYRHEPLHPDQLLVEI MSHYVAQAGLKL\ITGVSHRAPH/YR F*LGHC*SLVRRPWTISYSLCLGPPMW EVSD
6327	20228	A	6381	13	77	VIFLQLQPFK*SSCFSLPNRQDYRVPY PANE*FS\CRHSLTMLPRLLF*TLGQAC ATIPS
6328	20229	A	6382	342	77	KGQGFYFHLFFFFFF*KDSFSLPRVEC CGEISAPCNL*LPQSNDF\ASHAVGG KLKQKRGGAFFS*GGGFFFF*MKHSV LNSSRN
6329	20230	A	6383	1	208	RGRVDKIYFLFFETDSQSVT*AGV*WLN PGSLQLPLPGFK*FS*PQVI\TCLDLPK CWYYRREPLCPVY
6330	20231	A	6384	277	50	LVLKLGKCKTSSFI*FKGQPIAKTILK XNKAGSLT\LPNFKNTYKATVIKT*YV HGH*YRHGFIISGLSILFH
6331	20232	A	6385	2	354	AAASTNFRDR/IL/LCHPGWSAVAQS*L TAVSTLN*AQIG\SSHLSSLNLDYRY APPLLAVALLCGPWPQNSWQVILLSQP PKALGYRCEPPCAPLLLNFFFFKRL WFCCPGWSA
6332	20233	A	6386	2	188	FFKYICY/CINMYMCFYIFINISLYL *IHIYKIFYFINTYL*YICLYIKY YIFYIR**YICLYIKYIFYIR
6333	20234	A	6387	2	241	WATKCR*G*RRGTGLTG*WDCKASGOL *KTPQOFLISITY\PYGPAISLEIDPS ELKTYVHTKTRT*LFIAASFIITKN
6334	20235	A	6388	142	429	YCVCIYIIFLYLFIPTCTFFYSLSHL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LIFSFFFFLGRGVCSFPRGGGGGKYLGL WRFFPPE*IKKNVYIYA\QQYSAIKQN EILSFAATWMELEAIMLSEIRQAQNDKH YMSLICIGIKR
6335	20236	A	6389	468	250	VHRTPTPCPTIFFFF/CRQ*VLPLPLPKL VSNWPQATLLPWPSSLTVEFQALTPGWK NFKKMLFWMVMSWSIKKR
6336	20237	A	6390	616	1084	LCLCQYAGISVQCPCDCVQFHHVNDSTY EDYLKLLKTSLSFFWRRSPALVAQAGVQ WCDLGSQALPPGPK*FSCGLLLSSWDY RHPHHPANFVLVYEWKFIHVQGAGLEL LTSQDPASASQSAWITGMSHRTQCE\Y FNLKLFSTSPGELLCLK
6337	20238	A	6391	415	200	SPPPPPPPPPPPKPPKPPPPPPPPPPPP *RGPPPPPPPPKPTFF/YFFPKPPPPPP /RFKNPKPIFFFFNRGPKNPGGGGGKKK PPGPGGFSPLWGPFPFKKPPPPPKKNP PLFGKKKKKKKKKRAAPR*NPRARGVF FFPPPLPLGWAPG
6338	20239	A	6392	3	117	KLKPSH\DY*VGETYGRDITSRGKDKP IAVCKTFSPLS
6339	20240	A	6393	3	204	DRVSLCRPGWSAVA*S*LATSNS*\VK QSYHLSIP*GSWDVSCVP*PPL*LVIL LRQPPKVLGLQA
6340	20241	A	6394	501	187	AGVKNVYHGLWOPPPPLKRSSHLSLPS S*DRHREYPCPANF*KIFF\VETRSHVY AQTSLFELDSNPPTSASQNAGI*GMS HCAQPMQTFSLVKIGTNFLIF
6341	20242	A	6395	3	393	HACGAINNSKPHAVTQYHTPLLM\SVLI TT\VLILLFVTILNDGITILLDRNRNT TLFYPPGGGDPILYQHLE*FSGHAGG*I L/LLPFGGTISHIVTYYSGKKPFPGYIG MV*AMISIGLLGIIV*AHHI
6342	20243	A	6396	101	135	FDSFTFGIVPGTWTIRSLNVYLTRLIT SPSLMPS*FLFIFFCRDG/SLTILPRLV SNSWPAAILSPQHKMLQA
6343	20244	A	6397	395	187	SSYLSLLIGTWSYRNVPPHPANFLFCRD GVVYTFPFC\KMGAMLPRVLNSWAQVI LL*PSKVLGLQA
6344	20245	A	6398	35	334	QNETLSKTKTKTKKKKKKKKKGGPLKK PLKGPKLTRACKKKPPLSG/WRKNNL GIFKKPYPGGKKWKPPTKIKSFEK KKF*REKGKQKQPNQC
6345	20246	A	6399	464	146	HQIREFORTPTTRMSPKTSLSHKIKK QLVMNKRSPFIKOWIS*QKPCQMARDD*H NIFTVQKGTNCQIR\ILCPAKLSFKNER ETKPPFLGKYKREFITA*FIKFG
6346	20247	A	6400	723	632	FFN*DKILLCHPGWSAVARSQPTAATF RVQ\QSACLGLPSSWDHRIHPSCLATF* *KRGFAPLPRLLSNFWAQILPFPWPPDV \LGLQA
6347	20248	A	6401	522	46	FFPPFLSFFFSKIPKQSLGLVFF*NK VMVFCPGWRAIR*FFPPA/APPLGSKNS /SCLNLPSTWGYRISGMVPPKAH*IPPE IFFFFFFF/CRQSLALSRL/VVQWQVQA ILLQPPE*LRLOVGRVV
6348	20249	A	6402	103	261	NIPPTCLIKKKKKKKKKKKKKKKKKKK KKK/IK*KKKNVGGVVKKKLGGD

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6349	20250	A	6403	146	384	GFPLSLSHKELSLFFLPETESHVPAQA \DLGSLKLPDPGK*FSC\SLPRSDYR RVPPGCSVNPFCVSPY*PG*SQTPDLR
6350	20251	A	6404	3	395	ETESHVPAQAGVQWNRNPGLOPEPFKKP RFPYLSLSPSSWDHRIMPPCPANSAFVSVE TGL/IHAGQAGLQLTPGDPT*TSQSA RTTGASHRARPSLKVFLISFVSSLLHG LFRSVLGSMLRISQVFFCC
6351	20252	A	6405	30	205	CLRLTRPAEFRTRKTHITREKPYECKQCG KFFSCSKSNLIVHEKTHKVTMTGIQ*VMW LFL
6352	20253	A	6406	3	444	ARKITGY*ISKTIIVFLYT/DELAKEIK KAIPFTIVPNK*DN*ELNLTQKVDPHK EDYKILMKETEQDTK/WKDIPISSWIRII NIVKVAVLKAIYRPSAICIKIRVTFKT ECHWKKIIGKVAHACNPPTLENQGRRL SLEARSRLS
6353	20254	A	6407	480	307	QHDSPSAKKFPQKPKDS/HPSSRS/HPF PPPPPC*TPPPEF*YPPKGEWGARP PPPG
6354	20255	A	6408	923	833	KAMKHFLIKTRAPFFRHVTAHLIDQSIK TELLVYTSFIAIFALLWYKPEML/WP GAAHTCNPSITLGD*GRTA*AQEFKTS LGS*NKTPC*CLSAV
6355	20256	A	6409	382	152	ECSGTLLAHCNCLLCSSDFF/SLFHN VSLSSNSS*VAEIIGLCHHVLI FVSAK LFLGRVRVNLFSPTPKMFPSK
6356	20257	A	6410	553	173	CLLIIRNLTFAKKKKKKKKKKKKKK AR/WPP*K*RA*NPVITPGGSF
6357	20258	A	6411	38	562	FLKQSL/DSARQSGVQWCHSSQRAFPF GLGRSSH/PASLAGWSAVA*SRLAATST FRVQVILLSQPP*LGQSCSITQUGVQ QWRDLGSLQPLPGFKRLSCLSLPNS*D YRRLPPRPDSSITFSRKFQSPQARNLP PTPELKQPPVPAPSPSEIHLSSWSSGNK CHFLNFLCP
6358	20259	A	6412	414	144	FFFETESHSAAKLEC/ISAHNHLHFGS SKSPASAS*VAGTTSVCYHAQLIFVFLA DTGFYHVQDGDPLMFCPPRPKVLGLP RLPLICF
6359	20260	A	6413	3	455	AEAGGLLEPRSSRLQ/CSQ*SHFCTPA WAT
6360	20261	A	6414	462	162	TQGPRLPHFFHAGPGGPVFLGWEVRFPF APPKPPPPFPKQ/NSPPWGGQPSI PPP LEG*ARKSP*PPKGLVFTPKGPPPHF GQENTPFPKKKKKVN
6361	20262	A	6415	499	0	HFTSKHHGFGEAA/A*YWHFVDVV*LFL YVSIY*GSH
6362	20263	A	6416	187	236	MCHINGIMQFFFFFFFENEVFFCPARI GN*/R/WPNLG*LKPFPGLTLFSLCTPP RSWKNRPPPPARVILFFNKKGVFPLLP GRV*IPHTPEPLATTNLLSVTIDLLILN VSYKWDHAVFFFFFFF
6363	20264	A	6417	158	412	SSDPSRRSLCSFF/CFFFLEREFFFAFR VWRGPNPCLLTPPPGKKHFFAPSLRG GSDYGHLPFGVPIPTLTKAGFSPCGPG GS*PPPPGKKHFFAPSLRGSDYGHLP GPVIFGTLTKAGFSPCGPGGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, _ =possible nucleotide insertion)
6364	20265	A	6418	457	11	HTGQSPYRCSECQK/AFTQKSAITNHQK PQCKGRKSMQ*LR1*ESFFD*SHQLRHN RSSMNTMIVMGPFGLTVGKEPYRCNEYF KPSFLKISLVYRRDLTRIIQGAHWPMP VISALWEAEAGRSLEVGSRRPANT
6365	20266	A	6419	103	376	SALSILIGITFFFF*IFLETGSHFTAQAG VQW/PIHTCDHSILQPTPGLKPSSCLS LLSSWDYRHVPVPVPTSAFCECTILRSQ SVAHTVLWKAAGGSLEVRSKLACATQ GAPCLTKKKCDPQD
6366	20267	A	6420	463	6	FFENPHKKQNGTQ\PPKPAQOQKYTA DF/QDPGNDPKAQYKKSPPAATYPAAS SSPSFSS/RPSTTAHVLRVPL*GSPD GLVGNRPDPGGAQHPOPDWTQKRPA HHGLQSLASPPGIS*EPQLAPRNSPHW TRDL
6367	20268	A	6421	1	479	RGFAVLFSAVEFPSSSKSHLDETSKPA YKHGAPCSAPGSLQASLPKGNRNPNFG NPPFLV*DKISLCCQGSAAVIOQ*LTVA STSPGSDDDPTTTPPPHADPTWDHRHVP PHPAFYIFPYRDR/SPTMLPRLVNSWA QTVCLSSLFMLPLSLWLSLSP
6368	20269	A	6422	11	242	FEITFSAVEFGWSHDGSLQTOPPG/SSD PPTLDS*VAGTTGLHHHAQLMF*LEVEI GSPGLKWSVSAESEPPLYPA
6369	20270	A	6423	488	335	SCQLPWNSTIGQRSGIRNLFPVIALK EA/EAAG*LEPRSSRPAAWI
6370	20271	A	6424	454	229	RDPPASASQAGITGVSHHARL/VSLFL IVM*AEGCYLSGIWTRLRKMNPPQ*RKE ROIQVKSTRSDIFFFYFLFL
6371	20272	A	6425	1575	1309	FESEHSVT\RTSCSGTIS\AHCSRHRL GSSDSPASASRVAGITGVHHHAQLIFL LVELEFHHVGDGLLELLT*VIHPWPP KVLGLQA
6372	20273	A	6426	276	437	CFHPPEFDWQMGPPPLGNF*IFWKRG PPFVPIIILNFWPKMFFAWPPKTLG
6373	20274	A	6427	445	240	RPRRADHL/RSVG\DDQGHGETLRRLK IQKISWVWHAGTLNPFWRDGSRLISA RTQMLGSWACSPGF
6374	20275	A	6428	114	450	LLLLLLFESEESCSAQA/PSAVL/WILL GSL*PLLPQFKQLSILLISIEWYRGLP PYDANFFKFLVEMGFHHVCOAGLELLTS GDILASASQHSQGITDVSRAQPVITFLK GLS
6375	20276	A	6429	380	224	LRHCLPTQAGIQROEHGSL*P*SPGLKQ SSHLSLPSNNY\GVKLPCPNKFOH
6376	20277	A	6430	509	228	PHNKGKRVSPPPPNFFSPSRNLGGGWL PKIPPPKRVFSKKDPRGKKK/PPD*KK KKNFSPPPFFGPPPKIILKPPPPFFFFF FFFFFFFFFFFF
6377	20278	A	6431	3	117	HSWEST*RRGACFNIFIAOFTIADIN *FMCLSGDE*IKKGLGIYT/MDCYGVK KKETMPLATTNIELKVNILSEIGA*KD KYHVF*MNR
6378	20279	A	6432	417	271	LSKRTKFRNSPOPFLECSFL*NDKX/WF RVVHTCNPSLTGGGRWIT
6379	20280	A	6433	385	145	TFGIKQSSCLHLPKCFWFCPEPHLANL NF/CKR*YIPIVNSKV*TSQEVFSYT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6380	20281	A	6434	65	383	UPHSSSFTGKEVITLFPKCEPQMFK LFPNLLKKKKKKKKKKKKKKGGPIKK KP*GDKIKTRQAKNFFPARGSKNQPG KFKKKMFWGKKMEKPP\KKKTCCKEK KKI*KKKSEKKPCIADEKKKGS
6381	20282	A	6435	3	454	EIQRTDURYVTK*TLDRHLYTLSEKSTL K/EKKKKKKFLRAPTKGGQIPPKKIP/I KLTVNF*KKS*REKWD\PIFNILKKKK F*PKIFYPAKLTFIREGKKKFPKKQGL GKFVTTAPLKKILTVLNLKMKKGYLF PONTLEYLAHNHP
6382	20283	A	6436	424	410	NFFFPFGGGGGGGFFFDKPPGPNPSSL FFFLGGGKKRGPPTPPKG/QTPPPGGL F*KWLGGKKETPKKSPPPFFGGGGKI FF*KPPPPGGGFF*KSPGGGGPPSVKK KKEKHKKKKKKKKKR
6383	20284	A	6437	3	214	EIDCCAAVWKQPKCFPSADE*RKKMWLY TMEYCSATNKNKIQSF/VNNKVEVEIM LS/KKSQAEEKHGIF
6384	20285	A	6438	83	420	QSFP*ISCRKYS/WLGAHAACDANTLG GRGGRAMGQKFKTSLGNLEPGPKTADP RTSHGCELRSSSYTYALTHGFSSTPETA RPAPLLPPPPPTOREDYKEEDLYDDLL NK
6385	20286	A	6439	163	289	KMYCYYYY/C*DRVLMLPRVSNLWAO EILPPWPPKVLRLQA
6386	20287	A	6440	459	431	DKRIRTRITPLAIRKQIKTTV/RKQLQ SHYMVVVKETNNK/CGIFIHSSWCKM VQLLWKTVSQVFKRLDLPYNLATLLIFI CQLQIKTLSSPKYLHMKVHSIIKIRKK YIKKNLKCPSDDEWIIKI*C*SIHTEM ERA*K
6387	20288	A	6441	478	36	VFGCRVILVEKFLCEPLRVFLRLGQ LEKSL/WNFHDLNLSLHKQPNRCVH QWRIG*RRKS*CSE*R/TWQFINSLT LIN*IPSCHTAMDIII IACH/ITHVEY YSAIKNEIMCFPATWVELEAIIIGBIT QKQSQIWRSP
6388	20289	A	6442	464	206	LVQRSGIHLFYSSTVPL*GL/HQKNED VYRNTRMFTAALFLIVQNK*HNYLQTG EKINKLPYIHTMEYFSVIKSNQHSIT
6389	20290	A	6443	414	216	CYIYTCLPTQOSRSWAT*ASSKEWIN KLWHIHTMD*Y/SSNKNKLGINTWTN LKSIMLTEISLT
6390	20291	A	6444	7	411	SPYCLHSFAPSRVSYCWNQIYIAFLDWL LSRNSNLHVPFW\WD/CKMV*PL/YETV WQFLTCLNILLHDSALTLGIY*K/DM KSYVHTKMCTQIFIAALFIKATWKNL* CSSVGWERNKLWYLOTMEYSSSVLKK\N ELSSHEKTWRELLERSQSCKAIYICIFQ QYDTLEKAKLWRO
6391	20292	A	6445	257	419	KSLPFFF/CW*ETGSHSVTQVRVQCNH IALQPTGPKQPSCLSLQGSWDYKFHF TQACPY*RP
6392	20293	A	6446	20	417	HOYCFASFPPFNNFFKTESHVAEAGAQ WIDLKSLKPLRF*FGLSLLSSWDY RCMPHLDNH*FLNVTGFHHVQAGLE LITSDPPALAS*SAGITGVSHRRAPVE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6393	20294	A	6447	371	3	LFLRRQGLRLLQNIIGRQ VIGCQFL/RKTKRYLPYDLPVILLCIYR/EKKNLCRH*TCSTMPMTALFIIQTH* KYPKCHSIGEWLNILNHIHTMEYYAEMKRNKLLIHEKTYMDKDLFGSGQGVYLKSSILSIKICIRQEE
6394	20295	A	6448	46	332	LGEHLRGGPILIKVCQVILTHQQYFESQWSIMALSNRKYNANCRYNKKCPNSYIKKEML/WPGAAAHACMLSTLGGQGRHIA* AQEFKTIKPCLY
6395	20296	A	6449	2	381	LCSLVFTHICSLIFLFFFFFKDRALLP/H/PCWRAG*SYLTASNGVAVQSSNL SRGKPLCRANFGSP/CPWFHKKGGPTMW PRLV*NAILLPOPPKVRGL*AAAHAGGQ GHDHTSLRPOTPGIKQSSNLSRGKPLCR ANFGSFWFLVLEKRGSHVAGASLKQSS CLSLPKLGDYRHEPSHRANMNFRLSPG LRKADCLPY
6396	20297	A	6450	2	136	KSQVCGWRCGG*IGAL/LHCWCECMVQL LQNAVWQFLKNCKIVPHY* PNAIKTATQRNLCAPMFIAALCATAKRC CK/PKCPISDKT*YTHTMKYDSA*KKCV LLARVWVNWSPVHCWCECMVQLQNAV WQFLKNCKIVPHY
6397	20298	A	6451	314	72	MLPLTNGSCRTKSVKDIEGLSNSINPLE LIGIYRTPFPKTAGTPFFFFFLV/PNGT FTKIDHILGHKTRNLILKMI*ILKYIP
6398	20299	A	6452	54	350	LRSFCSALFCFETVLLCHLGSVA* PRLPAGSSNP/CLPTPSSWDHRLVPPH QVFLAEFFFFF/CRKGVFFFLPGV* NSGVKGTTPRPNPCKALN
6399	20300	A	6453	368	172	WLTSVI/QRGRPRKREHRLPGA* LR*STHLRLPKYWDYRRSQCPARPVIL KEANMFLG
6400	20301	A	6454	1	365	NILKLNKLANNLVKEEVAREIKK*LV LKNENYTKDLNNEAKTVLHL* IALSA*RVSNQCSK*ASTLRNHHKSN LNPLI*QOKSITLKREKSMKPKAGSLI RSIKLIJRLT
6401	20302	A	6455	364	1	PETRSCSVNPRLGGVQRQDHGSLPPLSP RLKQFSHLSPSS*NRGMPPPCANLLE KFYLYIYL/FCLFVEMGGHHVSQGLKF LSSRDPSALVSQSVATTGMSRRANDWII LQOKCAATAA
6402	20303	A	6456	91	300	GHARHFGPRRWGDCLEPVEDQPGHGE TLTLQK/KKN*PAWHTPAVPATQEQAG ITGVSHRARPCCPN
6403	20304	A	6457	2	195	RFSCLSLPSSWDYRHEPPRLAIFFF/C FWNFKRGGFPLWARVNSNS*PRGIGLL WPPKGWGLRA
6404	20305	A	6458	522	202	TRNWRPSLQIFTAALFLAKKWKQPKCF STDEMIHKMWYVHKMKY*SVIKRNEVLI HSA/KWMNFENMLNEACWERPHIV* LYEMSRVGKGTGKSRLLVV
6405	20306	A	6459	377	161	EMNFKCPSTDK*VKRYR/LYIHTMEHCS ALKGNEVLIHMTWMNLNINLSEKSC SQNTTYSMITVVKCLE
6406	20307	A	6460	92	484	LQACFLRTVLIDYKRNWAEKGNVGRVCL

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						MENMTVIIIFRDRVLL*HPGMHVVRSQ LTS/VKRSCLCKPPKC*DYRCILCQV EIAFTHRSFLNSFLKRSRVILLNWKD PSLGFCSYDSTGMALLNFS
6407	20308	A	6461	483	192	MGLMLILRANPOSTKKMKICLLKKSITF LNCIVLSNWPCTFNMVIFVCVFAVYKLH VWAE\ PVAHACNPSTVGGQGERTA* AQE FETSLGNIIRPCLY
6408	20309	A	6462	451	98	KQVWOLL* KQVWOLLESLEMKLLYDLAV LNLGAYPREEKTHVHTKTCTQMFTAAPF I\ IKK* KKNFSIDMKYEERDKMWTIHVT QHYLIK* SID\ YAPTWMNLENIMLSED SOTQKTHCIISFI
6409	20310	A	6463	395	67	FLRFWCTHWS/DILYFVCSLLSLNRS HSFPRVHSPLYHSYALCPHSLAPTYE* AHKMF/RLVNFLFLVETGFRHAAQASPE LPSASNPPFSASQAGTTDASHRAQTK
6410	20311	A	6464	485	220	FFPETWSHVSQARVQWNCGLSLKPLP P\GSSDPPTSAS* VAGIAGMSHAPTHEI PSIQARQOHLQGEKKIELLSLPTSASQV LRLLA
6411	20312	A	6465	1	371	ISIPFKYLRLINLTIVYQGLYEONKYKT KRNQSSKKRRDQSRIGKLNIRMSVL SNLIYSFNVLIVPASYFVSIT/RLIL KFT* KCSRPRIVPLFHLPLPLVPFVCS FILCRPGASLVK
6412	20313	A	6466	489	175	YRTIEISRCIK/GLL*LMETTHLFESHPI WRRGMAYEKNADFLRGTVAHAFNPSTLG G*GR/WNQGFKTSLANVVKPCLY
6413	20314	A	6467	2	367	FGTETLQAGIKGDPGEKSHNGEGLHQL REALKILAEVRLILETMIGLYGS*LTEL PAAAGSAGAPGQTGHPPGSHHLA\EPFL GSGAGPAGTGTPSLLRGKRGHATNYRI VAPRSRDERG
6414	20315	A	6468	472	260	TTLGGAGNSGYRHQPHVANYLFICRDR /SLILLPRLILNS*L*ALLSRPPKVLV LQT
6415	20316	A	6469	88	435	RGVLLHMLSCPLCKTCFCSSFTFHHH* TSFSFSFFFLGNKVSFYCQAGQGQPN LG*LKLPLPGLKQSCFT/LPEKWE*QT EPPGPVVRHFGLSYFPLTRG
6416	20317	A	6470	34	106	EFAIFFLTITYPELINTHVHTKICI* MST AALSTR* KSPTCPSM\ INKMWYHFMFY YSAISKGRNHANVHQIHKM*YIHTVEY YSAIKSNEALTYATTW/MNLENIMLSER SQS*KICI
6417	20318	A	6471	390	92	DFLIDAINHNKLVFFYS*FISMC/HPYN *SLSFSNIQSLIKTMINVLSFKY*YL ITYFS*KTTE*NRGLTMLPRLLSNSWA QALLPWPVKLEOV
6418	20319	A	6472	414	167	RHHIKTCA*IFSA*ETIAKK*KPKCPT ADEWINKWVYHTIYZYSAIKKNKLLI PMMLENIMLSTGNQOTOKATYCMIPFI
6419	20320	A	6473	3	244	FTILLGTYDALFSLIYTYTFVTKELL TSLFL*\IRTAYPLRYDQLIHL*KNP LPLTLALLI*HVSIPITISSIPQT
6420	20321	A	6474	12	224	IASGRPFPCYDVCV/WKRLCRHSTVIM *KKKKKKKKKKKKKKKKKKKKKKKK

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6421	20322	A	6475	417	155	GGALKKKPGGGEPLFPFH FQSFTENKMLSSITCSSEIFGERKSQL M*RPSSL/SY*EKLPLLASTTIVISQRPS AL*VQPL/PTAKNL*LTAGSKGHYYFLN SKVFSN
6422	20323	A	6476	1	131	RTPPTRTTRGRWLTFVIPALREA/EE AGG*LEPRSSRPANAWI
6423	20324	A	6477	830	513	WNSVKESLPADTWFLPFLGPLIDIFLLL IFALCLVNLVLFVSSRLQ*FHVMMMLA QGQRP*TPSSDPEDKDLLPLSLLEQVS/G ILPLOC*AGSMITTSAGSSYER
6424	20325	A	6478	399	196	SKGSSHLSLIS*KYRCAPWNAFF/SF FLINIFCRDE/SLTMRPLLNS*PQVI LLPWPPKVPCLQA
6425	20326	A	6479	1	411	NTGIMPANTVSIILLIDQEVLVIVTKCY LRNTFCGSDGSGHSU\QTFWIGSTILD AIKSL/R/DSREDKSTLIGIRKK*TP IIMEDLVGFKTSQEEGTVDGLNLA*ELQ VEGPRDETL*PODOTCMDEKFLMDE
6426	20327	A	6480	381	162	AGFTTHNFFFL*DMULLCHPGYSVVQ SWLTVASNSW\VK*SSHLSFPKH*DYLQ AVHFRMASNSPGLVLLQ
6427	20328	A	6481	379	85	SILFPLFHINIFFFFF*AWIFIIPPH \RAFKVVRVVGFFLADSVNFIKRLQYY FFFFFFGGFFFFFFFVFVFVFVFVFVF FFFFFFFVFVFVFVFVFVFVFVFVFV CG
6428	20329	A	6482	355	117	PKVKIFPPPPPLFRKWDPGRPP*SPGTNF SIFFLVEKDFPHVAOAGLKLDDSSSTPS VAS\QSV*ITGMSPHAWQLVLLSL
6429	20330	A	6483	402	97	TAFLHLDIYHKS*KIMFTNQPLKCPLE IIAKN*K*LKCPRRADQIWA/WCIHTI EYYSARKRNVLKRYTRLMMNLKSIMLCK RSQSDVTYYIVIFICH
6430	20331	A	6484	714	365	NGFALVAQAGV/QWCDLSSQLRFLPFIFK QVSCFTLLNS*DYRSMPPHPANPCIFSR DGV*SYNSWSLTPDLGLKCCDYMRBP PCPANAKSFTVEETHVTQAYETMLLSD HDESG
6431	20332	A	6485	408	146	LKTETQTETCPMFIAALFTLV/RRWNQ PQCLSTDEWISQ*YICIMNINSIDIKRN EALKHAVICMNLKNMVPFISPEKGKKK EKKK
6432	20333	A	6486	243	11	GMSQYQYKSKNFLLSNRVLCHPGWSA VAH/SRLTEALNRFK*SSCLGLPLKWDY RRVPLLLAQNATR*NSL*SCPA
6433	20334	A	6487	403	161	DMVSPRPWPVWSONS\SLK*SAVLSLPRC WDYRRFSCQASRNTSIRGNRKNQWNT CMYLLFILIPLLKMYCMNORVMEYFPT
6434	20335	A	6488	292	24	DWRGRMAIPLKKGSK*QCCRNLTGLRY *W/MECEVAQPLQEMV*WFLQRLNKLKS YDPDF/PLGLIYPKE*KAGT*TDICMPM LVATLFSG
6435	20336	A	6489	3	203	SSWDRCIPCLANFLICCRDR/SLTML LRLVLNS*TOAVLLPWPKGMPGLLFFV YGGIVLSYVNIS
6436	20337	A	6490	413	30	RGP/YQPGFLGFSPPNGLGFG*WVFLPL PPPPRKGKGGKSPRARGFGQAPPKKE

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						NQGGGFWISGRLAKKIGFWG*GPAGK KKFFFLCAGVWGLKVLIPIKKKKGFPF DPLFFFFFLQTHDIRG
6437	20338	A	6491	101	335	SSSFLGFPKYDYRREPL/WPS/LWQFF RINIHLVNPSPILAVYPREMKTCDLI KSCMRMTVAVF*ITQWQPNVF
6438	20339	A	6492	532	127	STVFRARQLPCLHEPGRQSSPVPVTSI LYT\PLPFPSSRYQONGPCLSPKLSPS PELGTQSPFVHKSFSPCLSPKPLTVPP ALPSTGPSQSL*QKHSLSLLHSHTP PAPSCNPESWGLDATAISTCFYG
6439	20340	A	6493	399	1	LCAPAPRGVYRGR/ESSLSWDGLHSVOA SWFLCLPTPASAMVDAPPA\SLPSRSS ILDCCISSEQSGVGMGPAEPAG*NLIV CCLLRPLEKCSIWAGVSRFSWYLSQLP LARKGKSPNPLSFPNEKMPRPVS
6440	20341	A	6494	319	75	KKIWGFLKKKGLQTRRPKKWFKPRPP FFFFFFFFF/HVAIFLLPCRDG/LA MLPRLILNSWP*RLIQFWLPKVPGLQA
6441	20342	A	6495	333	190	LPFFFFFFF*GFFFFIF YSFRDGVLLCHPGWSAAMPS
6442	20343	A	6496	1	299	LPRLEYSGTTTASNSWAPAILPPOLIK/ YNNFCCC*GRVLTVLPRVLNSRPQIVL PPPPPKSAETIGVNHVWPKKIISNEKT THCCSALAKQIIS
6443	20344	A	6497	51	266	PVNVILPSSWNLRHSPPCPARFVFLCL LFFGRN/RGLAMILRLVNSWP*VILFP QDPE*LGIGVQNTMLSS
6444	20345	A	6498	366	78	LLAHCHSSNNKGLITLDFNFIYHYGSPN TVTS*F\MSSIMLILSSP/*GTWSY LPYALKKIFCKD/RGLAVLPSLV*NSWP QVLLSWPPKELGLQV
6445	20346	A	6499	37	396	FPRPRTPKSSSPAKATQNTISFKKKKK SKOKKGNVTIIRVKNQRKRQKN*KLK Q*N*EQ*KINKISKPLAKLI/KKKRVKT *IANIRNERSIIT*STDIKRLWKYY* QL
6446	20347	A	6500	706	394	VPLLLPRLAVQWHLNLSLQPLPFGKRF SCLSLSS*DRHRTPPCPA/NSFVLVE TRLHAGQVCLKLLTSG/DTPPSASQSA GIKQMSHRTQPIELFYVFF
6447	20348	A	6501	403	216	ILNVLSFK/NMLY*HYTTVLRTVRPLSP R*ATVTCITYTSGWPEAEDPQKMTFPHC DLFLPHFN
6448	20349	A	6502	377	116	LLPY*EN*FLMYLPPTCCLPFDGNSGF CHQKKNFFFFFFFFKTSLSVA/RLECGGAI PAHCKLCLLGSSDSMNFLNEAEFFNLA FNGL
6449	20350	A	6503	3	401	CVQHLRASWSSRWAWAPHSSEQPAGP AAPGNEGLSIRASGCGGCTGYPPSASPP ALCISIS*PRP*LPSRRAGLATCSPPCLS LPPPKAPVRPEPRFVPPPAWPRVPS TTQGLRSASARHTQRLHLQ
6450	20351	A	6504	406	55	WKGFTTPTPRFRKEGSPVPPPKVLTLE *TRQPGOTKPPFPPIFKLTRQGRPP* FPDPQVRAGKPP*PQSFVPGAIFPP DPPLKGHPRPGQKKKKKERKERTPK RGGT

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6451	20352	A	6505	3	281	FFFCDDVLLCHPGWASAMVRVSRRLTATS /SFLGSSSDSHACLSSSDWYRHLPLLAN FCIPLKRGQFTMLRPVSNP* AQAMRLP QPKVLGLQA
6452	20353	A	6506	1	247	LGSLOPPPPG/SRHS PASASGAGIADIM SHRTQSI VFLRTNNKP* IENMMITIS CTTAYKYELLRHSFNKICARSLYEKL
6453	20354	A	6507	34	47	FDENLTPRHRTILWAVNKERMLTASRK KKQII*RSSNLSGDRLLNEASWEP*CK KSMOETIQATEGWNDIFKVLKEKNL\H SKLCPAKLSFYEGEVKAPPHKPKWRE FTVTKPLLOK*RNQRTDLTOI
6454	20355	A	6508	403	106	HYVPPSPSPS/YFFSPSGKRGFFPNPF ILVSPGPFSPPLF* KPPPEFFFPAPLKK IFPSDPRELKFFFKGPPPPFFFFF
6455	20356	A	6509	389	230	LSFFLFFFRDKVSLCNPGWSAV/VTFELK RSSCPGLPK/SQSHCLTKPQPGF* KYIYF SFFIK/KR*SLTTLRLVSSSDQVHS ALWHFKVLGL*AVAHAYNPSTLGCQSAE WIT
6456	20357	A	6510	101	419	ISFFFFFFFFFFLKKFFFPFGWRGGEF* LPQTPEWVKIIFPPPPKVGGFNSPP PPFPPFFFKEGFSPVPCGPFKTNPKK/ SPPPPPPRGVGLGGWPPPGWDP
6457	20358	A	6511	41	376	EWNCBTRGGAGGGRAGGAGGATGRVLA IQARKRRPKREKHPKKVSCSVAQAGVQV RDLVLLQLPLPPGLRVSLCHPS/NECGGV VSAH*NFCLPV/IKDGVLPCCAGWS*TP GL
6458	20359	A	6512	2	332	NEVKIATLTGFWK*LI/SGSSRTLMSG FERFKTSVEKVIADVVEIARELELEV ENVTLELLQSHYKTPGTLAFSLSPDVS L YSQLPETRSHWEQAASKIQPRKASTSQ
6459	20360	A	6513	3	294	FFFFEMESLSVTQGVVWHNLGSLQPPF PEFKQFSCLSLSPSSWDYRHAPHLA/NC FCIENRDGVLPFC*LGWVNSHLGFTGMS HCTOPLIALSLFG
6460	20361	A	6514	1	526	FRLGKPKW*GVN* PWSRGEPSGVAB AG/RS*SAPRRLHLHPAAGLATLSAGS RRSARWKMERASGLSPGGLGATSRQMS PGTQLANPPDHGDKDCLGRISPGSGQI QAAGQLPGPFTSLAPAQGRRLSLTFWLG QTPHESEPGIGHLQAATEAVLPSTQN LITKRNLM
6461	20362	A	6515	747	451	QAGVQW*DLGSLQPPPGFK*FSCLSLP SGWDYRYPNPANF*FLVEAGFHFG QAGFELLTSGGPPASASQAGITGMSHH TPLGVHALVGENIQ
6462	20363	A	6516	444	3	PGGGGPPFPFPWGGKPKGIS*/PFGGGG SNKPKLPCLPPGGPK/GNPPQKKKKKK GFGPGVVAHCNPIIPALWEAARGLP PDAGRYGPGGRREAVREAGPQEQDPE GQV*GDPRGCGAAHAPARGHPRKA* RGA EGSSPGLTK
6463	20364	A	6517	257	575	ASSVTWAGVRWCHLGSLLQLLPGFK*FS CLSPSGWDY/GHAPPGPAKFCIYSGDG VSLC*PGWSOTPHLR
6464	20365	A	6518	337	389	SGHFV*ISCLHDMPALASQSAGITGVSL

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						EARLIFTERWDSQCVPOAGLE/PEPELK RSSHCGLPKWDYRHEPOAPVCRFIRA TKCAVYSTQALSPADVOPGMTTPAKRGL PCQPPGSPCPSLCHIQIAGTPEPYE
6465	20366	A	6519	61	323	FMWDRVARKGSTEGASLEPLGSGVGGH GSCISMVVGALGHSS\THV*HTHTHTHT HTHTQTNTHTPSSDSKSSILDKEEAG CMTP
6466	20367	A	6520	399	101	KIGIKATMKY/HNIPIRMGFPPFKLSSQG /C*RCRK/IYTLKHQC*KCTVWPLWK SVW/RVFLKLNHPLHSPFPLPLGTYP /DMKT*TCM*MTATLEITITS
6467	20368	A	6521	1	276	RTGRFEGRLFFLFGFFGTVLCCPGWSAV E\QSWLIAASACLW\VK*SFCLSLLRG WDYRCIPPCLANF**R/CGSWAQVILPP QSPKALGLOT
6468	20369	A	6522	280	277	GDDPSCSMGGGHCLASRSE*GSVGVGPS KPGAG\YNLVCYLLRPLEKRSIRVGVS QFSRCHOSWLPFDRKGNSTPTCTYWR
6469	20370	A	6523	2	327	SLFSS*D/YRHFPPHGNFRIFCR/SAL TMLFRLVSYSWQVILLQPPSVGTST SHCPQPCIMFLKADLNPVRCQFRCALAP EPIYIQDPFLRDVAFPCLGASAPWHLA
6470	20371	A	6524	298	414	PGPQSEITLTKKKGGGRLLKGSNTFAGM EGNIFF/CFPLSKSHSVACARVQ/P*W LTAGSLQAPPPFKLSPLSL*VAIYAS P TLSS*DYRCTPRLANFCIFPDGVS CRSCAAVFNLLDTRDFWGRQSFHRLV AGDGRM
6471	20372	A	6525	376	180	KCKYPGGVAHACSPS*DYRNVFP/RFG YFLHF*QKHFGQAGLDLPTSGDPPAS QSAGITGVSHRTOPOLNYF
6472	20373	A	6526	415	86	LYLPPYDLAIFPLGMYPGRKKCAHTKIC TRIFTVVLFIARK*KRSKNPSTREW/I KMWNIYTVESHSVIKRELLIHASMILV H*/WMIFENILSDRSQMKITVMPVFF T
6473	20374	A	6527	391	166	FFFFFRDWFSLSHPGWNAE\S*LTVISN SWSQARLIFKFLKLRQGLNLLTRLVNS RLQGISSWPAKVLGLQA
6474	20375	A	6528	544	176	TMRYLLTPVGMATIKKAK\NT*C*CGR E/IGTL/LQCR*ECKLVPLWRTVWRFL KKLAIELPYAPFFFLSLEYGLFLSGSTN CAQLRSVYRKAVQNHOGVSGCAGFODS SHSAPVAIPTAQ
6475	20376	A	6529	392	139	TYVMHCK/WLGMVAHAWNPTLGSRGG QIT*GOASTKLSSHWSGLSRRESRFWLECY SRSCFSCLRPADCTSLTDSKQ
6476	20377	A	6530	362	87	NGPPPPFFFFGEIDKLLILLWKCK/RPK IAKTVFKKKNVGGLL*HYFKAYYKGT V IKLVQFWHVRKTDQ*SRRESPELTHI VYLVNARDSA
6477	20378	A	6531	1	346	AEFRPLKKTLSKLTNTLQLYDPAFS PLSVYPREMKT*RA*FAKICY*MFMA SLF MIVTTQ/NVPRCLPMGEWLNKWR*FIT *YHTGMKNT\VMHKTTWMNSQRI MLNEK SQSLTY
6478	20379	A	6532	3	294	FFFFRDRVFLYHPGWSAVV*S*LTAA LS

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						PWLKRHSHLSLPGS*GHRMF/PPHLGNF FV\FCLFL*QQCLAMLPQVLRSPQVI FLWPFPKAVLGLQV
6479	20380	A	6533	2	280	PRYLVRNPPTLGGSCVTVDK*LSLWASV LYIYIYTHHTDIDYRKIYAF/IFVCVYI YTFI*KHITYKEQAHAINDAEKFDLPS ASRWGKLVE
6480	20381	A	6534	96	183	DOLNVFHRKRLRYDTYTFVALLARHGG SC/LSLGS* D*RYTPTLQTH* K*FFL* ISLPMLDWLVSNWPAQAILLPLPKSSG LEA
6481	20382	A	6535	2	241	GFKRIDSNFSSVGKVTN/TIFCERKS LSMHQI/SLSYFKKLPOLPQCSAATTL \IS*QPYTLKQDPPTTLOPAEDSDGY
6482	20383	A	6536	485	97	PTTRPRLILLGPTYK* LKSWNKSDCFPM FIATFL/ILKCPSTDKKLKKMVKHTTD YYSALKKGNA/YM*QOMLEGIMLSEV SQSHGOLLHSTYVRYLK
6483	20384	A	6537	411	57	LPFSHIKFVLSWQSCFAKTSGPOTPSFF FF* LFFF/RDRVSLCHLWSAV/VSWLT VASTSQQAQCLSLPSSWDYRCPPFPAN FSRRGFTILPRLVSNRAQEICPPWPSK VLGLORRGI
6484	20385	A	6538	438	201	TYKEMKT*VHTKTCI*MLIATLFTLAR KWKQTKCSSTDENKMMHIQ/IMEYYL AIKRNEAQLHGETIMLSERQSQ
6485	20386	A	6539	466	131	SFPKKGGRAPPPPPPPPPPPPPPPVEA VLSLCCPGGSQTLGLKRSALHVLPRK*D HRHKPPCLASN/SFNNRHRMTNCLMC IKSWCLCI INPFFHLDSLLMWSLIYR
6486	20387	A	6540	419	50	PLPFFPKGPRIF/CLGAPKKKI*VPT/L REIKLFLPKGPPFLFFLNGKPLCFPGRK GRGVFSLATPKSWGQKIFPPSKEGASF PFFFFPFS*EMDITMLPRLVSNWPHV ILPSQPPRVGLQV
6487	20388	A	6541	1	341	STIKTAREKCLVY*GTSIRLTGDF*KY I/SARILQVRRQ*NDIPKVIK/IRKNCP RIQYPAKLSFINERKIKSFPHQKQLREF ITARDLQEMIKGILVLETKE*YLP*S*K HMKV
6488	20389	A	6542	409	290	NCKQFTCPSTNEW/IKL*YICITEYSA IKRNLQLHTT
6489	20390	A	6543	32	397	AMIVPLQASLGNRSRRTLKSKKKKKKG EKETLPGGST*KEKVRKKQNNLLV*KTH IKPG/AGAHGPNPNINWGGGROITRSGN KNHPG*HGKTPFLQKKKKRGAALLKGTNL TARGQSKTF
6490	20391	A	6544	402	0	LSWTQ*CKPIAPATGEGGTGGSLEPRES RLWCAMIAPVNA/NCTPAWVT
6491	20392	A	6545	1	365	RKVTSLSFSTRCLSLPHFSDGPRPVK LQ*LRCSICASLPTLHHTARAAGILLP \LASSTAVNQ* SRELGAACVKEHSGIK YGLF/RD/RGLTMLPRVLNWPQAILP GQPPKLLGLQA
6492	20393	A	6546	1	331	ISTFKSYLRNIFSKAIAAVDSNSTEGSG QG*LKTFPWGYYIIIDAIKNYDLNKEGK TSTLPGVWK/LDDPFG/FUTSVEEVTAH VVOIAKELEMDPFDVTKMLQSHDTN

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6493	20394	A	6547	1	417	TRFKINKTKLFFERINKKKP*VKLT KMKNKTPHITIKINESEFAFTIEKLS LRE\YMNVCVYNLYANRKPQMDKPLE RYKQLKLTQOETETLTD\YITSKEIKFV I*NFSTK*S*GPNGFNSEGRVWLFPTV
6494	20395	A	6548	410	288	AHFLFFCINK\SLTMLRLV*NMWP*VI FPPLPKTLGLQV
6495	20396	A	6549	1	216	IDRGFTMLPOLVSNLS\KRSSHLSLPK CWDRCRCPCEACPFHFLSECNTCIKQQL HVTLPFPNT*GLTSEG
6496	20397	A	6550	479	146	VPGFKFSCSLSPNS*KYQRAFPCCPANG FAFSVETGPFPHVGAQGF*PPTSGDPPAS ASQSAGITGLSLHAWP\ENL*KRLHAT GLRLHDHVP LKVPNYLKVCFSKFEIADV
6497	20398	A	6551	42	484	SMRKNMNVTIMPANTTSI PQPTDQEV SVFNS\YYYYRYCKATAIDSNLGGGS RQSKLTKFWKGLTIIYAIKNICDSWEEV KIST*TI*KKVIPTFMGDFGGVKNISK\ EITADVAEIIAR*L*LEVEPRVGLTPIVI PALRKAIEVG
6498	20399	A	6552	304	74	HTGKAARKKEC\WRGTVAHAYNPNTLGG *NGWIT*GQ*FETSLINMWKPRFYSCIC ISGYTHKVIHRIIICKGKKLE
6499	20400	A	6553	432	62	FWAGNSRMQWCTDT\VSARCSLDLGS SNPPASAS*VASTTGAHHALMLITMM EKPLQARYCKARIFENKLSIYPSVPT KTNAHVSKRSCFSDHPDGHYIYLS SGLIVNKIGKVK
6500	20401	A	6554	2	174	YCNLCCLPGPSDLPTSAS*VAGTTCMCHY TWLIPFCI\LVETGFYHVAQAALFIYS I
6501	20402	A	6555	3	268	DAWADNICKR*GYGAI*TLIHCWNECK\ W*ATWFLIILNMLLPYNPMV\PRTC IQIFMSTLFIINTKWKQPRCHLVGEWIN CGTCR
6502	20403	A	6556	3	402	DAWTDNIQCR*RYGAI*TLIHCWROCK\ W*ATWFLIILNMLLPYNPIIMDHK\TC LQIFMSTLFIIDTKWQPPKCHLVGEW/I KLWSMPAKYHSHWARTL\I/P*NT*R RLSCT*LWEKSQYEKATYCVVPTV
6503	20404	A	6557	396	2	KKQNAFQSPSFLPRL*TPKITILISFHN IYIYHTYIYIHVCIIFTYIHTHYIFF/ RDRFLCLCPGWRAVVSQSLTAASQQAQ GIPG*FFFK/SIPCRDW/SITMLPELVS NSWAQAIPPPWPKVLWDYRCGS
6504	20405	A	6558	393	175	FKSQGLVLLPRLPFSGMLTAHCSLKLPG FSDSLNSA\SQ*LG*GCTATPGPYLL IYAGELGNKRSISSK
6505	20406	A	6559	401	188	SPPEFFILGGPRVFPFPPFLKPPPRI*F WGPKKKNF/CPPEPKNPF*KGPPLE FFFFFFFFFFFHRS
6506	20407	A	6560	37	343	YEPAVLLDIYFKELT*AHKRCRTRIL IASPEKTVKMWOPD/C*ADE/WDK* TACLOVE*CSARKKSELSTM/IDMWKRL KCVALSERGSEQAACYVIPTL
6507	20408	A	6561	792	141	LEFPDPV\YSTSRNAGA*TTSTPLPQPL YHSPRRQSGTKPPFFSKK/PEPSP/S PNKFYDGNWGVSPFFKPPDPQKS*GPK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
						KSPLPPEAF/PAPPLTQDCPPFVSNPGG KKKTPP/SAKKKKDTPPS/PSPPPRH* I GGPPGFSPPPLFKTPPPKLLGPPKKKK IFPPPGGKFFFLKGGPPFFFFFF FSLFPVGVNSRWLRSEADLCGECYSS
6508	20409	A	6562	1	356	FFNFIFITLYL/NFLRWLSLSPRLNGV QWSDGLSLQAPRPLMPFSCLSLPSSRD HRRPPRLANFLYF* *RWGFTMLARMVS IS * PQ /CDPPASASQ/STGITGCHGTR LIPRNPMA
6509	20410	A	6563	416	84	LSLPSST/DVRRPPPCLANFLYF* *RRG FTWVSS*PHDRPPTSASQAGITGVSHH TQPIISFLKSFPTLSNRFRVCDSEL LLQCKDFYLOKPNLHIAPOEYTHCHGVH Y
6510	20411	A	6564	2	51	FVVREMQIKTVLRYSFKLVKIKK* DST FFWKGC/GETGNLHKANW/R/ST*OYL KKLYVHFLFVPVIPLEIYLNKKILST K* LFAVFIIVTEK*KKRCG*T
6511	20412	A	6565	2	511	VVR/SCAGL/LHTAV*IFGRTITSEKCA QOVDETHRN/LORLQPALNRRKGPILLH NNTCLYTAKPMLQKLNELGCEVLPHLSY SPDLSPTNYFFNHLDNVLOGKHSHTQON AENAF*EFVKF*SMDFYATGINKLIS/H WQKCIACNGSYFD
6512	20413	A	6566	3	248	GDICT/SMVLVPAFLTVPK/TWNPVSTIS K*TDKMWIYIPVEYYLAIKTKFC/SFS ATWMILEDIMLSKPGTER*ILHVLVLCG R
6513	20414	A	6567	3	258	WRDHSLHS*PFGLKWFSLSPSLNNDY RDVPACANFEKVL* K*GLIMLPRL/LL SSPFEW*ILSSRLPASSFQSGVITHMNH CS
6514	20415	A	6568	392	166	GGGGPPRGGGLEPPGGPPFFFLKNNK*/R PPGGGPLFPFPPGGGREGKFFYLGKGNF H*TRVGGPPPLSGGKKKIRG
6515	20416	A	6569	234	411	PGAVHRAVNTLGGQGRHS*GQEFKT S/LGNTVRRPLY
6516	20417	A	6570	1	175	FLQHV*KKPQTMSDQITGKIDDMNTLID LEKNVKDL/LITQTEVEELEGENKIPIL PG
6517	20418	A	6571	392	140	LPSSWDYRHVPFCPANFVLLVETRLHV SQAGLELPTASASAGITGVSHQARP/E **NSIRKGATTIORDLGPVLQVRLVRC
6518	20419	A	6572	2	228	RTCTQMSVATLELAKNKKQPRCPSTGE WINKL*YILTMYYLVK/NDPSSHHK TRGNPKCILLSSRSQSEKA
6519	20420	A	6573	412	100	ALHSHPLGGPGGGVPSKRI/NFPPCPGG TPFFPKNPKLTPGFGARLPFFPKLKLK EKFPNPG/MPGVPLN*IPPPVSHPGVQ NFFSKKKKARGFCLVLNPSSS
6520	20421	A	6574	406	257	NKREKTRKRLDSDIVIRKRIKSOBRCY SAPIQMAKV/SNRQSPKFWRCRQTISL *HC* *ECKIVQSMW*TLQKFLPAIVFLC IYHTEKLRTQOP/CT*IFLAALLMTV/ RTV/KRLVCPMSGENLSKLW*VNLSFSV
6521	20422	A	6575	370	68	EQSGVMRSEPPGGYNLLVCR*LRPLE KRTIAGVVS*FSRCSLRLPLARKGKSP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, =possible nucleotide insertion)
						NPVCTS*VFESNGLS
6522	20423	A	6576	1	259	IDLTIDVLEPFLTVT*AVVQWCNLSGL*P *PPG\SGDPSASASRVAGTIGQHHRLW IFVIFVEIWRHILVYFHTAIKNYLRIG NL
6523	20424	A	6577	418	218	KGKTRLGKRVVPPCPNFTSLG\GGGSWIT* QOAFRTSLANIVFPLM
6524	20425	A	6578	1	401	EKAGCSGSYL*P*HFGPPEQEDHLTLGI *DQPGQCSENLSLQKNF/TNISA*WPG IVAHCNPNFTSLGSGRRIT
6525	20426	A	6579	3	356	HWYRHEFFFPV*MHFFIWLPGCHSLLA SPNLTGCFFSISITESLSSLFIYLETRV *DLQCSYFWERRG\SLCCPCWSRAPGLK RSCCLRLPSSWDYSRLTPPHLANYCILG GEGESS
6526	20427	A	6580	411	158	IGSVAQARVQWRDLSSSDPSAN*APFGL KQSSC\PASLPSRLWDY\NKCTPPDPLANF YIFFVETGFPFYVARLADCFYPPPL*KMT GSY*VTMCQIPH*AFYKF*FI*FRUGE DKNSLPAWQHRETL\SLQKQYKN
6527	20428	A	6581	399	218	GGAELKVPK*GGGPGSPPLPPQLQKPRP KGPLWPGG*GPPRPPGEAPSLKNN*/ PLPG/AGPPVPVPPNWGGGYPRG*GEG* LPLGP*TLARGQORDPVFKKKKK*NVN KKKAKL*KS*OFFFVKTKGSRCPRAK VQPGMSYKPPQPRG
6528	20429	A	6582	392	214	GSSDDPNSTSERVAGTTDEVLPCSPGWS* NSW/VSK*SACLGLPKWDYTRPQHILA RSNF
6529	20430	A	6583	390	257	PKRPPPPAFFC*PK\SLGMLPRMISNSW AQAIIR*RNPPKVLEKQA
6530	20431	A	6584	65	251	HYFNSFNFFPLMGSSNHPTKNP*FFPFL TFYKKN/SITILPRLVLNSWAQGILLPW PPKGLGL*AQGILLPWPPKGLGL
6531	20432	A	6585	2	143	RHMFPCLSSF/SYFL*RRGFVFLPRLFS KSWVQVILMPWPPKVGLGQA
6532	20433	A	6586	142	334	GRWLSQLLNLNFTTSVLRQMSW/MACV SETWPA/STLGGRGGRIT*GLKEFKTSL QNMARPLYK
6533	20434	A	6587	485	377	RTRLSCRFILSLIFRFGNFYCFTLKF/ H**VLLSFFVFC*GHP/FEFIFKVF FIFHFVKVFCVFKYLLFFLILAEIFYF FVNIFSFKFVSVMFVLLIEMFYGRFT IPLR*F
6534	20435	A	6588	241	251	NSLPTFKKKKKKGALLKEPILRAGGSEG IIFFKGPKSIPGPGFKKAGREKPGPSP *NWPF*KGPPFFFFFCKE/RSFTMLPR PASNSWAQAIQLPQPPKVUGL
6535	20436	A	6589	429	54	YFLFLPSLPTFFPSSFLPSVLSFFLP SI/SSFLPSLLPYLSSPPLSSPPSSLF LSFFLSRVSFCHPG*SAVAQSLRTATS SWAQAILP/CR/NRDFTLRLALNS*P QVIRPPPPKVVLGQA
6536	20437	A	6590	411	137	KCIGITTHCSLHLGLSPDPPTASRVV GLQAHHTIQLAC*F*LID*LID*LNVM ESRHVAQGLLELSSDPPTLASQNAET TMSHCIF
6537	20438	A	6591	412	196	QPQPPGAKTKSGGFPPIR/WGHQFPFPG

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						AKKYNFFFFFW* RQALAMLRVVPNCQ T*AIILWPWKVL*LQA
6538	20439	A	6592	28	400	IMPNCFPKWLITFTFFFF* RQSL/DSV AQAGVQ* HSLGSTATSAFLGPK* FSCPP AFLE* LDYRHVPHTPTNFCVFNKD/MGF TMLARLVNS* PO/CNPPASASQSAGIT GMSHRAOPHLFVLKMEKPPNLFILLM NOSTHVLNFFR
6539	20440	A	6593	414	23	OTHLFWFDPGFSPPFFPKNRRIIFLGA LKKNFFPPPRHKLFFLKAPPPFFFK RSFFPGWCAIGL*SLQPPPRK* FFC PSLPKKNYRPLPRPGKF/CFPPFFVI LVENGFFHVGGDGLDLLIS
6540	20441	A	6594	91	274	ILHWS*PLNGYHL/WLGUVVAHARDLSTL GGRGRIAGQDQDFKTSLSGSKQSISARK KEKKKK
6541	20442	A	6595	391	251	HLKRCSTSSVIREVOIKTTTCHFS* K R/SEINMCN* ECGTSLALLIR* \WD SEMVOPLWERKEYLKOISTESSWAPAIP LLDI* P*ERCASLSLRKGWGYRPEPPEL ASFILGYSI
6542	20443	A	6596	465	268	ILLCHLGCSAVAQD/LTLCSLKRSSHLL SPSSWDSRRGPSHLTKPF/C* RGLNTL PSLV* NFWAQL
6543	20444	A	6597	3	229	CHGSPQPCPPGLK* SSHNLNFTPK* LAD YRGMPPRSANFLFL* RWGRCAQAQGLEL PDSSSLPASASCPROPVLYF
6544	20445	A	6598	122	418	IIIVNELCHIMCFFFFFFKQNLIGTQAG GQGGKNN* LKPKPRLKGSPLTLPGG WNYGGFP/HPS* FFFFLGKKGYPFCP PAGGKFFNLKGPFFFA
6545	20446	A	6599	1238	930	FETDSCSFA* AGVQWRNLSLQTPPPV SNNSCASAS/RIAGITGTHHARVIFAL LVETGFHHIGQGSWRTPQQAIRPPQPP KVLGIQTVTSRAVAISKHF
6546	20447	A	6600	398	78	PSSPFYLIFFRQSFPPFARVEKGGHFG FPNPPSGLKKEFYAAPGSKAPQCGP PA/RFYLIFFRQSFPP/CCPGGKRGPS GPPQPPPGVKKIFLCPSPPRK* GPRAG PPRPRIFFFFSSLFFFFVRWGFTML PRLVNSGAQAI* CPOPVKVLGLOV
6547	20448	A	6601	3	473	FFKGGKGGPPFPAGG/OLKNSKPKPK PGAPPRGPRGPKKGGGGLGSPPOSPQGG EKWTLKGGPNLPPRGLGGARPPPKIG GGPLFPKGGGPKGGTPPPPLFFFLRRS PALSRLKCSGAI* AQTSS/SPPARVGC PSPAPTRPTGLTVSPGSN
6548	20449	A	6602	398	156	NGRKHTDVKEELPSWVETDLTPTGTGA GAF/Q/RGYGYNYKYVTVKKSIAGVS TVLAA* VLFYSYCLSYREIKHEOLLRAH
6549	20450	A	6603	380	77	PPPKSPPL* NFFPPF* KKKVPPPPGK LPLSLFFFFFF/RDRVLLCRPGNSAMV HGHGLSPVNFICISTRNAL/SMLEPPI NTWQAIRPS* PPKVLGLQM
6550	20451	A	6604	352	204	KRGPKI* NFFFG* RQSLHMLPRVVPNSW AQMLPPPPPKVVOGLQA
6551	20452	A	6605	631	357	FFF* DRVLLYHFGWSAAR* SLTLTTS SWVKQFCSLSLSPSS* DYRCAPPCPASF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, = possible nucleotide insertion)
						CIFSRDGGFTMLARMVSN*PQVIRPPGPPKVLGLQA
6552	20453	A	6606	3	397	VLHKLTRQCSAVPLRAPTAFLIEIGTQTPKRWVKCR*P/RETQNNLLDKQDFKTYQKATVTKAVWCOHEDTIEQWDGIESTEKKFHTQAGGRDHDHSDSVKRRKESLEFFLKRGILILFPNLEGTGGISTP
6553	20454	A	6607	323	35	YLTKRIGKPGGLALQPLGFRPSPKNTQLGNRFMCTHTHTHTHTVHPHSTQYLYPHRSISFCYLDLSI/SP*VLTESSNSNPTPKCC*HFFSPCL
6554	20455	A	6608	439	252	LVPPLFFPFRSFLFSPPKRGGPKPV*FGPPRAFYPPIF/V*RGPPPPFGAPKKKIFFSPPPG*KCFFF*SPDPG
6555	20456	A	6609	3243	2602	PPFGRGDGVLLCCPGWSQTPRLKQSSLSL/PKC*DDWH/RATSSGLOVFLSICCSIISIFFMPSICDKSTKQFSN/PQRAYILV G*R*VIYLGVLALFLVFLRQHL/NIVAQAGVQWCNLSLL*PPPARFKRFSCLIPRSWDHRRLLPPRPANFFVFLVETGF/TILARLVNS*PRDPPASASLSAGIMGVNRHTWPIVLFLHPSVFVKVLQFLF
6556	20457	A	6610	81	395	TWAAALKYSTICIFSSSETEFPVDSQSQITDTTACIMEGLPW/YRSIWTL*FHFHWDCGLTLLTRIVNWSQVCLSLPGPPFKVLGLQASATAPNSFILLREGIS
6557	20458	A	6611	1	126	GRIGDENHNLNFGGRCCEPRHLHCSEAWAIEDSVSKK/NKNGLRKCFHLRKTLKGEKRIIV*PGGRGCSEPRHLHCSEAWAIEDSVSKKKMD
6558	20459	A	6612	389	67	YLFMYLF*/DRVLLCHPGMSAVAQ*LTAAASNSWPQVILLSNRPKSWTVLLSSKIPUVQGSTPCPRCYSWHPKCLQGLGLDCSSPKYPRGPSLAAPRSLPKWHV
6559	20460	A	6613	1	384	RCFKVRLDKMRFPNTQVDPKSNCKPCPKRLKRRGHASLPPEWKRKRPKGDDGRGWNASAVTSQGT/VEATRSWKSQGSVLP*SL*REKSPV/ELAHF*QRLAMLPRVLVNSWPQDISPPWPPKALGLQEP
6560	20461	A	6614	385	174	CLRLSALKPKPLNSWY*K*LYIMEY*SA LKT/NKGILSPAITWNLDDILLNEISQTQDKYHMNSLICEI
6561	20462	A	6615	1	370	MNPRHLSSLKRRERRILLWALKGHIN/FTV*GLTGIALANSLSYIVLHDTYGVSHPHYVLSIGAGFAIIGGFIIH*PFLFSGYTKKKKNIRGGGTKNFLLCALVQREKVNPFALTNLWG
6562	20463	A	6616	3	342	YRHEPPHSAIFAQLYKL*K*LIYALKTGKYVYVKLYLNKAIKSG/SYNRASLSLT*PRVKRRRS*PGTGAHTCNPSTLGSQDGLA*VQEFETNLGNIKPCLNHQKKKGA PV
6563	20464	A	6617	1179	915	FFFETESCLVTQAGVQWRDLGSLQSPFSG/SSDPQLIFVLVHQAGLELLIS*SFALASQATARITGVSHHAQLVWSDPIKSNLFCCCL
6564	20465	A	6618	3	390	HASVKMELPYDAIPLPSIYPKELKARF*DLICIPM/FITALETTAKRWQLNCPSV

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						VIRSWGREGVKESCLMGMEPHSAR*KSS GDTFHTENCY*TVHLKIVSGKF* [*] L* [*] C VLNYGVFFYHNKNIKRLS
6565	20466	A	6619	392	49	QFLFERLFSSYSGYVSGVKMLGSTEVQL FPRKCEMKSCSVMPRLCSCGGI SAHCNL CLPGSRDCPASAS*VAGLIFY/IFLVEM GFPHDG/RELVLNS*QVIRPHQPPKVL VLHV
6566	20467	A	6620	193	282	TPGLK*SSCLSLQNSWDCIWDRRLPLY PVNCFCC*FVCFVC/IFVEPGSCIAQYC LELLASSNSPMSASQSTGIQMSHGACL ILT
6567	20468	A	6621	383	8	LDNTVSTFFF*DRISLCPMSVAVARSO LKAASSTSWVOAILPPQPKTNLLCSSDSS TSA*QSPGFF*SPCFRLPGSWDYGCV PFSANF*IFCRDKSL/WAQAILSPHPP KVLGLQALWEAEEGG
6568	20469	A	6622	395	42	HVSSTSFQGEHLHLRIVALPPLPLHNL PLPLSPRSL* [*] C/HSRGMTVLPPSRLTAT SLPD/SSCLSLLSANDCRAPPHLGGFC WSAVA*SW\SLQPPPSRPLWPPKVRRL QPLPSRHVP
6569	20470	A	6623	3	327	PSPPSRWNPKDVPFNPQENLGIFFFL* [*] T RDLATLRLVPNS* [*] TQVI/WPPKVLGLQ A
6570	20471	A	6624	395	47	KNRALFFPPPKRKGFFFKPLIWGTPRF FPDPPF* [*] NPPPYFFFGAPKKKFPS/SP PGGKIGSKRPPPPFFFKQNFPPVPPG GGPRDGFSLQHPFPPRVGGFSLAP [*] IF FSSF
6571	20472	A	6625	100	267	LSLSKKANISKFWLGTVAHVA\DPSTL GA*GRWIT*VQGFETSLGKIVRPLCYFC
6572	20473	A	6626	409	126	PSSSFSSSSSSSPSSSSSSP/FFFFFF FFFSF* [*] KWCVSLCGPGWSQTLGLQSS CLSLPKCDYRNKPLHLAFASLILFTF QBVVDID
6573	20474	A	6627	506	323	REAPGTLYPCWQYDMIKAGLVNQFLRK PNLYLPYNDAIPL*HTCPKINTQT/C FITKTCTRMFAIALFIIPQWQKQPT* [*] PF CPFTIISHSCSPRDNWF
6574	20475	A	6628	330	117	DVCPRIYTLVLOQLCTIRMFTALFISI AL* [*] FCXPMCTSIIEWIKL* [*] SIRITEYH LVMRNRPKLLYSMPQM
6575	20476	A	6629	396	139	FFSPPEKGVFPSP* [*] NLGTGFFPPPPF KKRPP* [*] FIFGAPKKK/HISPPPAEKFF FFKRDPPLFFFFFFFLLFFFFFAFKL KV
6576	20477	A	6630	79	405	VSGRMTALESYLLASSA/RNKCSSNCKI KKMTARLDVLAHRCNPFSGG* [*] GGRIC* AHKFETSQGHIIIRPLYKKKKGRPPFR TQFSPARWQNGGFFWGLKNSRAGF
6577	20478	A	6631	2	417	SFIFCFCKPLNGFISFYKNVCHDFDCNCV ESKDQLG/WPDAVAHTCNNTLGSQGGW IA* [*] AQELKTLDNMAKPCLY
6578		A	6632	74	417	KTVFRYNGWAL* [*] ASERNISLADLLPSF HVLCLPKAG/PNPLPSSIKKFPDLPD LIRSHKTHISEGVLPFPF/RRKEPRTER PRRI* [*] TDRSCWSSLSLIVLDHAFVQS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
6579	20480	A	6633	740	776	CSFFLLKKQTRSRAAVQAGVQWCHYSSLO PSPFDLKKQPPASASQTV/KD*GAYFWCC FFLFLKRWGL/NSVVQAGVALLPDLFVV RRLVTPSLWAVEPALMAAQL*LL/SP CLASQSPHOTOQSPGHKCFPDILGLH LALRSSSPCLERTLRLPCLASFHT* ATWLGNELPVK/PKRVNMYLVKADPE PFL*GTRGRKSVQMTHAKTLQSTLYSG PEQAAAASVTDEF
6580	20481	A	6634	2	296	FFFLRQSFALVVOAGVCMHDLSSLOPPP PRFK*FCSCLSLPSGWD*RHAPPRAIFV FLVEMGF/TMLATMV*IS*PGDLPTSA CQSAGITGLSYRARP
6581	20482	A	6635	407	212	GRPR*TPPPLGKKKKGAPPPKTKKKNF LGRDYSQKQKFFFF*RNKTRPGGGGPP GIPPLKG*AKKKLPRGPKFVTV*/NK PPPPPGGNQNPFPKKKKRSTR*IK IRISRFLYFPPFFFLERGGCSPRGGG GGAFLSYGLWPPG
6582	20483	A	6636	20	223	PCKKLPOPLQPSAT/TLISQOPLTLRKL LLPGKRL*LAEGSDSYQFLVAKYFKIK GLSFGRNLANI
6583	20484	A	6637	866	647	PFLDRVL/LCHLGWSAVKRSWLTAAITS GLKQSSCLSLPKLRDYRHPQHANNIS *SSWSDSNMOPRLKTL
6584	20485	A	6638	398	26	KGAPPNIFPPFLNIFPPPPPPPPPP FFPINFLQCLLYRALHFNKVKVINNF/ PLNFCAYHPL*NM*FSYISQNLKYFF LI/FGVFNLSGIYFNVL*IANF*G*LI LPGTIYLKLCYFTTN
6585	20486	A	6639	1	341	NWDYKHALPCSANFVILVETGFCQLPRL VLNSCPQVSHHA/KFLFIFPPFLFLEEG GVFGPPRLLEYREGSLQ*LPKLKGSTCL TLPKG*N*RGEPLPARSSFFFIKFFI ET
6586	20487	A	6640	391	118	NANFEKSFMSGKIL*NSLAWKKILCD/ RKNRSMQKTPLD**YFPKLPQPL*PSA NTTLIGRPALTSRQGLPPAKTL*FAEGF DPMILSLF
6587	20488	A	6641	352	285	KKKKKGGGGGAYSGITP/CFFFLNGVF LGPAQVQVQWQORSLOPPPPGVKLEFFLS LPSH*GPRHGPFRPMFIYNF/CFF/V RDGVLHPCGWSQTPGLK
6588	20489	A	6642	433	64	TGNFFLDLSLFYFNGPLGGGGILKGFSS FFFLFLETKFFFFPAGGQWRYFSSL*PP PPKFKQFFFLSM/WPRPGKFFFFFGIL VEAGFHRVAQAGLKLSSGNLPTSASQS ARITAKSHRTVF
6589	20490	A	6643	424	11	PPSIFLAPPPSRGGGPPPPPKK/OSPP KKKKKGGGGGKPNPPPKKGGPPKKTGF KKNPPQKKKKKNSPPKKGGPPANK*KP PPRPQPFYFLTPYKIFIIYIFLLKFLF YILFFFLKSSKQGRPLAI
6590	20491	A	6644	411	2	PPLRIWLASPPSKIF*POPLHI/YFSPP PP*KFFPSLKPLIFLGGFFPKPPPKKS FFPKNPGQVF*NP*KKKIYFSSP*NF ADPKILKTPPPPPPPPPPPPPPPPPPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6591	20492	A	6645	34	381	LAQARTRETRGRTRGRTRG AKLGTRGAQKEIKVTRI*WKEIELS QFTYTTQKNL/NVTDKLL*LVYMFSKIT GYKVNLIKNCIFHKHTNQOKILKMPF IIA*K/TIK*L*INLT*KTQDLYAEIYQ TLKAEI
6592	20493	A	6646	17	448	HFVAKLGTASLSCSGLHPV*ASQPLYL PTQASAMADAPFPARLPNSLIYCCST NEQGSVGVGPAEPGAGYNLV*HLRLPLE KHST*VAVSRFSHYLSRLPLARKG\NP QTPCASWVRQCPTLLRLALHGLHPLSNQ SQGD
6593	20494	A	6647	462	336	SLRLPGNSDFASAS*VA/GITGPFCHHA RLVFVFLVMEGLGS
6594	20495	A	6648	447	62	KDDIWIATITHMNRWISLAKRKM*IKIT MKFPYTSIRMA/IKQTNKN*KKSSIKC W*ECRTWTLIKH*HITG*PLMKTVW KFIIKLNLYLPDPA\TCTQMFTA/ALP IILKY*KOSKYPSSGYCVFA
6595	20496	A	6649	3	1492	LAYARAFDDTTRKRYPDNNKVLLEKEVE RQFVEACQALAVNERLIKEDOLEYQEE MKANYREMAKELSEIMHEQ/CPGGED ERLTETPSHLQRHWDNSKNHNGSRDDQL VFGRVITSHGFCVGTFCVICKRLMSKA NHWDGDAQ/ERTKKGREK*RTTLFLN R/RFYRSWKVCHIFF
6596	20497	A	6650	495	170	GAAREFFASQAGIAGVSHHARLEEFFSL DSGRVMRGTEVLKVLGGYITIT*SIFF FSFF\WPLGSLQPLLPGFK\LSLLSRW DYRCAPHILSL
6597	20498	A	6651	9	222	QTRFRERNSGDPHTLSL*SSWDYGHVC HHAWLIF*K/CFSGGLALLPLRV*NSWA QAVLPWPVLVLGLQV
6598	20499	A	6652	241	833	KKTFLAMWNPWPGFQIHPHILTKLVQMA G/QENGCLSGHDLFSIRPAGLHNSARGE VLGLSSSLGKELVFLQEBLDSIHIPE AOEVEMASGHFAFLHVPVDPGRAPYCKA SLASASSLSPTTPEDTAISLLRPPSAPE MLTCHGAQEQVEDHGP/Q*QPSPHSQSR PSPQKDFQALVIASLSRTERKQASHGG TRPG
6599	20500	A	6653	1	398	FFFDIGSHSLTQAAVQ*HDHGSGSLHPR LPGFK*SSHLSPES*DYSRHTPPRPAN F/EVETEFLLHVPQAGLMRCNLLPAT/AT SKSARITSVSHHVQPEVSIKW*MNISNL IKCFLFYKYKCI*INTKFVFTV
6600	20501	A	6654	489	282	PAS/WDY/RHMPLLANACAFIC*RDPS MLPGLVSNWNAVICLPNPPRVLRIQAR ATTPG
6601	20502	A	6655	953	908	SQSCSVS\RLCSCGALSADCNLCLLGSS YSSTAS*VAGTTGARHHTQLIFVFLVE MGFHHVGQGLLELT*VIHLSRSKVL GL*APSSARGQNSVSQ
6602	20503	A	6656	412	44	RISERRKSLGAVHTKDKKYSRRVRSN PNCARGSSSKQSFLLPGKRAPHGKIS F\KDALLVVDGITGVHHA*QIFVRSRE R*IRPVI PALWEAEAGGSRAQKIETILA NTVKPRPSLLRA

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6603	20504	A	6657	3	241	FTFLKARSHSVIQVGMQWCHSSL*TO TFGLKES\PASSPHRAGITGVSHHTYLF L*G*\SHSQPHPHDLITSKRPS
6604	20505	A	6658	467	42	FFFFFKQGGFLFPOLEKGESIPGCPNP CPPGANDSPPTPLGNGGPGGPPNPNGH FGIFGI*GGEGGF*TPGSKPGSPGSPK \IPFCWVIRERPHGPPRFFFLRQSL CFAQAGVQWCDLGPLQPPPRFKQFCCLR NS
6605	20506	A	6659	2	286	KNLKNNT*WLNPPVVSAT/WGGSLKPRGR LRLO*AVIAPLHSSLGDRARPLYSVSQY LYFSLSLSLSLSLTHHTHTHTHTHTKIE LLGCVAEIITHF
6606	20507	A	6660	3	249	LSFRP*CGDTISAHCNHLHSSSSPFA VSQVAGITGACHHAWLIFVFSVMGFHH AGQDCLHLL/NLVHPPQPPKVLGLQA
6607	20508	A	6661	3	1507	PEAPVPFLDSNOENDLLWEEKFPERTTV TELPQTSHVSFSEPDIPSSKSTELPVDW SIKTRLLFTSSQPTWADHLKAQEEAQG LVQHCRATKVTLPKSIQDPLKSELRLCT FOQSLIYNLHPALSWLPLFPRIAGDRKM AGKTS PWSNDATLQHVLMSDWSVSTSL YNLLKTKCPYFYVCTYQFTVLFRAGL AGSDLTALISPTTRGLREARMNEGIEF SLPLIKESGHKKETASGTS LGYGEYVIK ITL/SSSTDLWTHEIDLHNSL*NRDSN CSNF/LREQAISDEDEESFSWLEEMGV QDKIKKPDLSKLKREKHEQMDHPE SVVLKGINFTLLNELNSKSLVATSG POAGLPPTLLSPVAFRCATMQLKARSV NVKTOALSGYRDQFSLBITGPIMPHSLH SLTMLKSSQSGSFSAVLYPHEPTAVFN ICLQMDKVLDMEVVHKELTNGHLNPTL EOLSOIPLLGKSSLRNVRLDYIYNWRS
6608	20509	A	6662	326	1	IMI FLFFOTGSRFVA\RELCSGTITTHC SLNLPFGSSNP\PTSAS*VVTCHTRVIL NFSVDPGSRHVVKGGLELLDAILKPWFP KVLRTRGSTPEFRSGGSGVRIRGFN
6609	20510	A	6663	414	105	QGVKGVKVLNPLSRLHFFKQKLFVLS *KGQVKKLSLKIPPPGGFFSPPI*NP P*NKQPRKPNPFMGFT/IRKKILFLAPK STKSGG*NPSPK/HKKI*FSF/CFWETE SRSVTQAGVQWHLSSLOPLPFRFK*PS FCKPHKRKVFPLGLVLWGGISNRRKKTK SGGKRNFKA
6610	20511	A	6664	1	407	GCVPVVFAAREAEAG*IA*TRET/RLRW AGIVPLHSSVGNKSETLSQKKKGAPSKK SLQGVALLFSLQLGLPPLQKRRKRPQRG GGRGQLAPGYNPPAGKTIVGPGPHLSFC SKKAWKELRPWKKRGRFWFLINST
6611	20512	A	6665	1	280	FFFF*HRVSLCCPGWSTDLHLHLP*LAR FKRSSHLSLSSWDYRHTPT/HGPFVVC LPVFCRDV/SVLPRLVSNFQAAILLC GDRKVMGLQA
6612	20513	A	6666	408	89	WLPNSLILPN*NYPVSYSLSDRVSLCRF GSTAVAO*ELTA\A*TLGLKRSASFHS HSCSLSPSWDYRCTSSHLANFFPKWGF TILPRLILNSNPOVILLPOSORH

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6613	20514	A	6667	484	208	ITVVSAGLIHYSFLNPGFPMPTTKYAO EIDDIH*NLQHLQPALVDRKGPIFLHDH A*PHAAQPK/LQKLNKLCRVLPHEYS PDLPLT
6614	20515	A	6668	495	227	PAFVKVPPEKDQRQNSTHAGRNHLPMEI LLL*KKKLIETESHVS\RLCSGVITA HCNKLKLGSSDPPTSASDYRLKPWHLAP SSFSMS
6615	20516	A	6669	2	65	DGVLTL*LSLLARLV\NSWQVINLPWP PKVLG*QAGLOT*PGLK
6616	20517	A	6670	403	224	ILL*P*PFGIK*/FLPSSWDNRASLCL ANFLFVEMGYPRVAGAKFLGSDPSLA SQSAGVTQSVRGRFLRTVL
6617	20518	A	6671	406	162	RSVAQXGTQWLDFFSSLOP*PFGILQSS HFSFSQSASH/RHPDNYCIPCRNRVYVG QASLELLGSCDLPASASQAGITGSCIL
6618	20519	A	6672	453	32	VVSATLHTSVVVCACATRCVGMCTLGV CGCECVV*GCVCTSVN*HTSGMSEX V*LCVCGCV*LCVACMAFVSRQCWCDP VCCLPEKMRSLPSIVA*VCAPMKVSPCP PQLSELHLLSLNIYINKCVLSQNAWLF L
6619	20520	A	6673	378	180	NEVIRS YKVS LFSPRIERKWK/N/I/HWY IYPMEDSAIKRNEVLIAHATT*RLKENI TLNERIFDIIPFI
6620	20521	A	6674	378	94	PVKNRRTKELHJ KDVCTPMLVILFMYC K/S*QKPKCP*IDEWNKMYTHMVEYC SVSKKEGSPFICYNEITLNEISHKKTN IYNSTYIRYLE
6621	20522	A	6675	1	380	VCSL*VLCRHMSFCQNCSL*FSFSFWFF WRQCLPLSPRLCECGPMSAHNNLRPGS SDSCASASLVAGIRGACHHARVIFVFWV EMG\FHCVGQAGLELLT*VICPPWPPK VLGLQVLATVPQPHIF
6622	20523	A	6676	424	135	SHRWGVCCKFYNIFFFRD\RV*LCCTGW S*TELK*SSCLGLPKCQDYRHETLRVS YF*NS*QIGVLAMVSKVLNS*QAQI LLPWPPIVLGLQI
6623	20524	A	6677	408	91	HTHFVWFPLIF*PWR*ULLTPTNTNF FLRDVSPCHPGMSVEAQSOITAASN\Y GLKQFSPSPKWCWDRRELPCWVSLII FIYVHLHMYVHARKEPEYPL
6624	20525	A	6678	1231	217	PPYFNNPLTFQKRF*FGDKTLKKWL*I REILQNRGIG*KTDGIR*MGKTEAPLK EKFLLGALQPSFLPYMLGHFKEE*GEE FPGTHSWFFSPFVWGLGLSVNHRGTHG PRVSLQTWGPQGEAMECECNHGTEDTG \GAVLQPG*VT*GFHTPTSEPLVAPPC TCSGLKAE*\GFLKLPKGQ*\SEGALPP *SPLPSACFPGLGLRLGSSPGLMIHFG WGLFTSPIGLKILGRHPAGPALPQIA RPSLKFR*RLGWGPPELLPAQTCGAQSL GPSTAPLLGQGPWGLG*HASRWGLGLA VAPGNEVPSLSPR*PRGAGPLHRRV RSWG
6625	20526	A	6679	1	178	RGWDYRRPLP/RPG*CFVLVEMGFHRV GQDGLYLLT*SSQSAGITGVSHRARLQ PPIF...

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6626	20527	A	6680	3	135	KSEHLEREPTIEQLSTMF/TAKYGVHRL RSH*HRCQKXPEPPDR
6627	20528	A	6681	425	107	KGPPTPS/PFPSPVFPTEKILVPPPPF PPPPFKPPPPONIFWGPKK/IKNFSPPR GEKNFF*TPPKYFLGAKKKKNFSPPR GEKNFF
6628	20529	A	6682	424	284	CLFQGP/PGSGASPPSFQDNWQLRQA LPPP/RESFFFLFLFPPIVQTGFHIVA RAGLELLTSSDLPASASQSAETGVSH* A*PFP
6629	20530	A	6683	1290	449	PLSAPPPGDSF*KSFRAPNLPA*PP NLSPWPKCPRPR*PASS/PP*LPVPP KSPSPV/PVUATEASRGHQPIT*ELG SLVLRMTEKGTW*GIPDSIMPLFRRS EPRTCRE*GDTWRWRRRRRRTGAUSTF SPGFACGGSGA/PAHPGEQKLGASARP DE/PVCPAAWVLLPSARVVASPAAPPP LPSQPVH*RFKP/SPY*PP/ALPPLSP FEPSPHTGSVPY*QGVPP/SEGCPST SKPLISVRPVTINGCLPQSQPPKHTV SRLYEEN
6630	20531	A	6684	425	40	EWASLKN*HPP/GANQAVEAEAPTHCW *GCKSIEPLKTVQCLDKNLICLYDS TPE*MSEHVYQAACKKSFTAVLFMIPP *KQPCSPSTGWLQGANWTLVIPAWEA KVGGSLEPRLRPANATG
6631	20532	A	6685	2	107	SWLTAASTSQ/VKRSSRLSLFSSGDHRC MPANFFFLKDDVSLPRLISNSWTQAIL LSLPFKLEL*AHCSLNLPGSSDPPASA YQVGTGTGACQLIEFF
6632	20533	A	6686	12	224	TFPGSTHASGAPPLANTIKFNY/L*RLP RLFMNSNPQVILLPWSKVLQGVWATV PSPFLIFDRDIDRI
6633	20534	A	6687	404	2	TAARGITVGGPIKLLRPKADVK/SGS FKTAAPFFFLGTRLTLEFLIION*K QPKRPST/DRINKLWYISTIEYYSAMKR NKLILHTTAWMNYKGMVSKRGQSOKSI FSRKTGFRGNISGCFYLPPLRL
6634	20535	A	6688	410	163	PRGNTFPFGSPPEKENQKVFNPFPGNIV *KKGPPPPQGAQKKGPPY*GPPLSFLPP KKKKKKGPPPPPPKKNPPKNGS/SFSP KKKKKKFPPPPKKKG*GGPPLKTLFFW GGGKKFFFFFWGKEFPLGGFFGGGGG GGPFFFFF
6635	20536	A	6689	205	405	KSPSPSGGPFLLIGLEIGGAPKPINWFP PLGPKGENPPLALGGGGGAKNHPNPQF ILLFLGGKNP*KSPSPSGGPF/ANRKRIG NRRGPKTKLAPPLGAKGKPPPCPRGR GGGQKPPQSPVYSPFFGGKKPL
6636	20537	A	6690	3	199	HGSLQH*PPGFKSSSLSPSSWDHGHV QPRPAIF/CFFLILEKRGVSPGPGGPE TPGLKGLDLL
6637	20538	A	6691	8	350	SVCLGLP/RCDWYRYPHPLA*LAFLCQ IIFHNDWIYHVSILVVDGYLGCFYFLA IINN/V*AGLELLTSGDPPTSASQSG ITGVSHCTHPYCYTFLTREITTPKEVKI GLCM
6638	20539	A	6692	373	197	LFSSWDYRFMP*HNLFFK/FLFLFLCRD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						E/SLTMI.SRLVSNWAQATLPPQSPKVLGLQV
6639	20540	A	6693	369	100	PMLARMVSTIS*PRDPFASASQSGAGITGVSHRARPIYFFK*R*SHAGYSAVPVHRHDPTTDKHNLSFLCFLQTGSCFVVGVMQWHDHISL*PRTPGFKQYSHPSLPRH*DYKPTTP/HPS*FVVGVMQWHDHISL
6640	20541	A	6694	12	182	FLSSWNRYRCVPHLAN*KKNFFPYTDR/SLAVLPGLVSN*QAVLPLQPVKVLGLQA
6641	20542	A	6695	402	248	SSWDYRCAPPANFYKIL*TGS/LLC*PRFVSNWDQVILPPWSPKVLRGV
6642	20543	A	6696	301	309	VQEF*DRILLSPRCHPGWRAVA*SRLTASASRLKARPSHLSLLSSWDYR*VPPGFANFLHFPCR/DRGFAMLPRLVSNWTVQVIGLLRPPSVGITGVGHRARSILLD
6643	20544	A	6697	3	387	PCLANFF/VFVETGTHIAA*CGRLILGSSALPV*TS*SAGIQMSHCTC/LQITLLKTESHS\WAGAGVQWHDLSGLQPLDQFM*FFCLSIQSSWDYRTRSPRANFCIFSRDEVLPCNPGWS*TPDLR
6644	20545	A	6698	1	287	LNFLYQGNAGITGISHRQNSFVFFKDRVLLCCPGWSAVA\HSSITVALTSDQAVIFLPOPPG*LGNFICIFSRD/RGFAMMPRLISNSWAQVIRPP
6645	20546	A	6699	412	3	FEMESCSVARLECSGTILAHCNHLHLSSSSPVSAASRVAGTTGACCHTWLFFFFFV/FLVETGFYHVAQMGLNNWAKAILPOP*VLGLQARITTSPPNSSTFREHTSGSGVGYPAKFHSIVLLLLLLFHLGCGVF
6646	20547	A	6700	393	88	QKLYPYLTPIYAKVN*QWIKRLSVTAKNI*FLGENTGVNLHSFRFIKGFLDM/TPKSISTKRK*KIKWSSSL\KNFYALKNNIKMKMKROPTKYEKIHLTLNNW
6647	20548	A	6701	494	239	KAGSHS\VSRLSCSGMISAHCTFCLLS*NNPLTSASLAAGTIGVHHAWLIVFVSVQMGFCHVTQAAWVLI*PDGCFESPINKYNLL
6648	20549	A	6702	2	379	RPTWTVWQNPASTKKKKNNFFFKTSPTVPQAGGGGNGL*RKFLPPGLKRRFSGLKREAPKGGQCSLMGGGLCLLPP/WSGTPEPR
6649	20550	A	6703	220	47	TGFGSSQIN*EK/IWLTGVHAHTCDPSTLGGAGGQVT*GQEFKTSRHEPLHLTVLCSLF
6650	20551	A	6704	80	414	ICYFYIVFAIYLNQFNSVCYRSFTFFFCPFETESRSAAQAGGYNTLTLHPPLPIKQFSCSLTPSS\WARS*KPCPTWNGNSVFVGIYKNKLGSGGAIRVQTCNQTYSG
6651	20552	A	6705	69	416	NVEKRNINIKTKTPVYVFGFGLLYCYCKAEVFFVLDNPFIFVYFVFYFETHCVAQAGVQWHLNRLSQPSHP*SSSDYRCAPPHLANFCRDGVSPCWPSW/S*APGLKLHPWPSPKVL
6652	20553	A	6706	373	75	HAQLTFKFYFYFRNTFCKAVASTKSNSSDRSE*SKLTFWKGTLTILDAIRNISDSL\EEVNMSTFRGV*KKLTPIIMDDFGPDPFTRESNHRGARHGGSL

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6653	20554	A	6707	331	379	K*KINKF*GGLTILDAIKNICDSWEEVN IST/LGVWKKL/ITLIDGSGFKISVE EGWAGVVEIARELEIEV/EPFYVTKLLQ SHKKT
6654	20555	A	6708	578	152	LQOHNPGLSLPLP*GFKRFSCSLSPSS WDERHAPPCSANFVFLVERGYHHVG*A GLKLLASSDPTSAQSAGITGVSHRAQ PLIGFKVNSVKKSVSVPTRILKONMSM YEOL
6655	20556	A	6709	392	146	FFETESLSPGLECGTVAHNCGLSSDS PALPS/RLGSSDSPAPAVVLYSFKL*I Y/FHKTCNYVLKINILLHVAIPYPSWS C
6656	20557	A	6710	9	393	KSKPCN*DKSQSYRL*LFAQLFTF/SNF FYFLETF*ESHCVIQAGIHSGTMAHHT LKLQSSNPASAPSSWDHRCGPPLA TFLKIFL*QWHAHYVSQARDGLIMFPR LVFELLGLKRFLLPQPS
6657	20558	A	6711	34	387	QDGFPLSFLLFFPEKGLGGTCTRAGPE SNLME/GGPPGLKQFSGTLPRGTGNGR ASRSRAKFN*KGKGGPGPPVELETFT LRCPHLLSSPKGKNGGCKPDPFKKVG KKAPNP
6658	20559	A	6712	1	188	IQAWNYTPVPVATWEA*AGGLR/EPRRS RLQ*AVIVLHSLCGDVRPCLNNKKG FPQPLW
6659	20560	A	6713	377	98	SLGLQSSHLNLPSSWDYRPVPPCPRNW FVVPVFFF*RE*GLAMLPRLVNS*AOV ILPPQPSKVLGLQARTTAPGFFSHLLKT LVNNVNLNI
6660	20561	A	6714	353	229	SSCLGLPKSWDYRHEPPLLAFYYI* RQALV/MLPRL*YFLDVM*LPLPFHVP SHLLNSVGMV
6661	20562	A	6715	371	64	ENHGDCFTAMATRAKRLFKKKT/CYOMF ITLTETIAKRK*LKCPSSDK*INKWYI HMMEY/YAIKRNWTLVKLNPNYAL*KV LLRE*KQNP*SVRNIFKTHI
6662	20563	A	6716	462	232	HFNLLITKITPFY/C*DGGLTMPLRVP NSWAHAILLPQPK*LGLOARACKL
6663	20564	A	6717	425	48	GFGGVPFCKARGFPLHFF*TPPVLRFPR PPVFFGGFKASPKKKTKPK/PPGGGGPP PYFHPFPLSPFFFIIFEKEPPFFFWRG LGPPPPPKNPFFFFFWVEGGKFLPKK KKKFFQISITRSVIHK
6664	20565	A	6718	3	413	GTFLTKTSLGFTLLY*VISIMCV*FIS* /SYLVYIIFYKDICV/LLMYIFYIYTC VHISVCMYMYVCMYVCMYK*PANLKT CTQKHLANGWVQVLI SVISALWEAEARE SPEVETNLAQLGPTLSLPRKKKKKKK
6665	20566	A	6719	408	71	SSWDYRC/LPPGPANFCIPSRDGVSPYW PGWSRTPD*RLSPGGDVMPALVRHVPE LLKQKQSSVRSSRPANPIW
6666	20567	A	6720	375	57	SVIREMQIKITMYKPIPTGLIVIKKTE NN/RGWQRCEIKACIY*WGCMTQLL QKTIW*FLKLNIEL/PYDPAIPPLGM* LRELKTCPLRGLGVVAHCNPSTLRG
6667	20568	A	6721	391	164	RISSETCT*MFPAALFIV/DQNPDKWTN LMWYTHMTDDYSALKRNEVLHSSWTM

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6668	20569	A	6722	381	278	\ENLENLMSKRGQSPKTPFG SSLPQTGPGKQSSCLSLSNS\PPRFID *SISLYRQGLTILLRLSNSWSQAIVLP GPPKALGL*ASKKFLYSNI
6669	20570	A	6723	2	363	QRSLEHRPCKKC/CGLVV*VS*KVOYL YKESSSFKNLLRRILHCNPLFSGIVFHF* KLLRTPRSFCLGGLHIPINTIF*IKIE KFKKC*PGTMAHPNPSLTLGLGGWIT* GQDGLDLTTS
6670	20571	A	6724	352	58	HGGAIGARFFKVFNL*PNLVCKDE/SF SLLARAVINSWPRVILPPWPPK\VVGFQ AKTPLPRKGLFESLPSLKKKGLAYAR TITAIQILGLVCPIDQ
6671	20572	A	6725	383	54	KSSPFFFFQGLLCCPGWSAVVSPLOPK CPRLKQFSP/LPSN*EYCTPTTFSI HVCVSIHKYI*YIDQYIFKFF/CR/DRT LAMLPRIVSNSWSQAIIIP*PKVLGFQ V
6672	20573	A	6726	3	343	LEV*ARATROE*KINGT*YIKYKKVKQV SQNDMILYIQNPKDSAKKLPELVNKFSS FKVNRQNSVFL*NSNKS/EKEIKKKL /PFTIAS*RIKYLGINLTKVKNLGRAQ WVTA
6673	20574	A	6727	3	615	HTSQGNL*IOYHTFWHPSSSERVERMNG TLKSHLTKLVLKTRLSWTKCLPIALLKV RTVPQKEVGLSPCEMLYRLPYSHFTVDI PTFETKSQFVKSIVLGLSSTFSSLKAK/ ELFSTDATLGSSSPGTSAPSLGDDVLIRS WEEGKLKPAWEGPYLVLLTTKTAVQT/D NKKMQTHHTPVKASPSKSCAIVPRPI PTKLKIKKKKA
6674	20575	A	6728	2	228	SGAI/SVHCNLHFFPG/SSSDSSASAS*V AGTTGVHTMA*LIFVELVETGFHPISQA GLELL/NHMCPPWPVKVLGLQL
6675	20576	A	6729	98	359	KVEYTVLLF*GFGKEFTPLVLSFSSP LNHNLISNFFLNRLVLLCYPDWSVVG*FT NHCNLNLSCLSLPSTW\DSRCVPTGAWL RFI
6676	20577	A	6730	10	428	STRTRDYAALREVLDPRRCRPRTGAMS NGRRDRPDGAGHSGPKAEARETLEKGL LPCCPGWSAVA*PRPTATFASRAQSLTV SPRLECGGVSAH*NF\SPHFQWGLAV LRTLVLNWSLALLLLNPKVLGLYALA
6677	20578	A	6731	425	158	SGTHDLR*STCLGPKCDHRCAPPRFAL FLF/FNKCPSIRKTENAQ*LPG*KNK FCRDHLLPLLSRLIINSWAQGL*CRPL KVLGL
6678	20579	A	6732	431	22	RDRVLLCHPE*SAVV*5*LTTVQNSAQ GILSSI*DYSCVP\LPVNF*TFKSVVY YFIFIFEIYFCNSKALGL/LGVSHRAR PRLVLNSWPPQVILPSQPP*LGLEAL ATAPAI PRNSNLVWHQYSFKSIPDDL
6679	20580	A	6733	44	414	AIYDLFFLLIDLPMELRASIRAHCT* RPFVATLFTVTKRLNQTCPSDE*QNKM WSL/YIMNYPAIKRNEILIHENMLCK RSQSQAHT*PHICEISRIKSAETED ELVATRWGKRE
6680	20581	A	6734	375	49	QRLTYHCRFSYNTASNMKRLS*TMHQK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						SACSMCPGRL*GVHAMRPFKVLMLRLSRSH/VARPIAATCAQ*VCDRIK/R/SLLIEEKIVVKVLKATQSQGTAKFKNETFFRNK
6681	20582	A	6735	381	88	SLFPRLETPLGRPSFFFFLFLSLH\PGWVVVV*SRITLALNS*ARFSLLSNCVPLHQAHHFFFCRDR/SLTMLPRLVLKSWAQAIPPPPEPLKRSGLQV
6682	20583	A	6736	384	293	AHLSSLSSGWDRCMPCLDNCVCLC/RVFVCR*GOAMLPRLVNSMTQVILLPHHPKVLGL*ADQDEPLWGRSGPGLPQAASG
6683	20584	A	6737	24	300	NILSAFLCLSP*P*H*YGLVIL*NVQFPRFLPLFFPMQMYTHIFFKIRIRPGVSHAYNPSTLVGGQGR\SHEFKTSLDNIARPRLYQVQNKIR
6684	20585	A	6738	2	353	IHCW*KCKITYTLEKTIVQFPIQLNIVLPIYIPAIPLLGIHTREMKTHIYK/T/CMMQMGVVLFIIAKIVFQLVNR*IKL*SIHKVDYHSE/IRNKQLYEAT*LNKCTVLSE*S*TKTT
6685	20586	A	6739	2	336	IHATYTNP*HRH\VHTFTHVT/HVYTHNGTHHTARAWPAPPTSLILPSPTESPALQIPNLPGLLSSPHAGSSQGEPEEGCQRRAKNRVGHRAEKWETELCAGDMN
6686	20587	A	6740	3	385	KKQATLLWIHLATTFVSVEI*QSKIEVHDIFKVLKEKK*TTFPYKITNPQKIAFIHEGKIKLY/IVK*QLRDFINSGVLKAMLRVL*SKRKGH*QTRINLRVQNSLVATANQPTIEYCNIVVGN
6687	20588	A	6741	406	155	TGSCSVTQA*/CWSAVIVHCSLDLPSSNPASASWIACTTGMCYHAQLPSFNLCLQFCYCMGCVFSRFYLRFTFGLOS YTRKQK
6688	20589	A	6742	1	215	LFVSDLSPTD/Y/HFSKILDNFLGKRPHNQDAENAF*KFIESQSIFDYAVRINKLISHNQKRVDCNCSYFD
6689	20590	A	6743	376	109	YHMEVNNLYSLKSGSSYLRLPSSWDYWCPP*QANF*K\FFCRDKDLAMLPRVLNS*LAQAILLRPPKAEPQLLQGQFQRRESGVN
6690	20591	A	6744	382	148	NIPQFMDFILFO*LITLSCPASP*SKFP LSSLYFIQ*GR/WLGTVAHACNPSLTGGRGQR/*A*DQELTSLAEKARPHL
6691	20592	A	6745	403	209	HIVINRIIRKYCA*HYANKFNNDLKDITFLE\NTTCKNLQTEETENLNSPVSVKEIEQKLCSDRN
6692	20593	A	6746	366	40	QGSVLSLANVKIVWFKTCGVHFLFPLN FLSLFQNYVCSHTS/YFLSLIPHESLWSFPSPFNHSS*Y*HFLKTN*MPDAMAHACNPSTLGS*GRWIT*DEEFETSLANI
6693	20594	A	6747	392	57	APKKGKGGVYPLYPKSGRKKKEG/PPPKPKKKLKTGPKKNDKDKIPGGAFFFSKPKKRGAPPVPRLF*KPPQATI*GGPKKKKKPQOEGGKKGAPKAPPLFFFFLYF
6694	20595	A	6748	376	140	LEDNI/GYSNQAGAGRVS*INTPKIKV/S\QSKIAKNDLIPKRLCAKVSMMNRVNRQPFWDRIALASAD\RGFLNKILG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6695	20596	A	6749	540	172	FFLRQSL/DSVAQAGVQWRHLGSLQAPP HRFMPFSCLTLPSS*NCRLPPCPANVL YF*QRWGTFLVLRMVIS*PRDPASAS QSAGITGMSHCAQVNTLSLHAFSCDKV PQNDLL/WPSKSPFGTSLSHEKACKDNVE TTWAQWLMPIPALWEABAGSGRQGEIE TILANTVKPHLC
6696	20597	A	6750	1	353	WFLERESTRSENIVNEMTT*OLEYVV SKAVAGFEKIDSNIKRSFTVGKMLSTSL H/CYREIFHERKSQSMCQTSLLSYFKKL PQPPQPSASATLI/VNLIKAKISAKRIKLT ECSDDC
6697	20598	A	6751	404	231	SPS/PPPPYFGGPGGFFPPPV*TPPPE YFGAPKKKKNP*PPPGGKNFFFKGPPF
6698	20599	A	6752	77	371	ITCPVLYLTSRNTTKKYYLDCCEWF* WNNRDQTYLHLFF*/CFIKKNFFPQPKR GARGGFCINETPPLGGKGNPPPPPGRG EKRAPPKTLCPFFFF
6699	20600	A	6753	354	169	ETESHSVTHAGVQVHNHLSLQPPPPGFK RFSCLSLPKK/WFSVKLN/PNT*SECYH ILKALII
6700	20601	A	6754	1	442	CICRTAFELTGRATRSEKERKKERMVD *KKERKKKEGILLKKDQEEEBGRKEE RKEGRRQTQDEFGGQNLSTVTKQS*PK KRK*GIQ/QTGAPTQERDKETSQNKNEE KARHDS*QPQA*RTQSRLLQEGRKLWKR GLVSRKK
6701	20602	A	6755	366	262	FF*RWGLTPRKLVLSNAQVILLPPFL E*LG*QA
6702	20603	A	6756	3	223	GLKQSSCFCLSNEDCKHVPP/HLRFLF FVCLFCFVLFWF*RYGGLAFLPRLVLKS WP*VIQPPWPPQMLRLOA
6703	20604	A	6757	418	244	FSLLSSWDHRYMPNMTF/SFVLFCLR EGCLTRFLRPV*NSWTQAIFFQSPKLLG LQV
6704	20605	A	6758	46	256	KLKKNKTEARHSSACL*/LPGSWDHRYL PRLANF*TFWRDVSLLPKGVSNLWAP TILLPWPCVILQV
6705	20606	A	6759	391	55	FTFFFFHSHGVSPPCCGWSRT/AGSS GSPASAHAGITGRMHTRLQDIY*LE /TGQTVTQLQSVLADTTLTKRLSWSILC CVNKPETG
6706	20607	A	6760	377	2	FGPEPPGSPPPVLKTRPNLFLGPHKKN INFPFP/WELNLVPLKGPPFFFLR*G LAMLPRLVSTSWAQVILLPQHKLLELQ VHAMVLSRSTSHSPRSRLSPRFSQRL PVSCNPAQPSFMA
6707	20608	A	6761	2	259	LTIA*KNPFLGL*GQICQIPRDYQTS R*IKDNLK/WDTPCSWIGGLNIVEMSV LSKLMYRFRAIQMKTTSGPFFFPWKKG IFF
6708	20609	A	6762	1	169	FFTEFRSFA*AGV*WHDLSLQPPQPSG SSDSPASAAALPFFFLKKIFFFFPG
6709	20610	A	6763	1	496	MATCTPKHINTQICVSPLLSLSEFEQ MSIFKKGENELAGTGNI RPYDSCPGNR P/APFATSPAPRHPGSPWRPPTSGGV ARAECPASPNLPDGGFCQSPSRGRKEE *LRGESTSTLAIFF**APNRHSF*LPRQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						P*PHGDCPARKKKKKPNDRLOFTVT
6710	20611	A	6764	1	229	VLLLCFFFFVL*DRVLVGHFGWSSRLVLT KTKTKQKKNNIFVCRVGG\LTLPRLVS NSWPMQVLSPOPLNALGLQV
6711	20612	A	6765	580	273	WRQSLTHSVAPQGVQWHDLSGLQPPPPG FKRFSCSLSPSSMDYRRAPPRPTNF/*Y LVQTEFHHVQAGLELPTSSDLPTSVSQ SAGITSVSHHAQLMDIPLR
6712	20613	A	6766	220	239	AQEFKAAASTALQTEFLCLKKKKKKKG GVSLGGVSSNFRITGGGASVTSISIF/CF FFFF*DRVLSGVQWCSLOP*TPGLKRS SSLSLSPSSWEYRHVPLHFA
6713	20614	A	6767	89	387	FLSPSGSKEHLQQTGLRSTFSFFFFFKR EPREFRGVGGCQPNLG*WKPPPPG/RQFS GLTLT/SNWERWATPPPTNFIFKKKG NSPWKRGAKI FGPWDP
6714	20615	A	6768	397	223	IREVGVVINVQHKDPCD/KWNCVSY*L* *WIHKPTHDKT\HRNTHTHTHTHGMHS HTQK
6715	20616	A	6769	3	367	SWKVCSSKRPIEPSLSFF*KHPRVLLRAD GT*VSLATL*HMQLS*AGSVKCAEPRS NAPPHKATFLFLFFCTD/SSLTMLPRLV LNTWPAQLPPCPKVLGLPARANSSLT SVFKLTSFCC
6716	20617	A	6770	490	260	FFETESCSVV*AGVQW\LELLTSSDPPA SASQSANITGMSHCARRCGTHYLCERF LVSVFTALLSOLLEGLLAHSRC
6717	20618	A	6771	418	130	FSFRLNLRFLLNGPFLFFFFFF*DRVLLC CLQWSAVASN\FDLK*STRGLPKCLDY RHEPLCPAMWDTLSSL*EIFGLFCHPRS LPAPRTGPGSO
6718	20619	A	6772	311	314	PAVUGELFLLHHVGHACLFFCHDCKPFE ASPAMLPY/OPVEL*AT*TGIEVLTPGC RPOAVFGLKVGPHOQPTPVYLG I
6719	20620	A	6773	465	283	CFSLPSSWDYHFFPRFANF/*YF*YHV GQGLELPTSSAPPASASQSGITGMSH RANPK
6720	20621	A	6774	410	91	RDRSLQDPQTFRLQSSCLSPNS*DYR HMLPCLAGLWGLACQTDROTDRQTDROT QTDROTDR*TD*IDSRDR/SLAILFRM FSDSPQVQNLPLQ\WPKVRLWA
6721	20622	A	6775	409	253	LIFAFF\CRDGLATLLRLVNS*PCAI LPWPVVKVLGLQARAPVRDLS
6722	20623	A	6776	3	278	FFFFSLHWAPLAFFFFGATSAHYNLP I PG\SSDSPASQSVAGTIGACHVQLF\ VFLVEMGFHHVQAGLELLT*VIHLPO PPKALELQI
6723	20624	A	6777	79	442	RDEDRGLERRCVSACSTPOLGNASTI*G CPGVSDPFLSHILF/CFPEK/SCFAPQA EGGGHNLG*LEFGPPGLKQFSCLTPQRI WNNGGAPPPPLYFFFLKRRGGSPLWPGW A*TS*PRS
6724	20625	A	6778	77	417	HRGLHLSFFLF/SFLFFFLKRAALLWPR EQGRGWIWNCTLSLRGGISKALPS*E AGTKGGRPHTLFLVF*KKTSFSQVDQGG GIDLWARGNPPFGLNKFELQKETLCPG HIP
6725	20626	A	6779	62	235	IQLRLIREGKCLAYETARNKGSQDLHA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GLSCLCCCCCCC\CNCFP*STRKFPTKPE
6726	20627	A	6780	908	566	SKMEFRSCCPGWSDLGSPQPL\PLGFKQ L\SCLSLP\RAWYYRHAPTHPANF*FL VETGFFHVQAGLELPTSGDLPTSASQS AGIIGVRHHAHPECVQFQQLSEANLRRI WNQED
6727	20628	A	6781	11	483	TTALLKAVRH/G*HLSLQRLLSF\VCL CPAPGGAYRGQRAS*SCGGLHPVRASR LCLCPNQAWAMAGAPPPTSLSLPPCSLISD CCASHQDSDVGVGSEPHAGINLPVCRF LSPLEKRSIRGVTRFRCRLSPLSLTR KGNLSLTPCASRVSSASPCS
6728	20629	A	6782	225	589	SRSEFPGNFRSLGVGVTCMCLSLSLP SRSFLRPLSLSLVVCVFCGLGTRVPCAP EGGFLARRPFFWSASPRVSAWLVWPGN RFPGGSGLGVCCEGLGNVGI\WSEPGQFS FPPHPEOPLC*AGSRRALPQNGQRLPG AHRLPAGGCPQSFKKVVVTPVALCPHRE M*POLDAGTEKEAGKGMQACLSLKGWP SWPSPHFDTPPRMPVVWAPPRIPLGLW PLL*PPAGRNARRKKFETDRRGSAGSQ PQACADGVRVSLPKSGALVMSRTGLPVC PWAALSVPVARSRGDQNPATSGAANGVWL PAVCVLSLSLALSLFALSFSLCPSVCS CALGHVCPVRRRVGLHVLGSSGOPLPA SLPGCCGRLAIVFPVAFVMSVKAWATN ASASEPQGSFPPHPEOPLC
6729	20630	A	6783	458	170	PCIVTASASQSAGITGVSHRTRLVLNFS KVGSVTISLG*EVLGRHWP/NI/GRLDK TGPGEKHQFIIHAPQSAPSVYHCLGNTQ ELPPSLTAMISQPKR
6730	20631	A	6784	1	192	FFFG*TLPLSPRAGVQWHDLSLQPPH PFGKFQSCLSLP\RG*DYRACATRDGLI FCNFFLOD
6731	20632	A	6785	3	246	SLCVCOYVCRKCV*VPRQVSG*VTMG /CATGTFLVILCG*QCLCG/C/*EDPP YCEQLCVHVCVCLGRGWSVCVCISRL
6732	20633	A	6786	408	128	GPVYPYKARG*SPFWPFGKEFSFPKNPT PPGGGGAVLPFPWPRGRPEMSPPGCKR C/OPN*IFFLPPHGHKTQGPFPKKKK KISAEFLSVV
6733	20634	A	6787	1	418	LTILGVNMKNCDSNKEVKISAPITGAWKK LIPTLTD/EY*GFKASVEGTAAHVLETA RELEVEAEAVTEL/LQSHDOT
6734	20635	A	6788	3	237	FFFLT*VLTIV/PG*SAEVQS*LTAAST S*\VK*SSHLSPSSWDYRMPHPANF FFFGKKSLILHPGRGGSLLPTP
6735	20636	A	6789	282	3	PHPDNF\REFLV*TGCLHVQNGQLALLSP GYPPTLASPSAGITGVSHCTRPKRYFM VLSNKSINRFGLCTVLPTCLQAPRRTGP PPATVLGRGT
6736	20637	A	6790	62	328	FFDRILFCHPRWSAVIQ\SWLTEASKS W\IK*SSRLGLPKMCDCHREPLCLDNTT Y*CRQNTLPTILIGCFRVS\PYAKYTGK FWGAEG
6737	20638	A	6791	67	353	TNRKHTYLELNKREKPLQITVFFVF*REL RGLILANGNFFLRG*SNSPA*PSKVAGI

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						TGPPHQAQILLVLEKTFGNVVG/RRGP PPPPKELALQA
6738	20639	A	6792	744	382	MTPEKTIARIHYFYLYLFYILRQSL/DSVA QAQVQWHNLSSQAQPPGEMFPFSCSLLL SSNDYRRPQPEA/NFFPY* * RRGFTVL ARMVSISSPCDPPASASQSGITGMSPR AWPKLHITKL
6739	20640	A	6793	372	129	RVLPFCHSGWTAVVQS*LLAVSTQAARR SPHLIRHVPPHPA/NFKQFFCRDGLIM LPRSVSNFQAQAILPQQPKVVLGQA
6740	20641	A	6794	395	25	QFGLFCFTPRKKPDSFSKVFVAVLSF/FP PSL*FS/PLSL*VQEMVSICCPGMSAV\ TPGLK*SSCLSLPKRGYRCAPPHSANL KFFL*R*VLFMLPRLGLH\SWVQVVLCO WPPKGPSLRACKT
6741	20642	A	6795	412	176	KKS*/CLATPSENWVL*NGPPLFFFFL *RRDLAMLPRLVSNWAQVMLPWPPEK\ VLGLQAGATMDHSCVQYSHSFAPE
6742	20643	A	6796	444	95	NFVRNCSFLQSGCTFLHSYQQFL/PC PCQH*IMSVQILTTIVIGVMHLV*ICS ALMTDFLFMCHVLI CHLHIFPGEVSQVH FSLLLFLFESGSIYVQAGLHLLFSSNP PASAS
6743	20644	A	6797	378	732	FFFWNLGSSQPPV\PAFTR\FSHLGLL NSRDYRHLPPRLANF*FLVETGFRHV QAQLKLITSGDLPALASQTTGITGVITAS PSLDEGVFKALPPVPGTTLCLPWPWTGG PFLQPAL
6744	20645	A	6798	444	1	PLCFPPGGGGLFSSHQPPPPPPPKRGS VGAKKNIIPGPPFFFFFKKPPF*CPY PF/SEPKARKGPPPEPOGPSPRSLVS PLGEKKKKKIPPPETQPPSFGA*WKK RAPPPGPRAGGRNSFLEGGROQGRGGS VREFRAGR
6745	20646	A	6799	462	83	IEFLRPALCLSSNPASI*KPHFLLEF/ CLPFLSFFFS/SFPFSFFLFPFPFPPSF FLIPFLSYSLCCSGWSTVA*GLTAS\ TYGLKQSSHL/SLPASWFFCLTN*KKIF FRDGLITLIRLAYLFLNF
6746	20647	A	6800	433	185	PPPPGGRILLVEKTREGGOLKPGQPGROAG LGMGRNPGKAQRPASGAPEMQLPARPP SGGHLYGCGAKNNEGANPLLCGGTQSG SVAAAGEVSKSAPDSGLMGNMMLVKKE/ AGGGGEPQANQETEN*EG*PMSPEGAL LLTSPAAATLPLPVPQRQGFAPPFLFL APQP
6747	20648	A	6801	395	60	IEFLFLPLPSVDGRLNSHQLPVMNEAT /MSIP*HAFAWTC/SSFLRGCCIGA*ST LLYGGYMFSLYLRNQTIFQSSCCIVNGE QPRMNRFLS*FIQHLVFSVELTRAIL GI
6748	20649	A	6802	423	98	RGVY*PGGLQPPPV/REFFFFFIGRVS VLQAGAAAPTCAQSLPGSWDYRHLHA NMSS*FLYEV*RVYFMSLPRLVNSWDQ AHSOPHALFTCVSVKRLATL
6749	20650	A	6803	396	194	SLMKLAIV*VLHTDGGFMHPSAISCHD IFDSLHITGGSARKICRALYELIMOLME EHPAQEQTTIA

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6750	20651	A	6804	373	192	PALNPWAQANLPHQTPALSSNNFFYF/CVEMGLTVLRLV*NSWPEAILLLPWHPKVLGLQA
6751	20652	A	6805	370	242	KKGTSKFLFFPSYSFFSKFWYQKKVKIAFFFF*DRVSLCHPEWSAVN*S*LSAALT/CPGLQGSWGYRHVLPCLANFS\FFC*DGVSMRLSENWPFCLF*PVFPQPGHGNSISTKK
6752	20653	A	6806	464	182	DGPHRFEPPISS*FLPWPFPQKLEIG*APLAKQIFFFFFFL*RDIVLLCC*GWGTVYSYVSWSSRLTAAS\TAVLKQSSHLGLSSWDYKHHH
6753	20654	A	6807	3	228	YTCAGFFRRGSLCHLQCAVARSQILIVA LTL/VFPOLK*SSNLGLPKCWDYRCEPFLACVNPNTVKDVCFCSCILS
6754	20655	A	6808	506	173	NLHLPLGLKQFCSLSPPPSRERYRRAPPC TANF*FLVMGSRHVAQGLELLNSGD SPASASQAGTGVSHHGQISLPKQILT STRISEVI FLTLLRLTHLDLPCLKFLSL
6755	20656	A	6809	676	397	VSSCPDRDGGHGETLSVLTKQLARHGGCL*SQLRLSLR*QTRLNSGVGDHSEPLSHCAP/AWATEQVSVSRCKKRLQHQKERIPEWVRS
6756	20657	A	6810	367	31	QVFOELYSQDLFIYLETLSLCHPG*SAVARSA*VVTAAASDSWVKOSSRLSLPSSWYR*VPPYSAHFDVNSFLTCTCTSPGLTKIEDSWLGTVAHANCSLTLGGHSGQIT
6757	20658	A	6811	469	251	LLSSWK/YQVFPFHLVFIKIL/CRIGRETASCCI*PRLVNSWNPQVILRPQPPKMLGLLSATMPGPISVFCEPCFCF
6758	20659	A	6812	16	462	EIISYCGFNLHFSNDYKKRKRERERK KRKKENIGE/HI*DIGVSDILDLPKAWTKLNLIDKWHYIKL/QKLSS*RVAKTNKLSFCTAEIITRVKQPMWEKTFASQTSDEGLISNTYKELKQLNSTETNKKNNFDLLSADKG
6759	20660	A	6813	492	243	SSWDIGCTSPRPD\IFVFLVETGFPMPLARVLLS*PRDPFASASQSTLVDSRYKVYQNTHQGVME*NYGCEFDLFTASVGD
6760	20661	A	6814	32	308	EYTLHPHYLTGPPPPVPEETYSYS*YF LSPNTQICQ\PAFPTLNTASTCLSRRTARFPVPIYQDPSLEP\QLFENSLTLPTFLRHSFCV
6761	20662	A	6815	97	274	GRFLELVKRGSLGLGVVVHAYNLSTLGG*GGRIP\QGFKASLGNIAKSCLYNKKGA
6762	20663	A	6816	74	376	DFFIYVSVPTHLVNIKDVKLVLYKSLKYFFAIYRMENIYKLYLGLGNIQISMEYYTA/IKKD*ILLFAATNM/RLEDIILSEISHEQKS\KRCMFSLICGS
6763	20664	A	6817	1	1127	MRTVAPRTVLLLSGALALTTETWAGSSHMRYFYTAMSRPGRGPRFIAVGYVDDTQFVRFSDAASPRMAPRAPWIEQEGPEYQDRETRNMK\ASAQTYRENLRIALRYNQSEAGSHTLQRMYGCDVDPGRLLRGYHQDAYDGKDYIALNEDLSWTAADTAQITQRKWEAREAEQLRAYLEGLCVELWRRYLENGKETLQRA\DPKPHTVTHPTSDHE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ATLRCWALGFYPAEITLT\WQRDGEDQT QDTLWETRPAGDRTPQKMAAVVPSGE EQRYTCHVQHEGLPKLTPERWEALPS FTSPITVGHCAWAGAVLASWSSGAVVAT VDV*EGRSSGGKGG\SYSGWRPSRPVR QGFWNCLSALKKP
6764	20665	A	6818	34	382	STAGATHVCMNCVHVSTCVCAKMCVUV KF*IWDTIGAAQLSCCVLVAQTEIIVL QERNSSLEREVCVCAK\CVCMCMCVHVS TCVVCVVCV*V*KRNWPGMVAHVCNSS TLGG
6765	20666	A	6819	1061	305	FFLRWSL/DSVAQAGVQWRDLGSLQAPP RGTFPFSCLSLPSSWDYRRPLPRPANFF YF**RRGFTMLARMVIS*PRDLFASAS QSAGITGVSHRARRRNTILY*HLNFVIK SHKPPDIVFRDL*GPRLHLENPVL*GAK SHSSCPWLNLSPPPPHAGSHCLSSSPR MGARQDLLFNASSHTGLFPLQLNQTAS RPTSQVFKSLCFPLPWVQPFALPWVROD BGRASVNSPODPPRPVPCAGFTHSCNS
6766	20667	A	6820	610	248	ERRSHPVA*AVVKWCHLGLSLQPLFGS SDPP\T*AS*VAGTTGVRRHARLTPVFF IETVSHHVQPTGF*TPGQAIRLPQPP ENARITDVKPLCLAHFCYSKHFIWVPAP CISHQKVH
6767	20668	A	6821	3636	3332	TLGSHATPRCHGSHFSSCKILF*FFVF EW*SHPVQAQGVQCRDLRSLPPPL*FK RFSCLSLPSSWDSRRPPRLANF\CIPS RDGILSCWPGWSRTDRL
6768	20669	A	6822	563	146	APGLSFNCYIPPAFAFMGEITLFEVD/ NRSIFPTEY/THILLISSDILHS*TIPI LGLKLTDAIPRCLROTTLTGRPGLYYG QCSEICES/N/HSFIPITVLELLKYFK T*STSTLYKHCKAIQHLFPKLKIDGVYT SLQ
6769	20670	A	6823	399	201	KAEPFPAKSWSKGGYVLPRLS/IRLDHVK WALEPDDIAVLNFMKERRHPQSKS*TILO KNIQFPSPIVOK
6770	20671	A	6824	323	323	LPTVIVITLISFNFFPFSMRLITLSEFI CMYVCICIYVCIIYVCVYIYVCIIY /IYINISF*NDRIISFFMLE*YVCVYIH EWIKKI
6771	20672	A	6825	396	122	LPFGGHRPAVPGGREGMGFSRGNPGNPR F*KKGPPSPGGGPAAGGPPSPG*ARKM G*PRGPSLP*TIIPPGSPF/WGPPGVPT PETLVGFKKRGHPPRGGGPPGVPLPRR AKPEKWVNPGGQAFHEPKSPPRGPPRGA KPETLSPKKKKIV
6772	20673	A	6826	414	64	RGVEGGAACIFKGLSVAGKFG/YLSAMR SCFRRLMLFKS*G/QVIATKHMPLPTVLR MVGDPVANVRFNVAKSLQKIPILDNST WQSEVKPILEKLTAQADVDVCKFAQEAL TVLSLA
6773	20674	A	6827	2	519	KTKTCLVEEIS*ITGRFLERINKIDKPL VNL*KKVQVNLIN*NSKIVTERT*K /IKKHGYOLYANKFY/IDEMDKFLKRD KLAKLTQETIENLNI PVSI*KFLI*NIPI XMKTF/GPDGISREL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6774	20675	A	6828	413	114	GCKRGGPFIFHPFARGPQ*GFCHTFAVQV FEPPLGSFPHFRGGFSSGGCQRGEGRK ERRPSWTGDSWMAQEGRTPAARLEGAVL EG/APGPEAPGTGTTMSAPTWPPEP/G/ GROVDVPAPFPEGASARQAR*HEE*LHWK EILL
6775	20676	A	6829	479	261	PCFSFLNSDCRHAPP/RFV*F/LVERG FRHVARAGLEFLT*SGLPASASQAGIA GVSHCAMPLOQVGEASLQY
6776	20677	A	6830	492	313	HPFGWPNWGRASAVGEFRDKNLFYFEC EIRTMGGREHGQSFGAQTFFQLLLSFX VESK
6777	20678	A	6831	378	1	SNGLCQASSASPNKIVPSTSLKVCNS/ VVDGSRNPSVAFPLPTNMLFAVAPSIS SOMGSETPIQGYRVDEKTKCYIFF/V *ANRHSFGVYMINVHALVSGPLSDDS GVNKPOMKHQCHSA
6778	20679	A	6832	374	76	QLVERKNTGVNKSMTDRVLTMRCRLRL *ALRT*PGTNLINDQIGMF/KFSGLSPK QVCVLEVNKHIVLMPSGRINVSGLTAKT LGYVAASIQEAVTIIQ
6779	20680	A	6833	369	56	LKYLGTSVENRYADOKWLSVVISALM* FE/CWGIARSEDHRDHG*OSEIPS/PAN FLFLVEMGFYHVDQAGLDLMTSGNPPAC NTGMSHCTRPGRTDIALILCSDP
6780	20681	A	6834	457	142	DCIALSLRDLQWCDLGLSQAPFPFGFKQ FLCLSLPSSWDYRCLPFRPANF*FLVE TGFRHVQAGLKLTLSSDLPASASQSAG ITGLSHRAWPDSSFECSGS
6781	20682	A	6835	407	35	TAPAIRGVHLRGRGWTYGVAV*AVPPAS IPAYPGVVYQGYFGADLYG\DMQHSDM RGLMVSQHSMPMHT\LQQS\SVTVMAGC TQPSHTMPLPLPLVY\ELALRWVYAEVA TSYLPPEAVMLAPCK
6782	20683	A	6836	1	428	GKTLNFPFLSGKSGFLIGLPENDWFPDV SVFPRAAFPLRGRSVQSVVREMGSVAQ LLL*MLTFTPHKRISAFRAL\QHSYLHK DEGDFE
6783	20684	A	6837	3	612	FKSGSVFNKKKLEEHPLWQDVALGTAL CPQLFSLPGWGIWERRAACLPNCPQL CPHCQPEAQYFL*AGQ*GQJQKKEFG A\GHHP\SGPQVPSAGGEANTAMEKRL SPAVAQNPQRKNTLDRGLPFGCAITTT P*SLRPR*TPVGAGLAARISHHPCGSG QEALALCPDRPHKDRGVRRGAGGPRRR VOLGGIIF
6784	20685	A	6838	3	412	YRWGFTMLTRLVLSS*PR/CDPPASASQ SVGITGVNHRVRLVFFFPGTGPHS\MAQ AEGQGNLQ*LPQPPGAKGTLPTGNF KGGPHTPPNF/CIFFGKNGVSPYCPGWD FGAKAILPPGPPKLELEGSFPAPGKVF
6785	20686	A	6839	419	26	EETSRILWSIGQCPLLIQTAQVLSPTSGH GRHREHRKPTDSLPSACAP/RLTTPP SMCPASHSLPSSQCMGFTLTPTTACAR PDTHSPFPVCPAPL/CRVCPFPFSL PTPA*TKPRTOFLSSMYCGRSS
6786	20687	A	6840	365	66	LLERQIGRSVYGFSSKSIIDFVSLPHR GKLVFLCLHTSSWDTGVHYAPPA*SWH

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						TVVHPRPQVGG/AGFELLTSCHPSPSLT SQTARIACVSHRAPKFM
6787	20688	A	6841	445	188	GFQ*FSCGGLGQNDTRHVPRLADECI F/M*RWGFMASRLSSMS*SAFSAQSA GITOMSHCARPATLNSPICGTSPLGSGF FF
6788	20689	A	6842	3	412	PQSPQLTTVTAPRRFRALLMGTMTANLQ TRVSTSHLQGPRLTSALTQMAQAVAT PPVSVLAVVLSARVTVLP/LN/VNGI SVVIROLQKAAGROPSPPHQTRNNLS* VASNLKFLILEVAELFCHVLTFFSYQ
6789	20690	A	6843	113	410	NHKCNVNFYNGPRLSKRLITLPTLHYF LNFILCKSSYLTLNLKLOTLNLFCK/YE M/ESHFVTQAGVQWHDLGSLHPKQSSYL SLLSS*DYRGMPHHLAN
6790	20691	A	6844	2	357	FCPLARILQSGRFVLPWNSSGLVRGRRO EGPHGAFTRHT/SLRAPRSENERR/ RIACALRAAHQASGWRLTTPRAPSPSGC HCPAPETSR*EAWGARRKGHCQCAPH QPAQDIS
6791	20692	A	6845	392	279	HFFFPQRD/KSLAMLTRLILNSWA*VIL LPQPSKVLGLQV
6792	20693	A	6846	3	275	VNLVDKAAAGFERMDSNFETSSVTGKM LSSSIARYREIFYERKSPSMOQTLFLSH FRKLP*PF*PLATTITLY*QPSTSRQDP LPARRAR
6793	20694	A	6847	1	454	FFFFETQPHSLPRLECSGAISAHCNFL LGSSSSPASASQVVGITGWHHANIIF/ VLEPVEGFFHHVHAGFELLTTGCPETL ASIMCILVYLWFOHLSVSKNLKGQNAS FYFSPFGQHGSGFVKCSIWCCGSLSGLE GHFLPPHSDPLH
6794	20695	A	6848	13	148	GSARHTFAG/ELKLLKLRHRYGNPEGG CTEPIWCYRTPPNTTD
6795	20696	A	6850	204	30	TIFSRQVLRTQNLVSEKLVRSTVYANG S/VLOGTLWASVYHGKILIGTVFHKTLY CEL
6796	20697	A	6851	2	429	EVWASGITGKAIMAMPVIVQPKNPSSYP CRQFPPLQLEAKRGFQLLTFKQKHGHL IPYN/TPILPVKKSEKRYLVQDLRIIN EAVVPIHMPINPSVILPQPDAQWFPV LDLKDSSFCLSP/VDPSGQLFAFE
6797	20698	A	6852	3	160	SGWDRHRRHTQLIFMYSFLPFCRRDR/SLP MLP/LVLVNSWAQVILLQPKVLGL
6798	20699	A	6853	2	243	ACMILAAATILRVV/PLRYIILINGIN KFTKLRNPYSIDNNELLDFLSRVSDV QKVQYAEKLCSSSHPLKRSAL
6799	20700	A	6854	24	458	SRAARRAAGTTRRSSHTGCRFRADPGA RCLPRGSPHPRMDPPESP/PSETSPGPP PMGPPPPSSKAPRSPVVGSGPASGVEPT SFPVSEAVMEDVLRPLEQALEDCRGHT RKQVCCDISRRLLAQEQWAGGKLSIPC KEENG
6800	20701	A	6855	3	183	CCDFPVASQRAGITSVTY/Q/WPSLGS LQPPSPPEFRFSCLSLLSSWDHHPPLR PACKVFC
6801	20702	A	6856	2	242	GNHPYARKLA/AQRRASTVSSVTVQVEVD ENAYRCGSGMQNAKDSKSLKTHQTQGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6802	20703	A	6857	54	401	RRARDKAL\LVANGKRLWCTEGSVC EGERLQKFMHVLTHTHTH/AHTERAH THTHTRTHTPRSGMHRNNRNLAQNLFPK I FFLLSSPPSLFFLI I FFLLSLSLSL SLSLYKHTPLCILSLRTEHLHRMGALLG GHILE
6803	20704	A	6858	1374	579	CENPSKSTRPGQGPLLPHQLPFP/RPA PSQSSPPEQPSMEMRSVLKAGSPRKA RRARLNPLVLLDAAITGELEVVOQAVK EMNDPSQPNEEGITAHNAICGANYSIV DFLITAGANVNSPDSHGWTPLHCAASCN DFTVICMALVCHGAAI FATTLSDGATAFE KCDPREGVADCATYLADEVSGMLANS GAVYALNDYSAEPGDELSFREGSVTVL RRDCPEETDWWAALHGQEGYVPRNYPFG LFRVVKPQRSKV
6804	20705	A	6859	36	269	IALGSMVDLITILMNEHKNIEIKRTIFL KIATR\IKYLGILNT\RGKDLDTENYT TLIEEIEDDTNKWKDIPCSWTGV
6805	20706	A	6860	47	888	TLRARALQARFTGSSCTAATWTS/SGA SQHSLRALSWRLLYSRARLKASRTSA LLSGFAMVAMVEQVLESDHEYPGLLVA FSACTTVLVAHLFALMVSTCLLPHIDE VSNIHNLNSVHQSPHQLHRYVELAWGF STALGTFLFLAEVVLVGMVKFVPIGAPL DTPTFMVPTSRVPGTLPVATSLSPASN LPRSSASAAPSQAEPACPPRQACGGGGA HGPGWQAAMASTAIMVPPVGLVFAVAFH FYRSLVAHKTDTRYKQELNELNRLOGLQ AV
6806	20707	A	6861	3	391	NKISFFCRDWGLPMLPRLVLNSWAQVIL /LISTCOPPKVLGLQA
6807	20708	A	6862	322	175	GCRCVPPFRASFKIFGRV/RGLDILPKL VSNWSPQAILPPWPLESLVLAQ
6808	20709	A	6863	700	294	YVLRGGTLTLPL/ECSSAIIHCSLKL LGLRNPTTSASRVAGTIGACHHTRVIFI VFWVIESCLLQAQAPKLGSSDPFALAS QAGIAGISHAWPPYFYFVLSSTIPS VLSLHSHLILATILRGGDVTSOTDK
6809	20710	A	6864	371	77	RSMPAN\NLVYDTSDDDDYHLKVLLEG IQTLNGLREVSGRRRTQILKQTSKFTD NSINELVALLKNVGLLYCPKCDMDKVET LRMVQCRSVEGSCGF
6810	20711	A	6865	273	34	DYLPPTYLKFLRLFF/CLITETESHVYA QAILELLSSSNSTPSASRSAGITGISHH TQPNFSNNTLLKPYLRISYALLFA
6811	20712	A	6866	1	190	GAKGMHHTVLRVRYF/CCVEMSHYVTV VGLE/FPALKHSSCLSLPKCRDYEHEPP HLALFCFSF
6812	20713	A	6867	506	293	EKPSNGHKKPYTWISAILFIKTKWQ S\PRCPSAGENINC/WYTQTEYYSMLK RNELSNCEKT
6813	20714	A	6868	2	116	LPFFCRRD/SLTMLPRLISNSRAQGILL PWPPKLLGLQT
6814	20715	A	6869	10	141	GSANLFFIFCR/DRGLALLPOLVSNPWL QAILLWPPRVLQQA
6815	20716	A	6870	2	603	APTFTFNPFAKGPFKRGDTYHLQVRGSA EQIARWIADRTDVNIRVRPPNYAGPLM

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						LAALLAVIGSLVILARSNMELFNKTCGW AFALCP\VLAMTSQGMNDHIRO\PPYG PKDPKHGHVNYIHGSSQAQFVAETHIVL LFNGOVTGLGMVLLCEAATSMDIGKRKI MCVAGIGLVVLFSSWMLSIFRKYHGYP YSFLMS
6816	20717	A	6871	375	1	GFPGFVPVKFGIPAPVAPQNPFFPPSF/ PQGGPPSPGGPNNGKNPFPKTPFFFLK NSPQKKIKFLFKKRGPP\GPNQKDPFK DFKKRGLKPPKGGPLKKKKKKKRSN YSLKKIYSPFGHFF
6817	20718	A	6872	255	23	GRVDPSTSTONAGITGVSHR/GVQWRDL GSL/QPLSPGFKRFSCLSSSSRDYRLV /PFCIFSRDRILFPWPGWSQTPEHLK
6818	20719	A	6873	5	157	YLLFTSYTHARTHTHTHTHTQFLLLWTS GLS\SCCYIFSLSGPNTKCNMIF
6819	20720	A	6874	351	132	SPRRCSAYGVA/IYLFYFLINLLSLYS IFYGAPNPSFLCEVQEPSLG\SGWEPLS GNHSSIKMKIAHREVNM
6820	20721	A	6875	99	337	AGSFFQKKKKKTSRVNRQIQLKFIYM NCASDKGLVPRIYKELASAR\KYQSI PS KVG
6821	20722	A	6876	69	306	YVSHHLSFFF/CFFGGGEKALFFCPRTG IKWPQFGLLEPSPSGLQKQFGLNPPETL EYRVFPPPGKGFIFFFFFFFF
6822	20723	A	6877	335	169	WHDGLGLQPPFPG\SSDS CASASQVAGI TGMHHSFNSF IYLFCEYKVFLETTLD
6823	20724	A	6878	2	237	ELGYKVLFPFPYSPDLSPTDYHFLKHLN NFL\FHNGQCAENAFQVFIESQSTDLYA TGINKLISHWQKCVDSNCSYLN
6824	20725	A	6879	2	199	RGRVGRQPKKEIELKKLEEGEE/VAP SSSSSSDPLISEPDISGSEEDDDEEGE VGDEGKKKKK
6825	20726	A	6880	1	206	FFFTTESCYVAQAGLELLGLGDPFASA SOVVGTTGARHHAQLIF/VFVFLVEMGF HHVSQDGFLLTS
6826	20727	A	6881	1	123	WYHTMEYYSALKRRKFLSPATTWMNLE \EIMLSKISRRRG
6827	20728	A	6882	15	105	SOLL/WRLQKQNLNRGGGCSFPLNCH CTL
6828	20729	A	6883	223	1	AASTFLFPLNKLNSLRG\SLRTFSSVTNV RKLTALTWNSQDIOFFSRRSLTLVARL ECVVRSWPAASRRGLCL
6829	20730	A	6884	193	3	QGEQDFLEPCLPNFFNF\FFCDRTVSML PRLSNSWPQAVILPEPHKVLELQARAT TPSHVFIF
6830	20731	A	6885	2	355	RLTSSDLPASASQSAGVTGMSHRARFR NF/CILPNLSPCNTHSPLSLPQPLAFTI LLSLWICL/SLDIS/WDYRHMPRLAKV FFFGDGVSQ\YRPGWSAVVPFAASTSGV EAILPQPPFK
6831	20732	A	6886	1	151	HSVAQAGVQWWDHGSRLRPGTGLKQ/FL PPLKQSSCLSLSSWDHRCATY
6832	20733	A	6887	314	203	FLFFCGDKVLCLPRLVNSNSNTQVILQP WPPKVLGLQE
6833	20734	A	6888	334	86	QNRSTFKRGM/MGWAANWLMFVIPATWEA EVAARIAPLHYSGLGRARLSRGGMKCTS IFCCKSAKDCQTLFVKKKISLPTLPSI

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6834	20735	A	6889	345	152	QHARIMSVFIVETGFHHIGSGGLEMT/S/GNMHASASQARITGVSPHARPSLPY YKCS KQKLCNE
6835	20736	A	6890	2	169	ARECSGAI TAHCSLDLMGSSDTFTSASQ VAGTVGVITMPRIYFK\FVEMESHICIA
6836	20737	A	6891	361	184	NQSSCFLLSSWEHRLMPPHLANF/SFF DRDE/SLTVLSRLVSNSTQAILPPRIFFENS
6837	20738	A	6892	3	330	HESAAITGVSHCTQTFFFF/CETGPRFV PQVQGGHDLSSGEFGFPRLRNWPGTLT ONAGNTSTLPFHRTNFGDFRRGSGFPCG PGCGFTDRDLSGSPHILGKRLSTLPPP
6838	20739	A	6893	2	348	ARXFFNNFFCK/NRGLSNLPRALNSG ACGILPPWPKKLGRLPTWDTGSSG LEGHS LYPHHSLLIFHHCKSPCFYKQW RLFLIRITENQGLTPLNAKPAEPVMNE ARTQA
6839	20740	A	6894	340	240	CRD/RSRLMLTLVLNSWTQAILLSWFP KVLGLQA
6840	20741	A	6895	155	1	HLCFWAG\PAVHSCHPGTGLGGRGRITR GQEFETSLGPGTDQVLAKCSRA
6841	20742	A	6896	454	294	PSSWDYRHA/PPMNNVDDFFCRDE/SL PMLPRLWNFWAQILLPWTPKALQLOA
6842	20743	A	6897	49	333	IYICLSFYQSIITYLYDKCHDVLETSHS VSLDLPGLRFSHLSLNDHRLILPLWASS NNFF\CRNRGLLVLPRLVSNWQAILP PWLPILVGLLPA
6843	20744	A	6898	434	324	FFFFCRD/RSFAVLPRVLHNSWTQAIRP PWPLKVLGLQA
6844	20745	A	6899	127	365	LPERRRVYSISGYRYHLQSLFFFYAQH ATFNNEML\LGIVAHACNPSTLGGDRGR MALGQEFELGLDSI\VRHLCKNKK
6845	20746	A	6900	208	1	FFFFPWILVETRFHVA/RAGLELLSAG NPPTSPSQSARITGIWFFVWSSNLSQF CYAHSFFTCWYSRA
6846	20747	A	6901	1	162	GTSGTRLFTIGRWQPKCPMAELINK MW\YTMHYSVLKKEIFCTNLTQL
6847	20748	A	6902	120	313	DKVL/WRLRQENPLNPGGGGSEPSRSH CTPAWATRAKLYLKKKNF KGTLSNMYS FRRVANTNLQMGSGSNYMQI
6848	20749	A	6903	340	234	IFPCRER\SLPRLVSTIWQQAILLPRP KVLGLQV
6849	20750	A	6904	1	327	GTSGTSRILPWGPGCIRTPELKQSAHLS LPRCWDNRYRHPYYSFAMLIKLEF EHLHSLVILWFLLANPQQTESSTSKT /PRLVLNSWQAVLPWSLKALASA
6850	20751	A	6905	532	359	RDG/DLVNWFPMWMEFGKQSSHLGHFK CWDVRCPELCQDFSYSIITVFPSPSREL RR
6851	20752	A	6906	270	3	GGTIVYPRKTKT/WPGVAHAHCNNPILG GRGGWITRSGLPVSTKNTKISRACCAA VVLATPEAQENKLPKGGDRDHHCQHG ETPSLSC
6852	20753	A	6907	1	312	GTSWKKMLPTLMDFRG\KTLVEELLTPD VVEIAREVELE\MEHEDVTELLQPHDKT WTDEBLLLTDEQRVVFLVSGVPPVEDAV NIVEMTKDLEYISLLIKY
6853	20754	A	6908	331	61	FRHVGGAG/LQKLLTSSDLPAPASQASG

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						TTGWSHHIRPKLTLRKKSMAKLDSRQT RLQPPVVEQGLLEQHEVYNVMAHVSX SSERKLS
6854	20755	A	6909	419	199	SAVQDGV\SWCGLGSL\QPFSLRLKQFP CLSPSTWDYKCAPHPAIFCIFIRDGV SPCWSDSWSTPGLK
6855	20756	A	6910	341	69	EAEVGGLLKARSLRPAWAGQDPTSLK KSFITLGGQGWITRSQDRDLRASASQA GTTGVSHRAQ\LIIFAFIVERRFHHAQSG GLDLLTL
6856	20757	A	6911	174	356	KTYLMPLRSLRSPGMVAHACHNPSTLGGQ GGWITRSQ\ESRPSVPLVNLRLTRCQANT VKPCLY
6857	20758	A	6912	391	3	SPFPFPFPFPFPFPFPFPFPFPFPFPFP FGPFPFP\YFPFPFPKSPFPFPFPFPFP PPLGKQFPFPFPFPFPFPFPFPFPFPFP FPFPFPFPFPFPFPFPFPFPFPFPFP LMICMLFFCKYILNFCRYS
6858	20759	A	6913	43	331	IRDTYSFSLAPALAPMLGTGCVLLAVA SLGSRGASLCVFCVCLCVRIH\IGVQA SGCVCVCAC\CVCCVRCVCVCVCPHWA SLLT\KDQLCPLPTV
6859	20760	A	6914	250	11	TPNLWGLFLVFCFEM\EVHYIAQAGLE/ PPGLKFPSSLLSLSSWDYRHVMPHAQI CISVFSLAQKGVPPSPNNILITHYSIKS
6860	20761	A	6915	532	53	SQMALHEGFLLLFLKEKELHGFSPHPFP SAPNSSMSKVVFYFSETESHVSQAQGVQ WCNLSLQPPFPFGKQFSRLSLTSSWDY TYLPEHLANFLFLVEMGLHWGQAGLKL PTSGDLPAIGSQSVGTTGVSHHTR\PRF LFKICPLFLFSKSNISQDEARI
6861	20762	A	6916	2	373	NHTPVVLATHEAEGGSLEPRRKLQLA MIVA\NCTPAKVT
6862	20763	A	6917	1	270	GTRQSPRLSLSSSCDHRVSPHPADF/ SFFYFYFPCR/DRGFTMLPQVLIWAQV MLLSQPPKLLGLQVGVVSHGARPPHCLG YSWVYNKP
6863	20764	A	6918	2	367	RCAPHCPDNSSFFK/RVKTGLTTFPRQT SNSMFPVILLPWFP/KVLGLQA
6864	20765	A	6919	3	354	HEVNIIVETAKDLEYSINLVDTKGFEKI DSSFRRSTVSKMPSDSITCYREIFCER KQSMQLQTSLLSYFKKLQPPQPSA/IT TVISQQPSTLRQGPFAKRLRCAKGLND FQHFWL
6865	20766	A	6920	366	41	STSGEDAVHIVEMTTKGLPE/YTAVPGF HPSSERRSVGNMMLNSVTCYRGIFGER KSQC/RQTSLLPYFN/KPQQPQPSATIT LI\SQQPSSTRDPLPKRLQLTSSND H
6866	20767	A	6921	3	368	QLLMGLHLEPATLDELQLKT\TIQCGSH SHHITAI\PS\FTRENTLMFIHLSPL LLSLNPDIIITGFFLLKKKNKPKNHKNG PSYKRTPEGLLLLVAQKTLPPKGGLY KIAPLRLFGEDS
6867	20768	A	6922	3	91	FSVLPRLVQNSWPQVICLPWHPKVLGL QV
6868	20769	A	6923	334	91	ERCCKCAHISEIFLSSLDYIYIPVYVF FFLFFFFFFFFFFFFFFFFFFFFFFFFF

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6869	20770	A	6924	375	37	QFKFNTSKSEKMFNKMKKVQVTF TKAGVQNHDSLSQPOPPRLKPFSSCSFL PSSWDYRHAPP/RP/ALFLFLFLGLVWFG LVFLVEIGSCYIAQAGLKLGLSSDDPPTL VSQSARIIGPTHAWPTLTTSIQCTIRG PG
6870	20771	A	6925	647	1054	CFWKAHQAGETNNIQGSEKHFHFCPAD EVVYHSGPAVEDQPPRRSFAL/SAQAGV QWCNLSLLQPLPPRPKQFCSL/SLPSSW D\HRHVPACLAFCIFSRDEVCHVGQAR LELLTSGDPPASASQSGAGITGMNHV
6871	20772	A	6926	3	204	DAWETTFGMIYDSLDYAKKNEPKHR/L ARHGLYEKKKTSRKQRKERNRMMKVRG TAKANVGAGKKK
6872	20773	A	6927	1	112	PTRPRTKGVASVLYFTITILIPIT\ISL IENKILKWA
6873	20774	A	6928	1811	478	DRARSPKSEKRAKRSSSLRQRDPISLGR RRLRREIRPGLPESSEPPPPAALITAD QPPRRLSESGGGGMSVAGEAATTTT TTTLQPQPTAAAAAPQDPAPKSPVGG APQAAAAPAAHVAGNPGGDAAAPATGT AAAASLATAAGS\EDAEKKVLATKVLGT VKWNVNRYGFINRNDTKEDVFVHOTA IKNNPRKYLRSVGDGETVEFVVEGEK GAEEANVTGPDGVPVEGSRYAADRRRYR RGYYGRRRRGPPRNYAGEEEEEGGSSSE FDPPATDRQFSGARNQLRRPQYRPOYRQ RRFPPIYVHGQTFDRRSRLVPHNPRIQAG ETIGEMKDGVPGEAQLQGPVHRNPYRPR YRSRGPPIPRPAVAGEAEDKENQOATS GPNQPSVRRGYRRPYNRRRPPPNAPS ODGKEAKAGEAPTENPAPTQSSAE
6874	20775	A	6929	324	203	LIFVFLVETGFHHVGGDLGLL/NLVR PPRPKVLKLENP
6875	20776	A	6930	3	364	HEASLTQTRITMTMTHCSRTTGCSTASGRT WTRSRHS CAWCSAALWRAAVASRCPS/ LPVTP PQCLSWP/WKVPLOCPALS
6876	20777	A	6931	2	165	GRGVGFCVAQAGLQWHDLSLKLPPV/G SSDCPASASRIVGITSLSAHFHNVP
6877	20778	A	6932	1	370	TELKSYSPNGAITSQCNCFCIGSGYS/ RSFSQVAGITGA/R/HHTQLIFVFLVE TSFHVAKAGLELLTSGDPPASASQSV G IAGVSHCAWPHVYILKEIMLGNVRL MSICHEHTESTCLFL
6878	20779	A	6933	1	441	RRANTFNNPPEAPN/QKKKKKKKKKKKK KNPPGGPPPPFFKTPPPPEKNGGSPGKK XGGKKKRGKKIFPPPPGGKKPPQKKKKG GGGGKKIFFFLFGPGGGGNFFKKKKGPP PFPPRKKKIFPTGGGPKKKKKKXAPPK KPRGFYFP
6879	20780	A	6934	518	340	PKPNFPP/PSPPKIPPPKKVFSKKPK GGFNNPPHKKKYNPPPEKLGPPKEFL KRPP
6880	20781	A	6935	396	299	VVEVC/GVCVCVCVCVCVCIHSLCKSTL HRTGV
6881	20782	A	6936	486	272	PTRAPTRAPPPLADLFIYCSDR/SLIM LPRLVLNSQPMILPLNHPKVVGLOA
6882	20783	A	6937	1	264	YSNLRDRARSCLSLPSSWDYFCSDWYKC

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						ASLRLANF/SNFCRERGLAMLLRLRVNSNS WAQVILLPQPSKVLRLLCLAVSVFFGEKQ QQCS
6883	20784	A	6938	2	407	TTGTCSRUVMLTFVLVVTGFHHVGQAGL ELL/RFPQPPKVLGLQ
6884	20785	A	6939	422	65	LKGPPPSFFFFFFFFFFFSPFLP YILYFDACASNACLFFKNTWRYKRIFF SPTPTPIFFHEVENVNTSLSYNVFYCYCFL FF
6885	20786	A	6940	462	209	LSFNDYRREPPFLPAKFAIFMLCRDRGL DTLP LSVSS/SNHQAIALPQPPIMLGLQ VHSAYKGFCLPVLTFEEVIGNRPLGLLP P
6886	20787	A	6941	491	299	CABYSPESGPTHASAHAS/SNVQMVVSR ISCKEELLGRTSPSKNYMMTMSG
6887	20788	A	6942	429	256	FSHLSPSSWDYKHLSSCFANFCIFVOT GFHHVGOA/GDPPASASQSGVGTGMSHH S
6888	20789	A	6943	932	661	FKTGSYSV\TRLESGEISAHCNLRFLS SSDFFHLSSQVARTGSSQYARLIFVFF VEMGFAMLPFRVGLKFLGFKPLHPP\RT RVGLGQE
6889	20790	A	6944	381	55	PASLPPCSLISDCCASNQRDSVGVGPSE PGVGYSLVVRRFLSRSEKRNIRVGVTRF SRCV/LSPSLTQKNSLTPCASQVRQC LALLRLAHGACTHWPAPTVHSLVR
6890	20791	A	6945	816	513	FFFIYFFEMESLPLRECSRMLSAHCK VCLPSSSY/PASASQVAKITGA/TRHS RLIFCVCLVERRFHHLISQAGLEL/NL VIHPSRPPKVLRLQGVTRTA
6891	20792	A	6946	383	234	LIFSLMDNSEGLKTSVEEVTADVVKIVR ELELVKVEP/NVTDLQS YDKT
6892	20793	A	6947	423	60	LNPPPPPPFYKPPPKKKKFFSPPLPKFG PTKFFKRPPPPPPPPPPPPPPPPHGT PLNSLVGPKVGVHVSNAQLPRAVGTF PNPKWGLNPKFAGGLNKFHPFSLNSGS EATPPLIPWC
6893	20794	A	6948	1	327	MRLLAALLLLLLALYARVDGSKCKC/ SRKEPKIRYSVDVKKL\EMKPK\YPHCSE KMVITTKSVSRYRGQEHCLHPKLQSTK RFIKWYNWNEKRVRVEEAQGLRRRIG
6894	20795	A	6949	952	796	FFLHFLVEMG\PLLVGAGLELPTSGDP PALASQASGITGMSHRARPSVSS
6895	20796	A	6950	364	6	ITTHKNYFLSRTATPPKEGLPQRKKIFL FETPIFIFFVGPIFNWGGGRGLVFFV FFFFFFFFFFFFFFFFFFFFF\RVK TFIGKVLFFKINVFFFLIRAVPLDYMN HALTIFQW
6896	20797	A	6951	418	266	ISFFFFXXXXXFFXXXXFLLFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFF
6897	20798	A	6952	459	7	PSYLYKPGSPQPNRRHRSVP/HIRSNKD PPPPVPMKKWGPPTPKKKYFPFRKKKL GGGGGPIYPPKKVFFKKPGGFKKPK KKKKI FFSPPKEKRGPPSILKNPPHPI FFFFFFFFFFFFFFFFFFFFFFFFIGEKA MLLDMA
6898	20799	A	6953	325	143	LPSSWDYRVRPPHSAHFKFFCRN/RGLA MLPRLAKRPPPSISIFLNHPQVSEILGA

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6899	20800	A	6954	585	306	TLRLAR KTESHSAIRSQCS\GEISAHNCLRLPGS SNSPASASRVAGIKGTHQVQLIFVFLV EMGFHRAQDGLRSPALVICPPWPKVL GLEAWPALHC
6900	20801	A	6955	2	155	FLVETGFHHAGAGLELLISGDPPTLAK S\DSQDVRITGLSHRAWPFLDIY
6901	20802	A	6956	3	346	LAWPDANGK\RNWPPPHQANFYTFVE/TG FT/HVGGAGLELLGLSDVPTSSSLDAGI TGMSHCSRPPEISSRDVHTIPGALQET WHTPDLASSIRSLRCLDCPHNHCPLDK DGVTLL
6902	20803	A	6957	1	224	QCGIRISRKDARKNGVOITIPREGRRTS PRYLFPVTCQETDQGW\NCLPAMLLKTR STSPRSPRLHRRRGATSW
6903	20804	A	6958	102	344	GLLXPKSLKLCQTITTFVN\NHCTAATA T
6904	20805	A	6959	3	296	KEEEEGEGEGGGGGG\EEEEEEEEEEEE EEEEEEEEEEHAEFTGHVESITQCKLL CHLSLRVEAGITHLLCFTVAVTRSQRL LTKRRENGSVGHTSE
6905	20806	A	6960	3	172	RLGLPKCWYDKREPP/RPGLLELLTSSDL PALVQSQDGKIDVHDTEPQDYTLTGQD P
6906	20807	A	6961	2	224	LALLPRLARSGTIIAHCSL\NRSRLRLGL SDPPASASESTGTTGMSHCSQPAKLLST CLRNSVAETKYLYLMPKCK
6907	20808	A	6962	2	330	KGTLRQVITYRGTLIR\LVADTLAETFH ARKEWDDIFKVLKKHCOPRILYLAKPSF KNEGESTSQKCIITTRVARSKMAKGVLI LEVKDISTIJKMKIRSSLVEQIHKW
6908	20809	A	6963	1242	929	ETGSCSVQAVQVQCWGHGVLKQPQSHAH /DDPPTASSIAGTTTANHYAQLIFKKFF NSLCCPGWSQVSWRILGSSDPPASASQN AGITGMSHGAWPQLSIYRKN
6909	20810	A	6964	1	378	KFFLQLFLHSFIYEHFFLFFSFLFFFFFL RPSFAFVACQGVQWRDLGSPQLPPRKF QFSCLLSLSRWDYRHAPPQSANF\EFVLV ETGFLHVQAGLELFTSGDPPTASQSA GITGVSHRTRLAIFY
6910	20811	A	6965	393	43	VSPFPLKNFYFSFTKTFVGGGGPSGPP POKRRFFHTPNSPFFPPPPF/YKSGRPP GFFTFPPPEKKNFP\DLLRLGPPPVFF TRPPPPPPPPPPFFFERQRTCSFLHFLVVR PLFRFYLL
6911	20812	A	6966	225	2	TRVECHGVFFGSCNPLLGLKKEFSADAP RGSCNSGPPPPPPR/RNSFFFFFSVULLE MGFHHGQADLEILTSSDPP
6912	20813	A	6967	8	341	FVSVPPILHYLFIKFFFLRSLCLPPR LECRGTISAHGSLGPGSSDPS/STKN TKLFLRGGTCGLPQLGLLRHEKTWTLG GGSCSYPKSGKRAMALGGGVQNKTCVPH
6913	20814	A	6968	29	362	DYTCRPHSSSELKKKKKKKKKKKKKKKK KKKKGGGPPKKP/HGGQPPPPGRKKKIF PFGKGFKKPPRGFFKKNPFFGGGMLGPP PPDKNKPGEKKNFLGORGQKNSFLSAW
6914	20815	A	6969	391	17	VVFFFLKKFFPPPPDKLFFPPFFLKIF F/SPNPPFFFLGGFSQSSPPPKGFFPK

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						IPFGV/VFSPDFKKNFFPPPLNFGFP RVFFKGPDPFFPPPPPPPPPPFLGL RGNAGDCNGVGVSVK
6915	20816	A	6970	374	268	TMPLRLVLSNWQVILLFWP/PKVFRLQ VRAPVPG
6916	20817	A	6971	614	315	FFFGDALSPGLECGGAVILRLQA/CLLG SHRSPASASRVAGTCKRPPRPPSGFFVF LVEAGLHRVGQDGLNLL/NLVI RPSRPP IVLGLQGM SHARLFVFL
6917	20818	A	6972	861	528	FETESRSVTOAVVQWNLSSLQ/P/LPFG FKRFFCLSPSSWDYRRTPPCPANFCIF SRDGLPWNWPGWSRTSDLVIRLPRPQC WDYKREPLRLAKSRHPWNHLPEQVEHF K
6918	20819	A	6973	274	119	FPN\FVFLVETGFLQGGVKLSTPGDPPF PASRRAGITGVSHPACPGKEYIFKN
6919	20820	A	6974	370	194	KITNFAXLFGYILPYSHYFWCLEKNRNR /SLTLRLVLSNSWAQAFLLLPKPKVLR LQA
6920	20821	A	6975	2	239	ARGPCSSI/SDCCASGEQSSVGVGPAEP G/MGNLLACCLLRPLEKCSIKAGVSRF SWYLSRLPLT/RGNPTTPIQVQR
6921	20822	A	6976	361	270	PQWLVPVIPA/LLETVEVGSLEPRSSRP AWAR
6922	20823	A	6977	363	48	GPPKEMCPYPN/PRPYCNLFGRVFPAD VIKFKILRW\IILDYTVQDPKNSDECPY KKQKRGRHQIKRKSQADQGGGRDWSGAT ARNAFMITSVGEDVRRKRPLAYC
6923	20824	A	6978	9	163	AGYNFLVCC/LPRLLEKCSIRMGVSRFS RYHLSWLPFARKGNSPTSCTSWR
6924	20825	A	6979	408	212	LETGCHVAGDG/LELLASDDPPASASQ SAETTVDSHRAQPHSAFLPWFSKIPAY GSVNLVFPHS
6925	20826	A	6980	395	254	LIFVFLVETRPHRVGAGLELLTSSDLP SLASC\ITGVSHHSRPSASF
6926	20827	A	6981	408	2	KVSFFFFPKGGRKKKAGGGRSFPFFPF LGGCTKNFFYPPIPSQGGKK/QKPPPP EKKKNPNPAFWGPPPLVLNMGGRPGGP LDPKVSFMGAPFLFGAKKKTFFSPPP PKKKPKQKKGGGRSRSTRG
6927	20828	A	6982	2	302	RKHLPPH\FVIFVFLQATLHRHVGAGL ELLTSSDHRASASQAGITGVSHCSLPA TSFSTPPFSVAKMLRGTQMKVPLIGPL POPRLVAGHYFIYT
6928	20829	A	6983	2	375	RGVRGGPVGGPVGRTIFFOAGSDSARI LVLPFYCTLPHPLPGLFFFFFTGKSKW VLLNPSRFRVIFLEKKIFLPQPPFF/HI LSPPHPGGAGGGNPTARKIKGLSYRDPK EGHKRGVVAHTPT
6929	20830	A	6984	1	146	PRPANFC/DFLVETRFRHAGQAGLKLST SSDLP/LTVSQSAGTTGMSHRA
6930	20831	A	6985	2	95	LTMLPRLECNDTIPAHCSLNS/SGSSHS LTSTSKVAGTTGVHHRFNLWF/PLFIQ
6931	20832	A	6986	340	169	VCSSGLSSPLLQHTNLI FYASGDICT /ANGKSGFNQPOPFLKTCTCHIRMSCT YL
6932	20833	A	6987	346	218	PCLTNF/SIFCRDE/SLTML/PRVLNS WAQAILPRPPRLRLRQA

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6933	20834	A	6988	345	141	NRPKCPMSIEWIKXMMHIDTMEYYAAIK KDKFMSF\ETITLGEVTQBWKTGRLLS LIRGS
6934	20835	A	6989	154	236	ELISFSRSVERCISSFIKVLVETDLFT LSLSPPFVSVLFPPC/RRWGFTMLPTLV NSWPQVILLPWLPLKVLRLPT
6935	20836	A	6990	2	156	PLVE/TGFFVHVGVGVELETLTSGDLFASA QSVQGIIGVSHVRPCCFLFVCICTLV
6936	20837	A	6991	310	96	KNFFFFLVKKSP/LNVAQGGKLLGSND PPASVSGGGITGVSPARPLNPKYKAT DPNTSV/LKGLNTKKKN
6937	20838	A	6992	15	279	NLLCTFFSISPLIGTFFFEEGGFHHVQGA GLKLLTSGD/LRASPSQRARITAMTRHP HPLVCGLLNSTHCDWRGRIPHWGFDRF REGFS
6938	20839	A	6993	127	352	KLADTPQSRFVLVCV/LIETKYSLCCPG GLQLASSNPPTSVSQSATITDNNHAE SQVFLNLVVPKSSKPTNTGL
6939	20840	A	6994	323	119	SSSEDHKHVPPHSAHFCC/CLQSLTM LPLRLVLSWAQVILPPSPKPFLLDALKK KSSKMMSSLLIT
6940	20841	A	6995	230	1	FFFETESCSVTAGVQWCDLGSLOPLFP GFKFSCLS/LPNSWDYRHALPCPANFC IFSRDGVSPGWSGWSRIIDLG
6941	20842	A	6996	346	121	RDICTPMFVTALLAKIRSPPHKCSVD TIRKMF\IYTMYYKAILKNKILGMHS HASLPVFNHMKLYLIS
6942	20843	A	6997	2	198	SNNTVAFREPGITGMCHQAQLVLLVLY QPHVDDGLDVR/NLVICPPWPCKGLG IQALNQSPDI
6943	20844	A	6998	183	31	MRLKSSQIQGTGVHACNPSTLGDHGE RITQGEFKT/GNIVRPCLYKD
6944	20845	A	6999	3	471	LALSCSGTILAHCNHLGPSLPPTSAP RAAGTTGVHHAWLIFVFFGKDVQAQPG LKLSFK/VIRPPOLPKVLGLQA
6945	20846	A	7000	483	239	GNNILFLFFIETGSHFVT/RLQECQ VQSSAHQSPSPRAQVLIFVFLQTGFH YVC\OAGLGLTSSSPHSAALLKVRD
6946	20847	A	7001	132	353	YAKLTGFGARQVPPGEGFLTVAVMSF AAGINPFVCIFPSNRELRCFSTTL/PL LQKIQVTKGTLLCYMREHL
6947	20848	A	7002	2	399	EDAQEVLEQGVHSESDKAITPHSQEE PQKQRESAE/SELTES
6948	20849	A	7003	2	135	IFQFLVEMGFHHVQAGLELL/NLMIHP PRPSKVLGLQAYWHSTRP
6949	20850	A	7004	2	114	IFQFLVEMGFHHVQAGLELL/NLMIHP PRPSKVLGLQA
6950	20851	A	7005	455	1	ALFPANLWLPSSSSQGLKLSHGTLTLE LLPSSTLKDLWPQONL/GTCNSQHFG PRKADRLAPGVONRPGORGETPSRKGG EGNWGGGGELHIYTYTHTYVHYIHA NWTWCVPVVLAFCQTEVGGLPEVAP AWVTVRPCLKKK
6951	20852	A	7006	371	172	QVILCLSLPSWDHRTTPHFA/NFLVE TRFQVDLELLASNDPPASASQSGVITG VSHCARPCYDL
6952	20853	A	7007	486	252	POTVFFFFFFFFFQALFSTFYILHVF FFFFFFFFPKQFFPPF/LSLKKQKGF

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6953	20854	A	7008	1	113	FFFFFCYLCNSLPTVVTVFFVNE KNFCR/DRSLDTPLRLISNSWPOVTLTP QPPKVLGLQA
6954	20855	A	7009	105	383	SLHRPAHPGLLKFGKRAIHSFFHLCRDK GDLAAILPRLVSNWPOVILLPWST/NDL RLQA
6955	20856	A	7010	609	348	ESHVTOAGVQWYDLDLSLOLPFGS\SD SPASASHVAGITGMRRHTQL\IFVLVLE TRSHHVSQTKFVLFDITTKFVVFYSGKR TRIRL
6956	20857	A	7011	382	233	DLEIFRGKTFLHHIFPFFFFFCC/RRRG LAMLPKVLNSWPOVILPKCWD
6957	20858	A	7012	359	199	DLLFSLPPFLFSPFLFPLETESHSSPR LECSGAI\PAHCSLGDRAIRHLKINK
6958	20859	A	7014	3	274	CFFFFFETGSHSVTOAGVQWYHLDLSQF PPPGCKRFSCLS/LPSSWDYRHV/PSSP LLVRNSSICLLSCFEMTPELFDGLAIY CCVTNDLKA
6959	20860	A	7015	372	54	LPSAWAEAMRGPLEPKGLRSQRAEIAP\ CTPAWVTEQAYVSNKINTERPPQKIEHV EGLSCTTQKFSND
6960	20861	A	7016	548	158	KFDT/GATLFDGRPAVFDEA/DFPSSVAV YLTGAETGSELDSDTWQAEHLHIEVFLP AQVPDSELDAMMESRIYPVMSDIPALSD LITSMVASGYDYRDDDDAGLWSSADLTY VITYEM
6961	20862	A	7018	396	34	QKNETKPTWQLHLTPARMAIYKIKLLKNG QWIGCOE/METLLHCWQCKLVQPIKMT NWRFLPEKPVKVELPFDPAIPVLGIQOQS WESSNDSGDPAIPPLGIQOQSPRRKVI KKRYLHTRL
6962	20863	A	7020	2	241	PPGPTAARRRKEDRYEYDVKVLSDRLK EAETRAEFAERSLTLREKS\IDDLQDEL\ YAHKLLQYQAISEELDHALNDMTSI
6963	20864	A	7021	347	3	NDLKLSTHSVAQARVQWQNISSLRPP PQFRKFCFSLPSSWDYSLNCKFYHLH FADEIETLTSQRQALECKSNMYKDIHN TVRSYKLYKVPQKLESRNRTKSSTRE VRS
6964	20865	A	7022	2	160	LREDDRRGRGFHHFGQAGLELLTSSD/L PTSASQASAGITGVTHRAPDWSFCQF
6965	20866	A	7023	3	248	DRVSSVAQSSLELSSSNPHLGFFPKCWD YRNPPLPFSSRSLLFLPSFLIFCRDRV SMLPKLASSFW\VRPWPWSKVGLQA
6966	20867	A	7024	483	143	PLNPLKFFFFFKAFKFGVGVPICSPFR RVLQSQSQGVFFYPFPQKEGYTFPSPG KFGPPKEILKRAPPYFFFFFLLRRDK/ SLTMLPGLVLNPNWQAVLPLQPPKALGL QA
6967	20868	A	7025	414	81	PHPLKFFFFPPTFFYFWMGVSPSPSPGR KVPPQKSPGSGLLAPPKGSFPFPCPFK IGPPRGIFKRAPPYFFFFFNNRRDK/S LTMLPGLVLNPNWQAVLPLQPPKALGL QA
6968	20869	A	7026	16	218	KFAPKCRNSARENTQNPKRKSDTPELK K/HKINNNKLGRGTHLWSQLGLRLRW EDHLSFROSRLQ
6969	20870	A	7027	28	272	EFVGVGCFSEFGAGYNLL\CAFLSPSEKC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SIRVGVTRFSRCHLSPLTLTKKGNLSLTP CASRVQRCLTLRLLAAGHALPLSSTP
6970	20871	A	7028	277	480	LGIFHMLSDSFLLLLLFLCLFVFKIFFGGI FCRD\RSCEYVWAMLPRLVSNWAQVIL PPWFLKVLGLQA
6971	20872	A	7029	24	153	SVWNWSF/RSSGEFRKTVGHDADFEAHI IDMLAKASKIEVYRGN
6972	20873	A	7030	2	470	IEIPRPLWHSAYRGRQASLSCGGHLFHV R/ASMLLCLPQAGAMAGAPPASLLPC SLISDCCASNQRDSVGVGSPFVGYNL LVRRFLSQSEKRNIRVGVTRFSRCV/LL PLSLTRKGNLSLTPWASQVWQCLALLRFA HGARTHNPAPTVMHSILVR
6973	20874	A	7031	487	107	SPFAPGQAPAPFPPTRVFSKKKKKFFFF FLKKIFFFKPGDGGIFFFPFGPPGPGP KKFSPPLFPKKGQGVVFPPPPGKISIFI FFFFFFFFFF/CRDR/SLAMLPRVLNLF WAQVILLPWSFKVLGLQA
6974	20875	A	7032	576	36	GYSQMGPRGRGAPHFPPDKAAGQRRSSL PRWGGAEALLTSMQGWPRGRGAPHIPD DQGPGRGAPHLPDEQLGRGAPHLDPDE RPGRGAPHFDPGAAGQRCASHPTRGGRA EVLPTSTGTQGPGRGAPHLDDGRPGRG PHLPDG/GPGRGAPHIPDGAARQRHLSF PRRGNCNTRIVDQ
6975	20876	A	7033	2	129	YGPTHASGAMLRSCAARLRITLGAALCLFP VGRRLP\EAASRDP
6976	20877	A	7034	1	287	RLSLALVARDGVQWCDLGSPPQFPPTGFK RFSCLSLPSSWDYKHVSRPANVFVLVD TGFLHFGQAGLELPTSGDDPALASQSAG I\TGVSRAWPK
6977	20878	A	7035	3	315	HASAHASALFYFIFFETRSLRVAQAEVQ WRKGLSLQPPRFKQFSLSPHYRHAPH FANLVFLVETGFAHVQAGLELPTSSN LASQSGOITGVSGRARPGLNF
6978	20879	A	7036	430	304	VTFYLIFFCKDGV/LTMLPRLVLSNLH ATLPQPPKVLGLQA
6979	20880	A	7037	3	256	FFFNKQKDLGNNFOTCQKNSPSEBPT /APHQAPKNTSPSPSLPHLTASTCTY PTPQAMLENWSVSPAPQAAGEAALWHFR R
6980	20881	A	7038	13	481	FARLHEFGTSRVIYLLARLVSNSWQVI CLPWPPKL/LGLQA
6981	20882	A	7039	455	255	SLCLSPSSWDYRRAPRHPANFR/PLVET GFRHVALAGLKYPALASQNAIGITGVSH HARPEQFILT
6982	20883	A	7040	490	172	KCWGG/C/GETGTLVHC/WIGNCTMMR PQWQAWQVFKLHRELPSDAMPLLGV QPGLKIDTQ/RYMYMALITVKNKQK ECPEVDK/LDKLWYHTTYEYVTKKK
6983	20884	A	7041	438	37	IFPNLFPKLHYFPQFSPPEKLPKPLLIK MAKRQSQGKVETFPKEK/SRAGPPPKFT TGFSAEKNGQPKPGYISQRVQKKNNC HSRLHSAXLSFKNRSEIKTFLNKQKLK /DFTASRPALQKILQEAHFRTD
6984	20885	A	7042	292	463	IEAISLFPFFFGDSLTAQWRDLGSLQP LPGLKRFSLCLSPSELP/CSGRQCS
6985	20886	A	7043	59	257	LASLVQSQSMKKMWYITTKMYAATK/G

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						NEIMSSAGTWMKI\FAILSKVTQEQKTR HHMLSLRSGS
6986	20887	A	7044	279	14	RTADTEIGRSSLCWRYGSLQIQVSKSH NFFETGSHSATQYGVQWHLGSPQPQT YGLQSSHCGLPKCWYDRE/LPPSMCS GTISAHLSLKLGMSSNPLTVASQAGIT GNSSRLHDINYGLO
6987	20888	A	7045	578	253	AAASTFCFFVFFETEPNSVA\RLCSG ATSAHHKCLPGSSNSPVSAPQVAGITD AHNHILIFVLVETGFHHVGAGLELO/ NLVLSLWPPKVLGLQAWSHHAQPFV
6988	20889	A	7046	3	229	FFKTGSLGSQAGVQW/PNLSSQLQPPP RFKQFSCLSFFPSSWDYRHPHPANFCS FSRDRVPPCWSGWSQTPDLR
6989	20890	A	7047	367	151	LSSLSSWHYGHVPTSPANFFYF/CVDTG PRCVSNWTAQVCLPOLPRVLGLQA
6990	20891	A	7048	370	141	CQPPHPANFCIFVEIVFCHVGQTGFKLL TSNDLPWASQASAGIWD/TGVSHHAWPS RPNSEVQFDYVSNKNVDLSLS
6991	20892	A	7049	104	361	VTAFGLEAAPKERVWPGAVARTCGPSTL GORGRI\RGQRIKTI\LANLTKCLY
6992	20893	A	7050	2	325	RFSCLSLPSSWDYRHPRLAI\FFFFFF GIIRKGGFTH\VGRRGFKPWTSNGMPAL PSQGVGPGLSPPRPVRGFFYPLPKWG GLFLQGVKFKKGGSGDLPKRKK
6993	20894	A	7051	14	208	AHETLSIEINPLEPGNDHRCVSSCPAHF PVE/CYRDGGLPMLPKRVLNSWAQAILP WAPKVLGLQV
6994	20895	A	7052	103	368	GNRVHTYMLTALFMTAKKWNKPKC/PVS DEQIRIQISVHAMEYYSALKRNEALICV TTWVNLENIMLSESSQKTMGMLRRSIY MKGPE
6995	20896	A	7053	421	2	LFLFPEVARGFPKGRGRASPFGGFFFG PRGGPIFFPP\SFPTRFWSKGEVFPSP TPGKGFRRGFFPPPKGKGGVFLPFFKK YLGEGEAPQNKGGPVLLWPPHSGPFGP PKNFFFFFFFETESCYVYPGCSAVVQS Q
6996	20897	A	7054	489	40	TPFAPGGPGFKKREDSPGANKSGPKALYF PKTTHPPWEGRFRFSQKGAPPPPVFFPP FFPLPFFFLRQSHSIPOAGVQWRDLGSL QPPFPFGFKQFSCVSLPCFP\RMGFRH VGAGLELLTSGHPDPSASQSTGITGVS HCAEFHRTD
6997	20898	A	7055	3	261	TGSGSVTQAEVQAEVMAHCSLNLGSSD LSALASARAAGAAGTCHHAWLIFVFFIEM GFHYVPLR/GLELWARVTHPPQPPRVLG LQV
6998	20899	A	7056	1198	1040	FLWKIALLFYFKLPLQSLQPLVATTLSS QQPSTSRQDPLPAKRL\RLAEGSDDR
6999	20900	A	7057	271	33	LPFFFKNESRSVARLSCSGAILLAQCNLA RLFLV\QGFPHHVGQDGLLIHPWPFP EVLGLQKQATPESSEKTYEATVM
7000	20901	A	7058	2	194	CYRQPPHLLANNFFLLNFCLFFC\KA LSLARALLNSQLQASLPQPPKVLGLQ ACGTTPCP
7001	20902	A	7059	3	272	NMKKLNLILLNNQWVNGETKMKTFKNCK E\NGNTTYQNLRDAEAPLKGKFI\AVNT

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						YIKDYRKTCRLRFYSYHFFNKEKEYTL KTMIV
7002	20903	A	7060	397	129	FWGPHKKNFPLPARGRKLGSKFTA/LPL FFFFPSFSLSLFFPSGSCSVS\RLKCSG TITAYCSLEFLGSSNPASFSQAAGTTT TFFLFIG
7003	20904	A	7061	3	351	SCFRLLCLPKAWAMAGAPPASLPSPCS LISDCCASNQCDS/VGVGPSEPGAGYNL VVRFLSGSEKRNIRVGVTRFSRCRPS LSLTKRGNLTPCSSQVRQCLALLRLAH GARTH
7004	20905	A	7062	60	324	DDFVSVVQTGVHWCGRGSLKQPPRLSS TSRLSPSSWDYGRVPF\NIFCDRVSLL CFPGWPTPDRLGSSCPSPKVWKLHTRV TAGGO
7005	20906	A	7063	481	160	RPGAPG/PDDFARMGRPRKGGAFETLVHP MPSGAAPFGLLSEP\PHRGPRSFARS TLRYCPGRAPSKGSGEDPPATGFGCPN LIQDGLVLSLTENVC
7006	20907	A	7064	65	481	CLCPAPRGGAYRGQASLSCGGLHPVRA SRLLCPLKQAWAMAGAPPASLPSCSLI SDCCASNQDSDVGVGSEPGVGVSLVVR RFLSRSEKRNIRVGVTRFSRCV/LSPLS LTKRGNCLTPCASQVRQCLALLRLAHA
7007	20908	A	7065	392	183	GGLKF/IFGNPNSLFSOKKKQKPGAGG SPRGSPPGGGLGGGIFPGPKLGSINPN FGPAPPPGGQKKKSLF
7008	20909	A	7066	558	248	FFLRQSCSVAQAGVHGYLSSQLTLHPR F\KFSCHSLSSSDYRCAPPRLANFVL LAEMGFHHHIAQAAGLEPSTNDLPTSA SONAGITGVSHHT
7009	20910	A	7067	2	127	VTGQAVVHACSPGTLGARAG/WIWAQQ FRISLGMVRPCLYL
7010	20911	A	7068	379	217	KKMFCKNE/SFTTIPFRLVLSNAQTILP PWPPKVLGLQVQTTVPSSYSPLSLYKE
7011	20912	A	7069	386	176	KRDVVKLKKM\CHIMEYLLATIKRET LFFATWNLQ\TFLSEISQEQDKYHMI SLICGIKMLIYRIE
7012	20913	A	7070	30	408	NSELSGVGVPTFCTGGNLLVCMWLR LWEKCSWAGVS RFPQ/CTDYDGFHWG KGNPPTPCASQVRRHPALLRRTLHGLHP CASHEKNQVPLEMQSSVFCIDLGTSC RVLEFPFHLGSKNP
7013	20914	A	7071	310	414	HVPKRSFAPAHCLGSLQPPPGPKRFS CLSLPSSWDYRCPPRIAN\FCSSGLQS WLTATASWVQAILLSQPE
7014	20915	A	7072	353	243	IFIFCRV/RGLTILSRVLWVFWEDQVILL PEPPKVLGLQV
7015	20916	A	7073	1	276	ELWDFKFPNTIYKLSKERKECVCEGR RDRNKLTLEDIMAKNFSPNMKIINPOIQE AQQTPN\QETGRKLALRHITIKLLKTN KKKILKAV
7016	20917	A	7074	362	133	GGGGGGGRYSPOKRGTLTLPSPSNWPK GAPPPRGNFFFFFFFS\RDGCLAMLPRL VLDSWQVMLLPOLKVLKL
7017	20918	A	7075	3	177	KWSPHSLPNN\WLYRHMPFCFANVEFF CSLAVLPRMVNSWPGAILSPNPTRMIG LOT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7018	20919	A	7076	1	169	PQLPSSRNVEHVFPCWNECFPS/RRRC FTMLARLFLNSWPQVTRPHWPPKVLGLQ A
7019	20920	A	7077	402	231	PSCLSLRSSWDDYCMPEHLTNYYYYYY YFVEMGSHSVTRPDILPPWP/PKVLGL QV
7020	20921	A	7078	422	316	FCCKDK/SLMPLPKLILNSVQTHLPQ PKVLGLQA
7021	20922	A	7079	58	293	DPICCTKSKLKKQTQTDKEDETTKKAK KAKSKI KI EEDGEGKV/VVEEVS VKK KKDKKKPWLGMVAHTCNPNLTGG
7022	20923	A	7080	363	123	GVFFRDHARAFSLHTGVCVAHISRCF/H VLTHFKFLPHWFLTITHTHTHTHTH HTPSFPFLGKAVPMHRIVIVPTNYQH
7023	20924	A	7081	3	181	YFLL\FPWRDVLPCHPGWSKGWSQTGL GQSAHLSLPKHWVCRRPFPALFLFLFK NTIS
7024	20925	A	7082	453	142	FFXFXFXXXXXXFFFFFFFFFPFFFFFF FFFLKNSFPYFFLFFFFYPLFLPLFFFF FFPNFFFFFFLFS*NNFFFFFFPPPLLEFF FFFFFFLFFFFFFF
7025	20926	A	7083	268	92	KNNLPSWQ/YKCSPPHKGNNFFFYIKD GGGLIMLLRLISNSWAQVILLSPWSKVL ERQA
7026	20927	A	7084	413	0	SCSVAQDGVQWDDLGSLQLPFRNKDFP CLSSTPAA/PPSDNDYR
7027	20928	A	7085	400	125	KIRSFVVRGGVQL/CI/GSLKPRTPGV KSSSPSPSPVGRNTGCMCPQQIFFFLV ETGSHYAAQASLKQSSCLGLIILFLSQP LGEKEGPTICT
7028	20929	A	7086	377	38	NPGQFFVWPGKKKIKFPFPQVKLVSP KRAPPFF/CFPFFTSFPVQTSLELL DSHNPTTSASQASITDMSHIAARMISI CMIQLWKSXYRHFPI SQGSRDCSSREE T
7029	20930	A	7087	1	151	SFCRD/KRLTMLPRLVLSQAQVMLLPQ PPKVLSSHHTWPIKFSFMHNLFP
7030	20931	A	7088	405	111	PRLVN/SELRRSAHLSPKCNVYGPPEP PCPAQMHLVLSGTAHKVHDFLASWSHL PTHSPFVLCSKTQISVAFFIQNLRAQ RSGQRHFGKQCSIH
7031	20932	A	7089	1	309	KQINKSLRISGKPPNCECVLHLGKSVN KSLLEPHKLASDP/HLCDFLESS/EQVK SVKELNCHV/TSLTYLGALESDMAEYF\ NKYTLGPGMLAHAYNSSILOG
7032	20933	A	7090	414	240	FSLF/CINKKGLTMLPKLVSNFWPQAI LLPQPPKVLGL
7033	20934	A	7091	460	328	RHPFPYLGK/FFCRRD/SLTMLPRLVSN SWPQVILSPWPPKVLVL
7034	20935	A	7092	388	199	KQFSCLSLPSRWY/SALPPRPAHFCIF NRDGFSPYNSGWSLGLPKCSDYRRRIFL RAKAHVR
7035	20936	A	7093	18	271	MHSFATYLLVNLHLVLCRLCPLSMYSG EKSYYLLTKRPMWF/SSGPPPSWSFSS ITLRIFLTCLTLKLSCCSCCCCYCCCC C
7036	20937	A	7094	415	291	GDIGSPQAPPGP/SRHSPASASRIDGTT GARHIMFNKLAIK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7037	20938	A	7095	21	428	DKGLTVTQARVQW/HDPSSRQPPSPGLK RFFRLSLPSNWDHRCAPPRVANYFFYR WGSYHVAQAGLELASSNTPTSASHSAG ITALFLRDLTVRFMGSGFCFQPSGGAFF TAQIQPGRTEELFIFLFLNDYLFSS
7038	20939	A	7096	320	134	LPL/PKTTFFLFLNRDRVLLCCPGWSR/ ILSSKQSTLLGLPKCWDHRRHEPPQQAVID HTLDFS
7039	20940	A	7097	402	221	DYRHVPPPPANF/LVEMGFHWHSQAGLE LLGSSDPNPTSQSGAGITETSHQAQAYTF IFIIY
7040	20941	A	7098	427	259	PPPRFKRFSGLSLLRRWDRYRPPSPCPGN FFFFF/CIFVQMGFHLVGAKMLKLHD
7041	20942	A	7099	422	275	VQWYNLDSQPASSGKFKRSHLKLSTW DYRHA/PRPANFCIFSNTKDTEI
7042	20943	A	7100	3	404	HSGATWRNPVSTRVWHIFIPVATQEG EMGSGLEPRK/LKAAVSGCTVNVVT
7043	20944	A	7101	539	336	FETESGSRFTEAGVQWRDLGSLQFPFPGF KR/DSPALASRVTTGTAHHHAGLIPVF LVEAGVSPHWPQWS
7044	20945	A	7102	408	287	WLILFFIFCRD/RGLIMLPTLVNSWAQ AILLPOQPKVLGL
7045	20946	A	7103	1074	705	SFLRWSFTLVAQAGVWRWGLSLQLPLP WFKQFSCCLSLSSWDV/YGRPPRIANVY F/VILVETGFHRYNPRMVSNSQDQ/CDF PAVGRPNASGI/TGVSHCAWPKMFLNNC TCTHSPYLOGIVSLG
7046	20947	A	7104	227	55	FSQHKINIQFYISLSPHITMSFFLCRD /RGLAMLHRL/VLNSNPHVILPPWPKV LRL
7047	20948	A	7105	479	314	PRLLLIFFFIERGL/LCSPGWSQTFGLQ ESSCFLGPQKSWGPKPEQPCALKLWTLQ
7048	20949	A	7106	37	143	NSFF/KRRGLTMLSRLVNSNWPQVILT POPPKLEL
7049	20950	A	7107	441	106	GAPSPASLPFCSLSIDCCASNORDSVGV GPSRPGVGYSLVVRFLSRSEKKNIRVG VTRFSRCV/LSPSLSTRKNSLTQPCASQ VRQCLALLRLAHGAHNPAPTWHSLV R
7050	20951	A	7108	413	207	CCIQAGPAFFGGPPPRWGQWGGVPPPGY /MPSPFPVRVGLLVFRGPPPNFVFMGL QPDGPGLGDPKKPAK
7051	20952	A	7109	92	409	PHLPDGAAGQRCPPFPGRGGCVRAGPQL PFGKGGWPGGGLPPFPKSTGWLPGGGAP HPSDCAVARQVRSSLLRGGRATLLTS QTGSRPGRGTHISDDGRFGRD
7052	20953	A	7110	408	13	PDWGPFGGQPFPEARGSNFPGFPWCTFLS PKKKYNSGQGGPLNPPPEG/SGPI PFSPEGKSLNPGQKQKIGAPSPPPGG PKKKPPSQKKKKGKKEKVIKGESSQI LLFKVSKILSVNPHLSSLI
7053	20954	A	7111	290	175	LKKNCR/DRSHTMLPRVLNSWPTILF SQPKVLGLQI
7054	20955	A	7112	1136	552	ILFKRMGCEAGORCSQVPIITLGRPRR ADHLRCGVDRDQPGPTMLKPRLYSNTKIS WAWWRVPA\IPA\IRRPKATRTFNPRR WRLPLNLRSHPLSHHPGRQSKIPIKKKE KKGQDRKKGCGQNWQKQKRRKEGKKE

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						MGMRIGGKNGKGRKERKEGRKEGNKW VWAELGAPPEGGKGLRRGPSEAVGVSP L
7055	20956	A	7113	570	199	LCLLKQAWLMAGAPPASLPCCGISDC CASNQDQSVGVGPSEPGVGYSLVVRFL SRSDKKNIRVGVTRFSRCV/LSPSLR KENS LTPCASQVRQCLALLRLVGHATH WPAPTVMWSLMR
7056	20957	A	7114	466	284	RTRGIGWTANRRMKATQPGLTFFHLHK QEGGNVGSQKQQRD/VTNSAFHWRLHDQ TANCLS
7057	20958	A	7115	474	224	DSNFEKSSITLGMKLSNICKYREIFCER KSQMQQTSM\FKKLPSPQSPASATTLL ISQLPPTSRONPPPAK\RLQLAEGSDGC
7058	20959	A	7116	377	111	PXXNXFSLFLLSLSTRKNWVAHITFFF FFFLPTPPFFYFIFLLIFCFFFLFYIF FFFFFFFPPPPPPPPPPPPPPPPPPPP FFFFL
7059	20960	A	7117	417	148	VPPCLANF\NFFVETGSPYVAQAGLELL GSSHPPTLASQSSQITRVSHCSLLYFLM HSNTSISFFSFWALVSLFLEMPSSCQDGI TVLAR
7060	20961	A	7118	2	196	RVPFFCPA/NFVFFVQTAFCHVAQAGPK LLASSNPPASASQSAIAVLSYCPLESL RLRSHLDF
7061	20962	A	7119	2	417	EAGGSLERPNRLHCA/LVAPMNSRCIP AWAT
7062	20963	A	7120	801	450	GPKFLGPPGVNR/RRPGGGGLPRVYKK NNYPEDRFIVLPAFFSQQGR/GPGPHDK HLPKRRKKQKNSPGRGSEPPPPPPPGFP GGERKNPLTPQKRVRVHMGGLAPFFPPS LSAKPKLF
7063	20964	A	7121	3	199	DWGFALVVGAGVCCDLSLQSPF/RL ANFVFLAETGFLHVGQAGLKLTSGNLP ALTSQRLRQ
7064	20965	A	7122	407	164	NVAGLTGAYLDSFFGRDRV/LTMLRLV LNSWAQAILPPNPVKVMGLOACTIEVSS LVAQIASKRLSGVQESDEAAIRDC
7065	20966	A	7123	33	192	RWDFTMLRLVLGSKRSARHLGPKWCNDY KHDP/PCPCGWSAQORDLPTLASQAGI TSMHLHQAIPKFLQFIRFSILVF
7066	20967	A	7124	3	399	SIPVDWFSRAPTPRGRESAAQGN/YPV GQRN/RMAGLSRPSRCWREVSFR/SHS C/ICWVLGKSAVLPPQSRGPGAGSGSR RRGSSPPPCPLQTLQVLSFQELMSAP IHRLSVTLQDCCISTGGAPFRCLA
7067	20968	A	7125	1901	1574	FFEMESCVAQAGVQVHDSGLQPLPFG FKQFSCLSLPSSSWYRHLPHRANFFVF LVEITGLHHVGO\SGLELLTLGD/LLPAS ASQASAGITGVSHHAWAKNPCFLTSDIT
7068	20969	A	7126	408	234	LPSSWDYRSPPPQANFYIFSRD/MGFTM LARLLTSSDDPALASQARIAGVSHHAQ PVYF
7069	20970	A	7127	88	277	KLSTEYKORPEDSFLLF/VEIGFRYV AQAGLELLSSDDPTTLASQAGITGVSH HIQPPFKK
7070	20971	A	7128	3	140	QRWCVPATRKAEAGESLETESRLQGA MITP/CSPAWEQDLAS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7071	20972	A	7129	1	212	PLLFVSPPLLSVPPLLPFP/EPAASFP PSTHLLSPVQSSESLGQFLHPPDPPLA FAPLKHQDLHLSH
7072	20973	A	7130	361	3	RNMISQDLAVIGNDSNRSRSGQSKLRFW KGTLLHAIAKDPD/S/WEVKISRLPGV WKLLIPTLMDDF/EGKTSVEVTADMV ETETELERLELVKPEYGTGLLQSRDKT LTDEKLLMD
7073	20974	A	7131	421	201	NFCILVD/TGFHHGVQVSELELLTFSPNP ASASQSGITGLSDHSQRKSELVLSFN FALPHILLCVMLAIDRND
7074	20975	A	7132	221	529	LKFTIHSFFYIYLIFFSGDGCFLASP RLESSGVISAHCNIRLPGSSDPSASS VAGII/CMRHITOLILY/CLVET/EFHH VGQGGVDLLTSGDPPASASQSV
7075	20976	A	7133	1	227	KGIFHSSANDVKKKTULVTWNSQDPOLF RDGLDGNVHRLKQCL/ELDEVVYVEK
7076	20977	A	7134	1242	300	DFVLDPGRVIP/KGIVUCLINITY/THYN PN/LWPTPLEVYDPFRFP/ENKERSP LAFIFPSAGPRNCIGQAFAMEMKVULA LTLHFRIPLTHTEPRRKPELILRAEGG LWLVRPLAGTSGRGNPRASSRPSLSDPW VLRRPLPPPIFLFLLLLTLPLFSVMAR EPPSPLRVEAPGPPEMRTPPAIEATPKG TLQPAGGRRLFLSGCVPIILHQVAGHRYG KDKMGILQHPDGTVLKQLQPPRGPREL EFYNMVIYAADCTDGVLLLELROYLPKYG IWFPPAAPNDLYLLENVTXKFNKPCIM EVKIQQKKL
7077	20978	A	7135	1	259	GTSCILASMLTHRLRFSF/CLFETEC SVAQSGQWYDIHSSLOQPPLKLFSPV NFPSSWDYRHMPPCLASASILKLLFTID LGFYS
7078	20979	A	7136	1132	900	CSGVISAHCKPRLPGSRHS PASASRVAG TTGTRHARLNFICFP/VMGPHRVSQD GLHLL/NLVVCPRP RPVKVLELHA
7079	20980	A	7137	1	501	FFLRWLSLTVTRLECSGVISAHCNHLHP SSDSPASAFREAGT/GHDAQLIFFVLV ETG/FHHVVDGVDLLTS
7080	20981	A	7138	2	229	WHSGLLWSQPPL/VLSLSSSDWYSHVS PCPAGLCLFLVETGSPYVAQAGLSLRGS ASQSTGIGMSQPAQFWKOL
7081	20982	A	7139	255	58	IFGKGFPPFFCQNGGVPVPPPPRAFFFF FF/CPAXYYTMLPRLVSNNSWAQAIHP NPLKVLGLQA
7082	20983	A	7140	422	274	TMLPRLVNS/GLKQSSRLSLPKWWDYR YKPPCLVYTFINRNPPEVPKE
7083	20984	A	7141	417	60	VWRFLLEETELFPDPAIPLLGILHKEH KLLYHKDTC/WNQPKWPSMVDWIKEMWY INTMEYYTAKKINAFRDLPLTSPWDPF SWRKFCPLLEIWPASYFLPGINTSLDE PLHIKGER
7084	20985	A	7142	391	70	SPPHPPRKGDRGDP/PPGKREIFF FFFFLVDTGCHVAQAGLKLASSN/LP TSASQSGAGITSVRHYIQPTLLKIIPOFL DILLGLKIFHSFLKSFNENLGSFY
7085	20986	A	7143	405	304	FKDRK/SLMLPLDLNLSWAQGLLWLP PKVLGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, ~-possible nucleotide insertion)
7086	20987	A	7144	3	139	HASEKIWMYTMHEYASQKKNKIMSVF ATWMLRVNLSKLMNEMMSVNGR
7087	20988	A	7145	343	115	CEFFYFLSCIVVFYFCR/DKGLSLLRH VSNWPQVILLPWPPKVSQAQPEFYFR NKQTKIDLSEFETAADLAYYS
7088	20989	A	7146	453	119	RCNKGCGLWISLRIT/NREWQLVQFPWK TVWRCLRKLKVEPPYEPATPLPGIHLKK TKAVAQRDMCTPLFIVAQPHHLLKRLFF SRCVFLAPLLKIA
7089	20990	A	7147	3	105	TIEWGEVIS/SSYSSTMANNEGLFSLVA RKLSRPL
7090	20991	A	7148	295	23	FANIFSHSAETLQTRREWGPIFNIL/EK NFQPRISHPAKLSFISEGEIKSFQDKQM LRNFITTRPALQEFLLKKEFMSFPQTMWK LETIIIS
7091	20992	A	7149	1	161	RTRGFFYLDGVSRLAMLP/RLVLNSWFQ AILLPNLPKVLGSGOTLAMVAAYTVFV
7092	20993	A	7150	1	219	DYRCTPPHPAHF/SIFIFCRQR/SLTMF LSVLNSWTQAILLPWPKLLGLQACTA MPIPGVELLWVSGCFVKES
7093	20994	A	7151	177	34	ELVSFLSFLSLSLFPPSFLPSFLPFLSF LPSFNPSF/LPSFLPSFL
7094	20995	A	7152	398	40	MNDRVLLFHEGWNVAQGSWFTGASN/FG LKQSSHLSLLCSWNYRHTPOCPASLLAY VCMYVCMYVCMYVCRD/RGLTMLPWLVS NSRPOAILPPQPSKIMGPLGAVAHAYN TSPKGSQRR
7095	20996	A	7153	418	179	RNSCTQMRNEALPNSGYFFPKLKYDYDF/ CORQDLAILFRLVYNSWVQAILLPWPK VLGLQHEPPCLAVIQFLKGNLKIV
7096	20997	A	7154	767	537	QALLCLPGWS\AQAQSWLTAASNSDDP ACLPSSWDYRHHVPPRQAENSFRVSVSSP VKRDGSPWRNRDCSE
7097	20998	A	7155	421	301	HQQLFFCRHW/SFTMLPWLVSNSAQAI LLPWPVKVLQGV
7098	20999	A	7156	410	269	AGGPTGSGFFFF/CYERGVSLLPRLVSD TWSHVILQPOHFKVLGLQA
7099	21000	A	7157	3	237	MQTKA/TMLYHFTPTNMTVLGPKKNSRG WQARGEIGTLVHCWNGCIMMPLWETVW HFLKRLNKLGVVHACSPNYSYG
7100	21001	A	7158	435	211	LFLVEMG\FAVLASLVLTLE/PRDSPTS ASQARMTGMSHTQPLFCFLVSKFHILA KKLSLIWNLRRAGICRLS
7101	21002	A	7159	3	220	SSASQSGGIGTVSHIARPSERO\SCSV AQAVVQWCNYSSLITPTGLRSSRLSL LSSWDY\GALPHPSVAS
7102	21003	A	7160	1	172	FRKVLGRGTSGNGLCTQVRVEFMDTTRS IMRNVK\SPVREGVDLTLLLELETLRL R
7103	21004	A	7161	1	180	DAAPVLKATARPTRPDWRK/IDIDSLDI HGETPSLQKNTNFRANWCIPVVPATRE ADMF
7104	21005	A	7162	3	108	KKKKTRGFKLV\WQYNRRFRVNVVTFGK KKGPNANS
7105	21006	A	7163	409	110	GQHGTLQSLPLSAPPREGAVPRWAPRPD/ SGLSLSPLLPTAPATTGASSANKFVSI PRDGNFLNIPQSQSWFL
7106	21007	A	7164	35	371	YFHLISLLKFLASMMWFLTVVVLLE

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						LLFFFLGETEFAFAVQFGR/QGPNLGSRLPHFPVSKHFPGLTPPRAGTSGLDPPSPATFGFPKKKRGSPGCGPRANTPGPRGGP
7107	21008	A	7165	3	382	YTGPAWWSMLVVLATEAEVGSLEPRSSKLQ/QPPLRHCTPAWAT
7108	21009	A	7166	1	305	TAVTVDPFVSHVYIEVNARPGACMNGGGLNGEQNSLKKRQVOTLNKRHGEELAMVDSLTLGPKLEEA/ASPPAFARVRLRARQACRRKGSRLCWEHLVSKV
7109	21010	A	7167	383	55	RDLSSVRKSKMLAJALCPTALMGMFNSIFGRVAKLFPFPLSVYIQQSLSHRNMMGDDTDCSFIPLYIFCTMSIR/QNFKIKVGLAPSRANTKQAGGFLGPPPPCGKFS
7110	21011	A	7168	465	166	SPQGAQIKGVGFOKLRFWCFPGFPRKRPFFWFKKKLPGQGGPLCSRFSGLSQKN\ASGPWGEIFFWQONGPPSPPGGKETFFSKKKKKKAVDYLNS
7111	21012	A	7169	2	323	IQGFKTLSEESVDADEVETVELGLQAEETEDVTELLHFNSTACCREIFHERKROQMQQTSLVSHF\RKLLQSPOSSAIATINQSQPSTLRQDMPMPATRLHLTGGLDNIH
7112	21013	A	7170	3	509	FGTIPLVLCADLNSLPGSVVEVLYSTGGVETNHKDFKELRYNESLTFNSCHGKNGTNGRI THGFKLQSAYESGLMPYINVTDFPKGIIDYIFYSKPLQNTLIGLGLPDHWHLVENNISGCPHPLTPSDHFSLAQLEL/YTAFAPASQRHPPSQWQEVVKGHLQRTALIH
7113	21014	A	7171	1121	320	SSCFQTSSHACFVTEFVPGGDPMMQIHEVDFPEQARFYVACVVLGLOFLHEKKI IYRDLKLDNLLLDAGGFLKADFGLCCKEGLGFGDRTSTFCGTPEFLAPEVLTQRAYT RAVDWGLGVLLYEMLVGECPPFGDTEE VFFOCIRLHGRPPTPAFLSVQ\VKFIQ KLLQKCPKPLGAGQNAEIKVQPFPRPTNQALLARTIQPFVETLGGADRGY FEGEFHRAA/PALTPPAPHSLLTAROQA AFRDFDFVSERFLEP
7114	21015	A	7172	355	3	GILLSMLGNILFTLPLLLPLSLMELGGVCGNF/ITNCCLEIDDNKVIDETAKI QKLAHVVPQIKWGSPTDLTGGWFSSIG RFKTLVGIVLVILGVCLTLPCLLLPLVK NIOANV
7115	21016	A	7173	184	2	EKKVEDDDDDDDFEMESRSVIPAGVQWRNL/LHLPSPSGFKPPCSLSLPSRWEHRCA PLHQCI
7116	21017	A	7174	1190	407	SLKRRPSARGSRPMSMYETGSGQKPYLFGMEASRPESRMRLQPPFAHIGRSALVTSSSSLPSFPSTLSWRDESARRASRLKQNSTPESDYDNTPNMDPEGDMGSSRKGRQRMVWPGDGLVPTDAEPHVAPSPTLPS TEDVIRKTEQITKNIQELLRAAQENKHD SYIPCSERIHVAVTEMAALFPKKPKSDMVRTSLRLTSSAYRLQSECKKTLPGDPGSPSTDVQLVTQ\VI PVCVRPFAKAAKQL VTITTKENN
7117	21018	A	7175	3	136	AIHLASLKVFFRYRYRVL/SL/LKRLVNSNW

SEQ ID No: of nucleotide sequence	SEQ ID No: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleo- tide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						FCVILLPWPKVLGLQV
7118	21019	A	7176	3	316	GIKVFEEFFFLTKGRTVTQAGVBNCSLG SLOLEPPRRFKQFTCLSPVSWDYRHLPI CLANFCIP/VETQFHHVQGMGLLELTSG YPTSPAPDAEITGVHHTQP
7119	21020	A	7177	529	217	LLPRLEYSGMVIHAGCLQLLGSQAATLG ACYCAW/HNFKAFFVETKSHYVTOAGLK LLASSNPALASQSVGITGVSHCAQATL PDKTVDKGPSFNLSFTPLLL
7120	21021	A	7178	3	150	YTLCKSKKDKSIYHIMT/HKTHHTHTH THHTHTHKPSTTSYTFETFM
7121	21022	A	7179	540	69	ACRGAAHVQGDSSALTVEEDGTACGPTM LSLDHLCLPALAFNFTCTDSGERRICS HHGVTAWSLQWREKLTGRDRPLLTSPGP ALPIG/CSNEGKCIQPDWTKGDCSIHN PLTSPPTGETERYKGPSTNI IIDSIA GAVLVAAIVLDETGWGYK
7122	21023	A	7180	452	279	CIDSYOEIYHLSISILSVLSIYRSIY LSIYLPFIW/SLYQPRFLRTRDPQLLS LT
7123	21024	A	7181	501	183	HVRCLAFICALIGFSSYFSIMPVVT/V DLVGIEHLNPAYGIIICVNGISALLGPP FAGWIYDITQYDFSFIYIGLLYMGIL FLLIOPCIRIIEQSRKKYMDGAHV
7124	21025	A	7182	446	245	LVRVSLALNGVSSASRYWDVATKLAT F/SLFWKDRNLDILPMSVFNFWPQVIFP SWPPKVLGLQM
7125	21026	A	7183	420	73	DSEDDSGSKLKF/FWKGFTILDAIKNI CDSLEDFKISLTGAWNKILPPLMDYBG FKIRVEEVTAADVEIARELEVEHGLG AVAHAYNPNTLRLRLSKPRSLRPGQHSK TLSL
7126	21027	A	7184	567	174	FFLRDRVPSLTQAGVQVQDHSSLQPRFP RLKQSSH/PALLSSWD/YRHRPLCLAKF LTFPLQRRGLAI/FARGVVSNSWSQ/CNL PASVSPSAGITGESHYSQPILLSDSQTK VYKTHRSTISSTITEMGCEKRD
7127	21028	A	7185	345	59	RNGSSCLMQVITQSILTLPLRECSQVITA QCSLGLGVSSNPPTSASCS/VESSHCFQD GLELMGSSNPPTLAGITGMSHCAQPLYD LFLYEYGLSVHY
7128	21029	A	7186	1	209	LSVVLEIGSHSVTQAGVQVQVHSSSLQP* MLGLKPFSSRFSLPKCWDYRHEPWCLEGL LRLKFDPSVGGVA
7129	21030	A	7187	3	225	EKTPVSDRGAGKCTESLVNRRPFCFSALV VDETYVP*EFNRETFTFHADICTLSDKV RHFLKPIALVILNHHIF
7130	21031	A	7188	1	377	ES*RNHNGDEDDSHVRAQGACIEAKHDK YMAIDMELFSQADNRRKKRDI PDIYLRGK ISFELMRQPCITPSGITYDRKDI EERHLE RVGFHDFVTRSPLTHEQLLPLNLAKEVI DAFISENGCVEDY
7131	21032	A	7189	1	359	SRATDHVQROGHG*GIHNSYDSENTDWF RETKNQSVPLSCCIEITVSNNGSLAHFY DLYABGCEALVGKILLEFMMHVIWAELA FAAIQLLSMLSACTVMCRKSTDPAYELL ITVGTYA
7132	21033	A	7190	496	118	ONQKFPFEPGTS*LGLYPKKYKLIYHKD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
7133	21034	A	7192	1337	342	PKTCMPTAALLTTEKPNHHKHLMSADWN IKKVWYGVTHGACNQSTFLFWFFFBMES HAVAQGGVQWLNLCSLQAPAWATERDSS QKRPKIDPHKVIYN ISEATRTTFRESTWQFQSSPREDDNRKL SASGSRQSHPGPRSTPGPGQHRSSHQG CAPVSSAARPGGPFRLSRGALSRSQFS VLVIYP*VAAGQFVKACLGASSPPSRL* GGLGTGHRTPGKEARSWPETSAAPAWHL LRSCLPSRGEKLAQARSQKHLGWKWL KLCPKTKYWSGPDSPSVLRDPEAGTT RWAPSGNPEEEVVLQKAKYLQNISEVL SVLHLLHIKALQHSTNPFVFNARHLV GQISSALTNNLSQILFLLRPFPFLSQV ERHSPLOKTGTETNVLVFDQTVPMNFP SSILLPSKYSCLPDKKASHFYQ
7134	21035	A	7193	469	130	SASWDYRPPFPSPNFY**RRGFTILA RMVVS*PRDPPASASQAGCAYIYLVQ ERFARLHPACAPRYMASDPLSLHHSV PPGLHLEHMLWHLCLLPQICRPGKLW Y
7135	21036	A	7194	430	149	TVWQFLKQLNIELSCDPVILLGICPRE LKTYYVHTKRT*AFIVALCTIVPKQKQL KYPVDEBWMVIMWVHTMDYFSVINKNK LAKHRSGL
7136	21037	A	7195	257	412	TATSNKEPLKVKRCLLWRKKDCMARGFT ACNPSTLGC*GRWIMSRDRDHFG
7137	21038	A	7196	1	124	PLYSGVHFCNPSLTSGRGNRIA*VQEF ETSLGELAEPCLY
7138	21039	A	7197	2	120	YGILFITSEVVFAGFF*AFYHSSLGK KISKKESVII
7139	21040	A	7198	234	416	GVHAEVLISFGQDRLEALVVIPIFGI LFAILLVLVFIKKVAKKPTNKVGH*EP GTEF
7140	21041	A	7199	372	3	VHYFVFTQSGPCCVPHPRGLSTHPLGH SRYTGLGMVAHACNCSTLGGOSQKIA*A LEMEISLGNMVRPCLYERTNKQSKPRHM GITFTGLTSLTLTKYSLISGFYLPQV LISLHPLPGY
7141	21042	A	7200	396	21	GLKESHKCAIPACQLORDPLVRVLKAG F*RKSLISISTELQSLFDSPPDFSKITGP IKLTQVEHRAGFEWNEIDAGTTPSPGLQ PAHLTPFLDYHLNQPFIFVLRSDDTGAL LFIGKILDRPG
7142	21043	A	7201	2	148	REPPHSHLANF*KFFVDKGTLLPLPLVS SSWPQVVLPPRPRELGLQA
7143	21044	A	7202	1	291	AEGFRMHALVSOACGTSGLKSVGMV QGPIHLMLGLLISLIFLSRSGRTWAF SHS*YKTSDLLPCRNAREVIEFLHYRNL HSHICLSVTKTFL
7144	21045	A	7203	262	406	ILARMTSVVNSIKHLLFLPK*SSHLSIP SSWNYRCULPHQANFLFL*RSPTLM PALVETVLQNSPTKIDSSPDDPSGKF YCTNLIVFENIRRGNTSNLLHKSRLIL PNLTKTLLHD
7145	21046	A	7204	2	247	DTVLERSGGGTAALPRSTSLDRDWAITE EQILASLLTEPALVKYVDKPECMARIT SAKNIIRMMGKPLT*ASDYISAMTG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7146	21047	A	7205	2	168	FFFLVETGPTVLARMVSV*PRLGPASA SQSAGIAGVSHRAQPALRFLMLENRMC
7147	21048	A	7206	1	237	GKCAHTHTHTHTDTRHHAHAHTHACTH THTYVQCGLSQNSQDCVRMWACHIFGV PRE*ASRYTSSLVYKFGCTGVC
7148	21049	A	7207	2	239	KVDSEHKLERSSGGVLGRFGKSGGGLN LGNFFASRKGYSTRGFDRLNTEGSDQDK EDDGSESE*EYS*PMPALEPCSS
7149	21050	A	7208	1	405	GSRDNMNVLICFPNAPKVASVKNDA QLDKYLECTAQEI*INWEDVPDLFHYM RTLPSDNMPSLPGGELASMTVIEAVY YRLNPYINDTDSSTDDMFNCSSSHG VYLDLHRRVONFDETFSSMPEL
7150	21051	A	7209	2	761	QDFGTRFATVLLFYGYFKCTRLKGTCL YNAILYKVCSPRNDQPDVCYNPSFLLP IKTGELLGLFLVYASREKRSIAGD*KDD KWPPERIIQYYGPAT*AQDSSWGYRIPI YMLN*IRLQAVLEIITNKTGRALTVLA LQEIQMRNAYIKSRALDYLAAEGGIC GKFMNTNCCLLIDDDGGQIVEDI*IKITKL AHVPMQIPDIWKNIVKIPVLFCSVLIT GTCSPOSGTFCWLSRSRSPHDPFRVVS P
7151	21052	A	7210	147	390	KTGLSDQMFRAIGLSYSVLSPLLY**SY KKKKKKKKKKKKKKKPNFPGKPN*SF WGGEKKSGPGAGLKNPGGGKNTFY
7152	21053	A	7211	433	214	WGRGNALTIHFFWVFQESSETSPFL*G ITLLDNPPSPIPKQPPPH*STITVPYLL SSPQPGFPHFPQADGLA
7153	21054	A	7212	532	253	KVINVFHKAAINSDFSDRSRHSHTLKAS E*GFTMIDAINKCDL*KEAKISILGTGI *KKSIPITLMDDF*GFKTPLL*VTANVGF QRFSKKFYW
7154	21055	A	7213	456	24	DAQAFSWYSQGYFNSSQGFYSISLPDGT SPVKIKRMGGPLFFS*LLKSTCKACSKTS RVFGKVLTKGLPRPR*PVYKDLGGFY RF
7155	21056	A	7214	2	445	ILRDLCORVFTWSGGFFSWANELLVERAI SSASSPQSPGDALRTVFECISSGILKSG SPGLLDPCCKDPFDTLATMTDQHREDIT SSAQFALRLRLAQRQIHVLGMDPLPQMI QRSNIHNNRRRRSDSGVDGFEAEGK*D *KDYDTF
7156	21057	A	7215	203	3	VRPGVVAHACNPSTLGG*GGRIA*SQEF ETNLGNTVRPCRNSGEVLNRTVSIIRRA LRVFSPLHTA
7157	21058	A	7216	1	285	GKCAHTHTHTHTHTHTHMTHTHART HTHMCRAV*VRGARTVCTGSAFPLES PGKEPKDTRLPLFVSQAARFLGKAKFC SVYRQREPPPI
7158	21059	A	7217	1	386	GDNSCERSVLYVLIATFGIGVALGILSW TVICNLKQKQKPKMKKSKXNLDAIQE SL*LPASRAGIKQKGLLSSSLMHSES KLDSDDAIFTWPDREKGLLHGQNGSVL NOCTPLKATSPREIL
7159	21060	A	7218	70	379	NILYENIEFFFF*FLKELNVFFFFF* VFFFYNNFFFFVFLCFVFFFFVVKLIEF WGFFFLFFRFFFCGLFGTQSWRNFFA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
7160	21061	A	7219	1	208	LPFWGLMFLPFLLEFLVFF*LVFF PRLAASVSPGMLGWVLGLTVASACN CSTLGGRGMTIT*G*EFETSLVKKART FYKRLKQKKSANL
7161	21062	A	7220	455	96	HYLYGSGQLSRFYFVTCQGVQWHDHGS QPPTPGVKQSSLSLKPCKWDYKCEPPCL ARDCPPFFFL*TSVDTGLLNQQPIL* IMTFYPYLLRKSLSFHHQIYEPTSI LLSFCT
7162	21063	A	7221	201	319	IYELWPGPVAAHCNFSILGG*GEQTAQV QEFKTSGLHLG
7163	21064	A	7222	307	3	NRQAGFPFAKLRPSPKGGFPNFKLF FFKSS*F*KNPKQGWGFPPLIPGFGPG VGSLGAPGLKPPWGTQPNPFSKKKKK RSNCTDTGTTIAHRRQM
7164	21065	A	7223	331	141	SETITANVSPNL*DANDVPIQCEISPLI SYAGEGLERYVADKEFHAPVIDENG VHVNGI
7165	21066	A	7224	157	314	WLPGRFDGGEDGVCHVAQAGFKLRT*GD PSIKASQAGITGLTHRTGPK*KF
7166	21067	A	7225	2	392	RDVRSQQLPPLSLK*FSCSLSSWDYR CAPPTT*LIFFILLVEMGFHIGAGLEL LTSQDPPASASQAGVTGVSHRTRPPSF VLVNPILPPLLFPVSPDGPNISSSTTSW RGYPVLRLWGLCSFWGCG
7167	21068	A	7226	84	204	FIFFFFKR*SLTMLPRLVSNWARVALP PQRPKVLGLHV
7168	21069	A	7227	3	307	DRAAPRGAGRAGAVGPHRTGDWGLAGTP AGRGHAIHIGRGPKOGRAGORGLHHPG GLLAGCGNSP*RKQTPGSMRRAAPLL STGQVWEGPASVGRVP
7169	21070	A	7228	52	1176	GSQQFLHISEAGQDTLLIKAPAEAAFP PLIAFSSGGRLPCSHES*SAAGYKRLDD TAAGGPPSPGGSPPSPATAFGLHVPWGG QLRPRGGRGLPATQSGEAFQALTLQSRG RACTGPPAPGSEDAAPSGCSAARNSP*M AGSSSCAIPDSASCTCPQGPWRW*SR APARNRCSASSGRSRC*QLRRRYIPGL LHPVLHEALPDSWGCETQLGPLASEAA PPRSRRREEG*RGSGRC**KPSLPSWS LCRNQAEAGFVSLVLWGLAGAPSRPA AAAPQIAPNQHRSPPLAPVPAASGSP WPERDLGVLETLNVGNFAQDPNPSACS GPQSTPDYYPVQKPKTGLRLHFHSRPN TIVKSVGNMCL
7170	21071	A	7229	3	112	ASNLSRGSCSEPRPCHTPAWV*E*DSI SKTNKQKN
7171	21072	A	7230	103	299	AMSQIRNAIPPTIAT*RL*YLEIQLTKE AKDYINENYKIPLKEIRDVTNKNIPCS S*IGAQLCK
7172	21073	A	7231	2	137	SLTSLSLCTFCL*RWGLSVLPRLISNSW POAIPPPWPKVLELQV
7173	21074	A	7232	3	273	LTHIVDGNPLFTMTYQCLMCVC*QELGY QPVITTRCHNVNDCLQRSFKAQVFSCH ACRDLGQNYIMIPNEIMQTLDDLAFPG YSLGR
7174	21075	A	7233	338	136	RPRWEDCLSPGVNVCQHSSES*PFLQEI *KISQTWCKPVVPSYQEVESGELLEIRG

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						STCFGLPKCWD
7175	21076	A	7234	437	261	HLGFPECWYDRHEPHQHT*FLEHEM*RRGLTTFPRLVNWSWFOAIFPRWSPKVLELQT
7176	21077	A	7235	41	264	VTVMEIKGKINLVLDIIRKDIYVEGFSTY YF*ROGLTMLPRLDLDLSWAQALPPOPP E*MGLQECNHHQAQLSRYP
7177	21078	A	7236	1	154	GTRDFSVKTL*ARREWHDIFTMKEKNF YPKKYALKI PFQNEAETKKVSV
7178	21079	A	7237	1	179	SCLSLSSS*DCR*PPPCPANTVKSFFRN GVLTMLPRLVNSNLPQANLLAQLPSGFI ILL
7179	21080	A	7238	340	140	KINWVWVVPVPIPTPEA*AOKLP*PGX LKFPLT*IPPLPSRLGHQQTSTFFKKKK KFYLLSDSV
7180	21081	A	7239	2	175	QFESKPSPAWATEODPVSKKKKKKKKK KKKMKKKNSKFKMIPFTRQY*EGNWK N
7181	21082	A	7240	336	192	QSETFSQSNQKFI*GGGIALLPRVLN SWAQALPPWPVKMLGLQA
7182	21083	A	7241	1	186	DRPGQHGEMLSLLIFCFCDRGGTLMLP RLVLKS*AQVILPSRPPKALGQDTVHC SKFDVAV
7183	21084	A	7242	2	111	VKITLNLGIDGTWLRIIRAIF*KPIANI LANMCSPL
7184	21085	A	7243	360	217	LPSRGDYKRKPPCLVNFYFL*R*GLTLL PRLISNWAQMIILLPQSPKC
7185	21086	A	7244	35	276	VQOORVQGRKKYSTLVKNKKKLKNYLR VGE*MG*RNIGWVQ*VAHTCNPSITLGR GGRII*PWEFFETSLCNIG*TCISG
7186	21087	A	7245	1	356	IQHTFSLITFGIKYSYYVLKTVSWLA AVAHACNLSTLGGRGWITT*GHELTNLPF AVKPWVVDKNSFPPTNLNRFKASHLWE PRGKNHGPPEPTPLSRVSPQRFFPGGT RPLKKE
7187	21088	A	7246	3	293	CRCKGFHNFYSFQNHESHTGEMLYDI RNVGK*SIFF*HHCQHKHTHRAEKLCEC KICREAFSHFGNLKVHEAGRSGR*SQ HLGWANCLTSGI
7188	21089	A	7247	6	387	ASIFCLTYPSWEFL*FI*OAGHFSFSKK KLFICAFPSNRDEVSMLPRLGLNSWAQ VVLLPWPVKVLGLQVRATTAKLGFPGW FMSVSLGQGVCLCRSLCPLPLGPGQVH SGCSQSFEKMNKEL
7189	21090	A	7248	373	146	HLGKVLIFWQVQYALLNPPNGGVSRYV PRCRPLMVFFFFFFFC*GRGLAMTLRV SNSWSQVIFOLQLPKVLGL
7190	21091	A	7249	2	184	ATLRGI*KKFISTMDDFEGIKTSLSEV TADVVEIAREVELEVEPEPKDVTTELQS HDTT
7191	21092	A	7250	795	544	EMKSCSCCPGWQWRDLGSLQPPPRFK RSPASASLVAGITAACHARLIFVFLID TGPHYVG*AGLKTP*ATAPGPIFYFL
7192	21093	A	7251	34	242	KNTSLKKKFPKQCLKNVSLVEFAFW GAVARAQNPSTLGRGGVA*GOEFQTS LGNTGRPLRYKI
7193	21094	A	7252	216	57	NIQVLKYVLTSLYLLKKKCAFRLGPVHT CNPGLIAGQRRIS*AQEFETSLS

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7194	21095	A	7253	126	366	INLTCCQQYLDKATFFFFFLKXGLFAP*A EWQGSFASLQPKPPRLKXSHLLTLLST WDYGGALPCRAFGSFFFWKKG
7195	21096	A	7254	2	213	RPTWATWQNPASTKKKKNSFFETEFRT VAQAEVQGGNLG*LQSLPPLKRFSCCLK MPEAPKGGSCSLIC
7196	21097	A	7255	150	263	EGVSLLEPLACNGAILAHCLRLPTSSD LCAFS*TTTRYKYKSGYCFSHPLMLIC SRFTLLSSHSLGLHLTLFLIVCFEKES HSCPGWRAMVLSWLTATFASRRQATFAP SLELSR
7197	21098	A	7256	386	93	PPGGLPQPSIPSPRAQLKPKSPRGKKRG GPKPGGSGQPGFWGFFGPGPPFKRGGGL NWLGAKN*KGVKGNQKKKKGMQPETK RGNRSIDMKFGGS
7198	21099	A	7257	153	369	KENSRLQGVGFLPSHS*PTNSCPGVQVW LTPVILALWEAEVGGSKDQPGHGTPTPR LLKIQKFARCGGGRL
7199	21100	A	7258	180	3	CSTLI*TRKVLGVAHAYNPNTLGRG GRIA*GVVFKTSLGNNVKTCLFLPSPHN QQ
7200	21101	A	7259	22	265	QLRAIPDLKLDPLMEGKEILSRTLGGSG TVAPICDPSTLRGGGWIA*VQEFKTS GNMAKPHLYRKKLLQVTKLEYKW
7201	21102	A	7260	326	2	KSAMQICIVDFLNAFLEICCHANLHCR PSNAFCFLKVDNVRAFVSPSIPQVSLIL KNFSWGGVVAHTCNSNTVRGGERIA*A QEFETILGNTGRPCLYFLKNNRKS
7202	21103	A	7261	1	68	VNLCPFLMWLGGVVAAHACNPST*GGREG RIA*P*ELETCLSNTP*PGVVAHACNPS T
7203	21104	A	7262	282	176	GLKKTFFFLVREVRVLCYPGWSAVV*SQ LTAN*TPGLKFLSCSLPSCWNHRRVAL HVAENIC*CHMPVVPATWEAEAGELEP RSSVCSEL
7204	21105	A	7263	588	351	NNTVCLLESISVNLCPHLQHSVPVKLE ILFFPSSDNFPSTHHITVRPLSPS*AI IFPVCTYTSRWPEATKDPOKK
7205	21106	A	7264	327	2	KIKERINNFIFICRDRVSCCGGNNAV TLNSWAQAIRFCLSLMS*NYRCAPTHQ QVTTFRCRQDIEIHMVFKYHLGNTLNY FFVLFCFVFLRHPFSAHRNFRLP
7206	21107	A	7265	121	270	AQEAQFELLTSGDLPTSASQSAETGMS HRAFLPCY*FYVTLHGLTVACA
7207	21108	A	7266	3	227	SSQVSLNNWDYRRPECLRFVFLFFVE TRSCYVASLELGGSDPTVLAS*SARVI DMGHCDPNLSEILLHVR
7208	21109	A	7267	300	1	KMLNTIMCNREITLCRRKSPRVQQTSTFV SYFKKLPPQPQPSATTTLISQGPSTSKQ DPAAK*L*FAEGRLLAFPSNNVLYQLR YIMCFLPHGTIVHLVN
7209	21110	A	7268	29	344	ASLLALKKKSGLGAHAHNAHASTSGGGRG GRIT*AQEFATSLGNMARTCLYKIKKKK KKGKNFTGVGGPQPGAPIPGPWGGGKS PAPGKPGGPNFPFGKGAFTPL
7210	21111	A	7269	3	209	LHLSFGPFAFVAAGIPGQASR*GPCR PDPSPDASVDASLPGPALSLWSNGSR GEYGTTPASQIH

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7211	21112	A	7270	86	206	COPGVVAHAYNPSTWGGGRQIT*GQEF ETSLGNTARPP
7212	21113	A	7271	45	274	GLGTVAQACDNPSLTGG*GGWLA*GQEF KTINNDKSNKWOYLAIETQINNRLICK NKKELTDICNNTDEFQKHRE
7213	21114	A	7272	1	122	VLVETGYLRVGGAGLKLTPGDDPALAS QSAGITGISHRA*SYMHF*LVETGYLRV GQAGLKLTPGDDPALASQSAGITGISH RA
7214	21115	A	7273	3	242	LLKQLDYRPPHPAKFFFFLEFLVKKGPH LVVKGQFKTQTSGLPG*ASKGVGIPGV SHCPGLIGVFNLTLLKVAVSLMDL
7215	21116	A	7274	2	169	LALVAQAGGQWHDGLSLQELSPSPQFF YLSLPSS*DYRHEPPHSANFSSFSNVR
7216	21117	A	7275	353	76	FAHLGLPQCWDYRREPLCAT*KLFLRGK *PSKQVQVFSGLGTGHSNACFSCVMWT IVLLIINFVWTGIDGRTSGSSSVKCGNH SIYPMVLL
7217	21118	A	7276	6	87	RRSLTLPRGLSNWPOAILLPWPFKVL KL*AQTPLGRQSSCLGLPKC
7218	21119	A	7277	1	203	FOVKMLCSGMMMLTPVIALGAVAHGTN PSTVGGRGGQII*E*FYTSLDSGNPPA SASQSAGITLA
7219	21120	A	7278	272	51	IFFFVN*CGHVDVHHFNPS*NNLSSWS SWFMPILPLWEA*AGK*LEPRSLRPAW ATKLDNSNKKKIIIEHA
7220	21121	A	7279	1	131	SRDYRHGPHLPTDFVFFVEMRPHVAQA GLKLLGLSDDLPAITS*SRDYRHGPHLPT DEVFFVEMRPHVAQAQLKLLGLSDDLPA LTS
7221	21122	A	7280	411	36	FLECVNFFPDKKKKFFKKNTGQVFFPV TFL*KGPALEFFIPFPYGGKFFPLSSAK DPPPRVFF*KGPLEFFFFFFFFFFF FFFFFFFFFFFFFFFFFCFPHIYKKVHF *SSVHFQPIIF
7222	21123	A	7282	395	181	RKHESIHDSDVSVTFTNMQSLRLFFFI FILSL*LFRIFFSFVLVFFFFFCFF FFFFFFFFFFFFFFFF
7223	21124	A	7283	392	2	IKFFGYNV*FNLYLKNGLF*QLLI*LIN LFILRQGLIFVQVCNVLVFFFFFIFF FFLFFFFFFFFFFLFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLTONMLFI VNFCKDTFKQONILHRTGR
7224	21125	A	7284	113	291	YVCVCVCVCVCVCMEY*SAIKRDKIVA FTVTWMELETILLSEVSQEWETTHHMLS LIN
7225	21126	A	7285	327	44	LKVSNNFSPPKKKVLPPKPPCTIFPFS PF*KTPPEPIFKPHKKKNFNSPPQK *GPPQGFKSPPPPPPPPPPPPPPP LGFSSKLLIR
7226	21127	A	7286	3	215	VILIIFMI*EAPAWKKVLIIVEEPSINL E*LYDGGYDGLVLTSLGLPY
7227	21128	A	7287	367	119	LKKAPAPFFLNPFFWGKNFILSPPKMG PPRGFFKRGPPPPPPPPPPPPPPFLG FFFFFFFFFLLQYNNMYH*ILLINO
7228	21129	A	7288	73	259	INKVLQN*KKKKKKKKKKKKKKGGP FKKTPRGAQISPVKKKKPPPPGFKKK QAPGPF

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7229	21130	A	7289	337	53	LRSPAPHLFPIRLLLTDTHMVTLPFPSS LCSHYLFNEVTVTTLFKTTTHLQCTMA HTCNPTLGG*GGRSA*AQESSTSPGNM AKPRLVLLNF
7230	21131	A	7290	1	96	KHIFGEAAA*YWHFVDV*LFYVSIY **GS
7231	21132	A	7291	288	2	SRVEFGPMAHCSVTIFGSSVFTSAS *VAGPHGARHHC*FLF*FLV*MLENG SRHVVOAGL*RVSSDDPARACSGGIP GVKPHAQSVSV
7232	21133	A	7292	121	233	YFPKKKKKKKKKKKKKKKKKKKK* KGGGRSRKSYLG
7233	21134	A	7293	3	346	NPLNPLVNLTVSPKRNSSLDTRKPCRE RHREKETLRKKRNQHTFARQRENHPE TE*ETGQRDRDKQTKKQKDDIQAYTYT DREKDKKRRQIR*AEAEIRDTERQ DI
7234	21135	A	7294	46	346	ETGLKKWGLDSNGTVRAVLNLAQADFV SIPSYH I KRGNTKNCGEGKKILVVT AKKSEPGVTHACNPTLGG*GGRVT*G QWFKTGLGNI VRPCST
7235	21136	A	7295	254	12	RKDAENNGSRAB*IKRVLDLVQSKLKPF QELEKEGILPNPFYEASITLIPKPKDIT SKEDYRPISLMNDAKILNKILAN
7236	21137	A	7296	258	1	CIGQCVLVAVGRELLCVSRSWCGLLHVD EVGGEALGRLLVYVWPTORFSESFGDLS TRDAVMGNPKVKAHGK*VLGAFSDGLAL LD
7237	21138	A	7297	191	263	VCSKCEFFIYIMDYAAIKRKNKIMSFA RWQLEVVSELTQEQTENNMF*VVEG FLLLC
7238	21139	A	7298	2	164	SRVAGITGAHHRAQLFVFLVETGFHV GQAAPKLLTSMNHARQ*LFHFYFPK
7239	21140	A	7299	307	8	VMTITFWLPHLSGYTEKSTFYECGFDBI SADRVFPISKFLVAITVLLCDEKALL LPLP*ALQTFNPLIVMSSLLLIILAL SMAYE*LLGLDCSE
7240	21141	A	7300	205	317	KSSPACTPSTLGG*GGWFA*VQEFETSL DNMVKPOLY
7241	21142	A	7301	140	22	FNFLFLYP*NYFFFFFFFFFFFFFL FFFAMNINVFY
7242	21143	A	7302	382	151	SIHRSEFRPRSRHSVSRPESRGITLVVC SLYFLGSGDSAPVVS*VAGTIGVCPWAS LIFGFFFFFNDRDGVLLSCPG
7243	21144	A	7303	318	17	LVPTKRPQVENNYVPHYTIWYCTGKGRK WAGIGGSCLSQHFGRPSWDPLSLGV* DQPGQHRETPSLQK*KNWQEP IVPATQ EAEAGEWCEPGQSLQ
7244	21145	A	7304	310	132	QWCDLGATTANFCIFFVRNGVSPCWG WS*PPDLKLSARLHQSVFFNP IISIGL FFL
7245	21146	A	7305	338	168	REPLPAANFVFVEMRSHHVRAQGPPEP PSSSDLPASASQSAGITGVCHAMP*TY YK
7246	21147	A	7306	276	161	ITNAAIKRNEFMSFAGTWMLKEATILSK LTQELVK*KLRFNTDTILLLILIKI F
7247	21148	A	7307	310	61	ITLVYCNFFYPINFNFLKLPDSFVITLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, =possible nucleotide insertion)
						LKQIYSCTAIVYLIL*AFVQFKFLCFY FLYFKNIYFKNIYFKIKYV*NMFFVF
7248	21149	A	7308	257	1	CGRVDLH*AVFFFFRWSLTVLPDLDL SWAQVILLP*PPE*LGQSCCTTPSSLS TFLYAPLHIPVNMKSCFVGKDRGMFFSY H
7249	21150	A	7309	2	181	RDGFCHTGHGL*LLTSGDPPASASQSA GITGVSHHARPCHLSTAFFKNMVMWFG QQE
7250	21151	A	7310	25	340	FCVFNMTDVRNI*IFLIFVVDVHLG*QK NLLDITI*KKKSIRIQE**QYKSTSKRN YNTVSDKSWLGTVAHACNPSTLGGQGG TA*QEFQTSLDNTVRPCVY
7251	21152	A	7311	2	193	FVDFSMHILDMLSLYLSIVICYITLFLS IIDNIYVNGPHKI IIPYFYCIKIYIYI IWFCFWFFETVLLCCFSVFTPDVYCSLY FLYLLGVFGLFHF*FLYLYMVLFLVP
7252	21153	A	7312	1	245	RTPLGLKQSHFSLSSNDYRHWVPLHPAN AFFFKGP*BEPLTLASSLHWYFGGHP LQAPKIDDPNESP L LKGLKKSP
7253	21154	A	7313	167	2	GKFCILVVGCRDSQCKEKGTLKREAL RMCK*GOARWLTVPVIALWELEAGGSP
7254	21155	A	7314	334	152	CHVAQAGVQVNHSSLOP*PGLR*FSH LSLPSGWNHSTPPHPANPFIMSGCHLP LINK
7255	21156	A	7315	2	164	PHVGQDGLLELTSGDPPASAFQSAEITG VSHHARPTFYLS*QVGLTVTSFRNPQ QRIKH*FHWLGAUVTCTNSTLGGQGW ITGGQKFETSLAYMATRFLY
7257	21158	A	7317	1	293	GIPSTWDYWCSTSPQPH*FFFFF**KR DLAMLPGGVLSWIPAILQPKGKVLGL QAWTILYKGYGKEMWHKEICKGTHOVL SKLLTTKRFRLL
7258	21159	A	7318	262	73	SNSLVYLIKPDSSVYIFLLFVETVSSHVA QVGLVASSSTPT*ASQSVETIGVSHH ARPKKVT
7259	21160	A	7319	169	265	GGRMALSPGRGGCSEP*GCHCTPAWETE QNPA
7260	21161	A	7320	169	260	KPKIIPVACDOOFTDRNCSHGDIYECNM VDFFFFFRVSLCHPGWSAVV*SGDH TTALQPG
7261	21162	A	7321	580	400	FFFFERESRSVARQPGVQRDLSSLKSP PPGFKRFPCLSLPSSWDYRRAQPCPANV FEFW*RWGFTTLARI VLLS*PCDPPTSA SQSAGITGVSHCAQP*FFFFERESRSVA RQPGVQRDLSSLKSPPGFKRFPCLSL PSSWDYRRAQPCPANVFEFW
7262	21163	A	7322	130	26	SPGFLGLIEPLPSRFKGFVLLNLP*TW EKLALTAPIKFFFLIKTFPH*GKIL RG
7263	21164	A	7323	17	303	KSSGTIKGRAGSPFLQLVAIEQCQDCPH FRSQ*YKKCLOQGMHMYNPSYSGR *SRRT*AQEFKSLGNITKLCCKINN SLFKITENIE
7264	21165	A	7324	194	8	DNWEVLKSTYRPDTPVAHACNPSTLGG* GGSIT*GQKFEIRLGNVVGPCLLKNLTN QLGVGG
7265	21166	A	7325	413	72	GVPIFLKTLTKGTISSERESKVPLEKGR

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						ANFRDKRGIPPHHKRVIPAEKKL*KGRS PFDDGFOKKLTQPRVSAFGHPPLQPLY AFIKSFRSGTHHQDCPFWHLILSARRQ Q
7266	21167	A	7326	394	177	NVNHTHTHTHTHTHTHTGWCSDTQYS SDS* CITPRCIHDPTWSSQT VNLAMG LT LAKEVLAMTQTEV
7267	21168	A	7327	232	22	SRPSGSKGAPALQSSCLSLSSWDYR HKFPYLTNFCIFL*SQSFFMLPRLLNS QPHSNLPKVVELQV
7268	21169	A	7328	232	3	YHRSSGSLSLIQLRLRSKI*APSIPII KEWLSSVAVHVPNTILGGQGRIT*GQE FETSLGNIARPCLENCLN
7269	21170	A	7329	364	3	PKARRATVRTRVSKAPSNRQCLGVNTH VLGHRPVPKGNAKTRWSASEQAHCTNI TTLGGQGGLIT*DREFFESSLATMNPVS VSGWLQKMFSSKQLYSKFFPNVAYKAFR IWLLCARA
7270	21171	A	7330	177	2	DPHLHKFKARCGMGL*SQLLRLR*K DQLSLGVGGCFELWCYCTPAWYTERDP SC
7271		A	7331	413	40	RHMYLMFYTYIYVLVDITYTVFFMYIYI P*CVCKYISGLHIMYRFISMYPGVVVV CMCVNVIHVIVENAGSCLALSALIEHE GMARDSKMTNFNPDHMKRLSYKKQLEKL NFMILCPTWKFE
7272	21173	A	7332	147	49	KNYIYFCRRGLPMLPRGLNSRAQEILL PQPPM* LGLNSRAQEILLPQPPM
7273	21174	A	7333	148	361	SWLGTVAHAYNPFSTLGGRGQIT*VOEF ETSQSNIAEPLLYSVLAYAVQPLPMVA MRKWLILPTSRITL
7274	21175	A	7334	305	2	CPGGFVTRVHR*YVRLSQFDLRFVTSGA MPASAAOSAGITGMSHRARPVCSTIIIFL NIFKVTCIFVELTIPNQNKQNTFLSSSTV ASCRILASRPTPIVVVL
7275	21176	A	7335	1415	1164	FFLRQSLLYCGWSVQAQSLIASSTIQ A*AILPPCSWDYSSQHTNLKFFFC*GDF SMLPRLVSGSWAQMYLLPOLPKAQAKL
7276	21177	A	7336	1	206	GTRADHLMSGFODOPGGHTETLSLKLQ RSQAWWHVPVMLPTR*IDARESLERLMT IALLKVENRYIF
7277	21178	A	7337	65	302	KSSLFYFLKIETGFHYVAQTGL*LLSD DPPASVFSQAGITSMSSHOTPKELLKST RNTLEENREWAKAREWAHRRNT
7278	21179	A	7338	208	38	NPVSANKNEYPRGTFDLGTQAEVQWHD LSLOPTTPGLK*FS*LSRV
7279	21180	A	7339	2	198	ARADHPRSGVRNHFGQHGSETPVSTKNTR N*AWWRVPLVPECWDYILFYMTNCMDN KLKPLWLTLC
7280	21181	A	7340	2	227	ARGEIMSPAATWMOLEANILSKLTQE*K AKYCMFSLLSGAKHWVLMNKVGTGDIR DYLGCSTQAVLNKLGTRAE
7281	21182	A	7341	3	300	HEGRNYTLTRGDSCTLAASAEKACGACP LWGKDAESSKVCREASDCBEEGISIC VDVNCKEQTMPEC*AVAL*CTVHLIYVT INNALCLPQLTLFL
7282	21183	A	7342	210	351	RGISGTVARACNLTFGG*GRWII*AHF ETSLRNITKPSLRENDML

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7283	21184	A	7343	306	164	IYMLFYIYITLIYIHTHTHTLYLDKIYIYL*CVHCFI*AYMICHOR
7284	21185	A	7344	442	8	SQMSKLKTWFRVAHAHNPSTLGGQGRIT*VREFETSLGNTARPNLYWN
7285	21186	A	7345	3	248	HELSSLSSPLFFPKNEKGR*VAHAGLKLTTSSDPPT*ASQSARITGISHCARPLLSHFLAYLALPCHQNRCLTGHLPT
7286	21187	A	7346	2	246	HELYQSILLSPFLPKNDIGSR*IAHAGLQLLT*SDPPT*ASQSARITGISHCARPLLSHCLAYLALTCHQNRCLTGHLPT
7287	21188	A	7347	1	130	GTRLLKRLTQETRLNPGGRCREPSLHYCTPTWARQSQTVAHN*KRLTQETRLNPGGRCREPSLHYCTPTWARQSQTVAHN
7288	21189	A	7348	516	288	FFETESRPTTGTGQVQCGLGFLQPLPFGFKGFSCLSLSS*DYRCLPPHPANFCIFSRDGVSPC*LGWSQTPDLK
7289	21190	A	7349	417	148	STSVVVQAGVQNHHDHGLLLFGPPRLK*S SHLSLPHG*DYRHILSLCLANF*NI FVEAGFRHTAHGLEPLGSSDLPASASQSGAITGMSHLA
7290	21191	A	7350	143	2	TQKFTSLSSWDYRRVSAHVANFCIPSKDRVSY*PCWSIPDPAZ
7291	21192	A	7351	189	37	EALAVRRII*NLFFDFF*EWGLTVLPLKLVNSWAQAILSPDSKVLRLQA
7292	21193	A	7352	131	2	KSLKETVAHACNFTSLGGRHGWIT*SREKFTSRANMKPRDRA
7293	21194	A	7353	1	106	GTRGGCLTMLPRVLNVAQMLPFWP*VLGLQV
7294	21195	A	7354	939	653	KGNFIFLRQSFTLVAQAGVQNRDLGSPQPPPQSGK*FSCLSRSSWDYRHGPHPA NFAPFLVEMGFLHVQAGLELT*GDPTT SASQSAGITGR
7295	21196	A	7355	270	26	EARFLGLLRDIAQLCYFGWSAAV*S*LTAASTSWAQVKASTHLSLPNN*D*ARATMPG*LKKYVFF*ROGLAILRLRLVF
7296	21197	A	7356	329	206	HHLANF*TFCDRDLTMLARINSWFOAILLPQPPKVLGLQM
7297	21198	A	7357	128	253	MRPDTVAHTCNPSFTLGGQGRIT*THEFETSLGDMMKPYLYK
7298	21199	A	7358	2	108	AREGSGGGQGCSE*WRHCTAAWVTEQDPVSKTIKK
7299	21200	A	7359	1	340	GTRERNWHLA*ALHTHTHTHTRHRTHTHTHFSPPANS*RDTFVIF*QSLLEIMTSFSPSLGLKCSFSQQPSGLLSSIAGERDSRIHGENTVSMCLHNLKAEKLSDVISLRV
7300	21201	A	7360	385	1	SVGPSKPCAGYNLIVCHLLRFLEKRSIRVGVT*FSRCHLSPLSLTRKANSLTPCTSWMRRCILLRLTLGVPHMPSCTHCPITLSEMNLGPQLEMOKSPICVAHAGSPRLLELFLGHLGSTPNLPSC
7301	21202	A	7361	234	29	LSTEPKSGKALKFNVTLLNLNIAF*CNSSCNLSNLS*SQY*RVIQSHLSQTLWLTPVLPALWEAEGG
7302	21203	A	7362	68	339	DRDIANKPAWGLCQSRILYLAQLQFIDGCELLPDRPIHYKVI*TCATAH*RRNRLDOWNRADIPLDNPQCANRLTPVILVLWEADVGS

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7303	21204	A	7363	168	2	CFYSTHAHIFKELQRPGVAHAHAYNLST LGGRGRLT*GQKPFETSLANMVKPHSC
7304	21205	A	7364	399	62	OPGQYQKHPVLTKNSKIKFPNGDPPVVE NAREG*A*KMVEPGKVRVQSAQIKALEF NLGPKKKVPFKKKNPWLAGGGLRPEIP AFGKASKGGSFRSLRLRPPGFLPYPAHF
7305	21206	A	7365	289	76	VCDVLRSAQLSLKCSGIT*AHCVNS IAGSSNCHASALRVPGSTGVNVESEGRD VDRFEAYGRGYVCA
7306	21207	A	7366	364	182	QNHDCNFKLLGSSNPFTLAP*VAGTAG TCHCAWLI*FLTWKIGFKTSLKIIVLLG YFWF
7307	21208	A	7367	155	2	ELGTRKREGWEKSATVAHACNPSLGGRG RWIT*GEFPPTSMMANMKAHPR
7308	21209	A	7368	342	184	LSLPSWDRRYTPPLRANFPKFFKFR*S LTMLPRLYPFYITHTLNSAMTF
7309	21210	A	7369	2	211	AREPKCL*TDWEINKQYIDAVEYHLAY KLNEILTHATTWMNLNMLIGRS*TOKA TCCVIFPMDSIYV
7310	21211	A	7370	190	344	YKNTVTKRILTWSTVAHACNPSLGGQ GSRFG*GQEFETSLGKIARPCLY
7311	21212	A	7371	24	254	KPGQIGAAHSSQHYGRPRRDLHSLGV* DOPGQHGEIPSLQKKKKGLPGRGGVCL KWFELKILGEKNVWVLTFG
7312	21213	A	7372	43	358	DSNLVSLFFHGEADLGTTQVLTHPSTT ANYFVHYCOS*LLYGTINT*PPVHKIN PTHIKTSPCLQASTAINLQLSHINCNS KATPHPLGVQOQYVPLTVHST
7313	21214	A	7373	2	288	THILTAFTSSLLGLVYRSHLTLALCEL HGIIILSLTIIAPLPLNTHSLAPIGPI AIIIVIA*QAAVGLALLVSIISTYGLNY VHNLALLOCCN
7314	21215	A	7374	335	1	VQWNDFGSLQNPPGVSEFFWLSLNNLL GFKGPPPRPGFFLK*PKGFSALTRMV SLSRPRDSAPLAPPKAGVSRNLNPARAP FFFFVFCFHFLLSGKKSLAHKGGI
7315	21216	A	7375	399	91	RIFFFPPLKAPHKQKPTFFFPKPKPL VFSIPPIFPKPLKKNPSPWEVFLFLS FFQKDAFFGPQV*KGNFFFKGPPPLTQ NSPGQVPPKKKKKKKKKN
7316	21217	A	7376	377	131	YLYIKFYNFITILFYPIFNIF*FNMIF NLLFYPIFYIILINFNILILINFFYFI LLIILNIIILYIIYVFIKNIKT
7317	21218	A	7377	2	156	PHHV*AGLELLGSSNPPTWAFQGAETT GVSHHAOLPHFILLRQKELSLGL
7318	21219	A	7378	319	59	DTKMSODILYSIQSNRT*W*LYRQ* TKQSAPRNGNEVP*THQSTATTLLISQO PSTSKQDPPAAK*L*FAEGRLLAFPSNN VF
7319	21220	A	7379	308	12	FSPTISNFNYKSNPSPLIYLFQ*PIITOL IPTNISTNTPLNL*FYRLIYISTSISLL IISNNVKKK*CFEHTKPTPPLTLIALT TLLEISPSPLIIL
7320	21221	A	7380	11	169	RRLDLNVRLESSSGLK*SLHGLFPEH WDYSEHPNSMLFLPLLTGFF
7321	21222	A	7381	300	2	KFFPFFGFFFKGFFSPL*SHQKKTQFF GEFFMGFKKFFLFFPPGGGFFFFF FFFFF

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						FF*INSLEIQNSFLT
7322	21223	A	7382	163	160	PQTSNDEIQRRNSRRNISPIAER*GLSL LPRLWMSGNEAHSNLELQSSNFPASA SKSTMITGVSHCA*PRLWMSGNEAHSN LELQSSNPPASASKSTMITGVSHCA
7323	21224	A	7383	1	183	VVCVCVCVCVCICIKWDSYSATIKKNELVA FVVTWKRLTIILSEVSQE*NTIYHMS LICGS
7324	21225	A	7384	2	196	KIQMPPGVVAHACYPNLTGGQDGRTA*G QEFQTSGLNIARPCLYQQOQQQQPRCS LTYDGDKS
7325	21226	A	7385	3	192	RNLSSLQPPFPGGLK*WCSLLPSSWDYR RPPPCPANCFMLCEFFRTNGVPCSPGV YFEPN
7326	21227	A	7386	266	198	TMLSGLRSAGLTMTIS*PHDPPASASQS AGITGVSHRARPLVFLRDSLYSGTQAG VWRDLSSLSRLAEQMRFCFP
7327	21228	A	7387	164	311	SKQKGLSGVAPCNPISLGRGRWIN* GQFETSWASWVKCLSLKL
7328	21229	A	7388	3	218	EINSFAATWOLEANILSTLSHE*IAKY CMLSLSGAKHWLMNIEVGVDTRDYL GCTYPSSTQLGYYS
7329	21230	A	7389	521	58	SDCGLTPIAQTVGVHMHLSLQ*LPWL G*FSLHLSPPSWDKYVPPCPASFLYF LVETGFCFHVADGLELLDNNPPSSASQ SAGITMSGCAGLRRF*KLRSWRYLVLL AMQVNEOGTSQAGEAVSEADAGQGCCG LCLHRLSQYALP
7330	21231	A	7390	169	322	APGNFKTN*RNKGFWAGNTLGVSVKNMK NGWAWLTSVIPALWEAEAGGSP
7331	21232	A	7391	1	353	GTSPHYGSGFHGQKDV*VGKGSQSRPR VLGSHARKNSLPVHEVKAYLL*KYLSIL RATHILISPDGCWPIFIAQSYIFLSSC GFPLFLFLLLTLSFCSWHLIISFLALF VIPLY
7332	21233	A	7392	372	3	IQAGACCAECIPSKGIRWNPISIVEGLHS DMSWSLCLFLSGAISVLNCFRLSGSSDS PMSA*QAARTAVIRHHTRLIFCIFSRRD ETGFHVGOENLMLLLQLFSGLGFSTIS ATLLTLLMLV
7333	21234	A	7393	362	176	ARMCCSGAI*AGLRGSSDSLASAS*EAG YTGKCGHAQ*TFVFLVEVRPHVQGNAI NIERTSL
7334	21235	A	7394	2	304	ARADCCARNE*GSVGMGSPRPVGVNLL VEFLRPLEKHSIRVGETFRSCCLSQL CLARTGNSLTCTTS*WVQCLALLRLMLG ALHPLSCTORPTSHS
7335	21236	A	7395	256	3	MYAARVWNAKKTTSLEHWAHGGGSH PVNPSLGG*GGQIS*AHKFTSLGNV KPHLSKNQTKNQTKNQTNISWSCTCL
7336	21237	A	7396	346	2	RDFYFRESHSLITYITCLNVKSNLCKGE GPLNFTFHLQRKNLGNHTRSPPGVYHV GRTEATGPIKRRNLGAVHTSNPSNL GGQGGWIT*GQEFKTSLSLPRWLTVP IP LV
7337	21238	A	7397	2	242	RRYSDDPYDAYTT*NYLSSVGSFISLTAV ILIIFMI*EA*KKKKKKKKKKGGGPF KTLGGGPKFNRRMEGNFSLKGGGR

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7338	21239	A	7398	1	289	TKLLGLYITLLQASNDFKSPFSIFDGIY GSTPFTVTGPHGLHVIIGSTILTIT*FIR QLIFHPTSKHFGLEADA*YHLDARR HSESTHQQCSL
7339	21240	A	7399	346	40	TIIFTNKIYIKLNRKLKFLIKLIDLYI I*IFFPRK*FTFKQ*KP*ININKIYIN NIK**IFIVLPPFFFFFPFLPPFFP FFFFPPFFPPFFPPFFFPFLKK
7340	21241	A	7400	1	334	NSCRQRLLDLLLPITL*LPQIGYIE KSTRYECGPHIPISPARVPFSKFFLVAI TFLLFDLQIALLLPL*ALQTTNPLIV MSSLLLIILALNLAYE*LPKGLD*AE
7341	21242	A	7401	2	302	HTINILGERVYLATTY*STMTLLTGL TVLHTGLYSVYLMTTQWG*LTPIINM KP*FTR*DTLVFHLSPILLSLNPDII TGVVLVLLSYELLYLT
7342	21243	A	7402	57	338	TTHNVIGYTEASTAYESGCDPISPARVP FSIKFFLVAITFLFDLEIALLLPI*P ALQTTNPLIGMSSLLLIILALSLAYE* LOKGLD*AE
7343	21244	A	7403	407	68	QEEVLDPITVIREQCEOLENCVKAR*RL *LCDERVSRSHSEEDCEDLPDLHAR DHCVFLLIYINKYMCET
7344	21245	A	7404	494	154	SLFIFLYLILFL*FFPHYFFYFILLST PSEKLPFFFLHFFPFHMFLLPFPSPNK IFPFPKIPPRFFLPLF*KKFFFLPFPK LSPGLFPF*SPFFFPFFFPFFFPFFFP F
7345	21246	A	7405	1	400	NPGRLSTSNSSLYERTREIRPISQSAF PRK*YHLKKKKKKKKKKKKKKKKKK KKGGPKKKKPGGQK*TGGEKKKFPKR GGKKKPPGPK*XTTFWGGKKMGKTPQK KINPLGKKKPKGKRGKTPPL
7346	21247	A	7406	2	257	RASLCHFGSAVV*SWLIALTSLWLOF SHLNSLCXNDYRHEPPLA*LRFEHRS GSSICITNLR*ILLSFPILSIRYKGLIL Y
7347	21248	A	7407	259	47	YVFFFLFLLLFFIRLQSVSPFFFPFF FFFPFFFPFFFPFFFPFK*SPIEMFSFV LYLLRQVSISIAITLFG
7348	21249	A	7408	3	248	VTFL*CDVEIAVLPLP*ALPTTNLALI DMSSLLLIILALRLAYE*LRGGLD*AE EHQATHSAYERAPPL
7349	21250	A	7409	2	350	RSQMPRRYSDDYDAYTT*NLGSVGAFI CLTAGILIFMI*EAFASKRKLIVIQP SINLE*LYGCPYPYHTFEEPVIKSRHI RKSNPPLVSSQPHGLHDFKKKLGIT TEKN
7350	21251	A	7410	2	232	LDQTYAKIHFTVIFIGVDLTLPLQHF LSGMPRRYSDDYDAYTT*NLSSVGSFI ALTAAILIIFMI*EAPAKK
7351	21252	A	7411	2	321	TSLLAVLLIIMTL*LPQINRYIEKSTPY ECGFDPICGRVFPFSKFFLVAITFLF DLETALLPL*SLQTTNPLIAMSSLL LIITLNLAYE*LPKGLD*AE
7352	21253	A	7412	2	194	SIECFVPTLLCLDEALLPL*AL QSNPLPLIVMSSLLLIILALNLAYE*LP KQGLD*AD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USPN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /possible nucleotide deletion, °possible nucleotide insertion)
7353	21254	A	7413	1	197	LYTTFYVTRKTLTLLTSLFL*GRTAVPLRL YDQLIHL*KNFLPLTLALLI*HVSIPIT TISSIPPOT
7354	21255	A	7414	1	185	STPLP*ALQTNLPLIVMSSLLLIITL LSLAYE*LQKGLD*AEKXKGAVALKDP SGGFS
7355	21256	A	7415	347	228	LE*LYGCPFPYHTFPEVPVIKSLRKRKE SNPPLVSSQPHGLHDFKHINKYRKNK RKEGLASVKENDRGP
7356	21257	A	7416	1	296	HAYDHASALNGLYEOSTPYECGDFDIS RARVPFCIKVFLVAITFLLFDLEIALLL PLP*ALQTNLPLIGMSSLLLIITLALS LAYE*LHKGGLD*AE
7357	21258	A	7417	3	202	TCSTI*HVLVRMT*LIYDLEIALL*PVP* ALQSTNPLISMSTSLLIILIALSMAYE *LQTGLD*AE
7358	21259	A	7418	1	321	SNITLLALVLITITS*LPQLSGCVGECTP YECGICRILNARALCCMQIFLKAITFLL FDLEIALLPLP*ALQTNLPLIDMSSL LLIITLIALSLAYE*LQKGLD*AE
7359	21260	A	7419	1	212	RTRGITFRPLSQSLY*LLAANLVLT*I GGQPVSYPFTIIGQVAVLYFTTILILI PTICLIENKILKWA
7360	21261	A	7420	2	257	GRVGGRGVGYIAFFLQAITVLVLDDLESA LLLALP*SLQTTNLSLIYMSSLLLIITL ALSLAYE*LPLGLD*AEYWGEMMTTLD A
7361	21262	A	7421	367	269	HCDLKLGGSSDPFASAS*VAMITGTCHH TKLS
7362	21263	A	7422	2	116	ALQTTNPLPLIVMSSLLLIITLALRLAYE *LQKGLD*AE
7363	21264	A	7423	2	336	KPECGREGILPCCSSSAWFECSFRPFQ NLGSFLSFFFLFFFFFEKGLFLCPVP* PYGKSNLLEPSASRFKQFCGLPLNNWD YRLFPFPFGNFGVFKNVRVFFPFSVL
7364	21265	A	7424	3	154	LFL*IRTVAPRFYVDQLIHL*ENFLPL TVALLI*HVSIPITISSIPPOT
7365	21266	A	7425	3	154	LFL*IRTVAPRFYVDQLIHL*ENFLPL TVALLI*HVSIPITISSIPPOT
7366	21267	A	7426	1	314	INTLLTLLLIITIT*LPOLNGYIN*STP YECGDFDISPARVPSIKFLLIAITFLL FDLEIALLPLP*ALQTNLPLIDMPSL LLIITLIALSLAYE*LHQGLY
7367	21268	A	7427	1	331	ILITINTLLALLIITIT*LPOLNGYIEK STPYECGDFDISPARVPSIKFLLIAIT FLLFDLEIALLPLP*ALQTTNPLIVM TSLLLIILALRLDYE*LQPGLD*AD
7368	21269	A	7428	2	373	SDRNHITHALVITILGLYFTLLQASEY FESAFTISDGIYGSTFFVATGPHGLHV VIGSTFLTICIRQLIFHPTSKHHFGFEA AA*YWHIVDVAGFLHVSIRYGGSYNHQ IIPSVAQESTPA
7369	21270	A	7429	378	63	PSFFFFFP*NFFFPPRLPFSGGGFFFF FPFPKQKPPPKIPGFFFSPPFWKFF FPFLLLPDPFFFPFPFFFPFFFPFF FPFFFPFFFPFFFPFFFPFFFPFF
7370	21271	A	7430	1	109	QTNLPLIVMSSLLLIITLIALSLAYE*L QKGLD*AE

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7371	21272	A	7431	358	290	FLLVIPNLFHFLIYIIISIVPNVSFFH IYILSIFPPFIIFILLSSFNILFFF FITSFPPFYFFFFFFFFFFF FFFFSFFFFFFF*FFFTN
7372	21273	A	7432	1	95	PTRPPTRPNLSQL*TPGLKQSYPRLS SWD*RHMPSPANPKFF*RWLYCPGW S*TPGLKQSYPRLPSSWD
7373	21274	A	7433	1202	870	HNIFKIRPHCLRTHRGKPPYWGLLVTPV FSPSLRPSFLPSFLPSFLPS*LPFLPS NLLFLSYSCPLSLFCLRCIPHSAPFWG NPRVQVQNGCVITVTVRYLSFTALHQL TV*GQFFETILAKRREPLACFLFL
7374	21275	A	7434	163	1	TV*GQFFETILAKRREPLACFLFL
7375	21276	A	7435	148	362	NDENSVEFPIRLHKG LGTVARTYKESL GQGGHIA*ACEFMTSLGHMT*SSLYK LTEYGNRDTASLLMC
7376	21277	A	7436	61	233	GGDLRHWPSSDSFFLSGFFF*KNKGK LALLPRLDLNSWSQAILPLKPPNALGLQ A
7377	21278	A	7437	44	242	FVCLFLFFFFKEKSTPOHDLSSLOPPL RFKRFSCLSLPSTWDYRLAPQCLANF*I F*KSQGTFG
7378	21279	A	7438	119	300	YCVSLLIFFIFIYIYIFILLIKFLFITL NYISFLFFYF*H*FY*KNFIFVFFGY FPRP
7379	21280	A	7439	1	221	LKLOHDDPTTISLVITRNWQKPCPNVO QIVH*SAIKRNEILLHAKTWMNLRGIML SEICQPKILYLEIPFI
7380	21281	A	7440	35	345	FSFCCVCCVCCVSLPKHATTEMLNQT YVPGVAYLPEREPIVPMDELTA*VE DYRTHESAQEPSEPHQLSRRSLPH*PGH ATRDHSPPTDSWGKRRTSH
7381	21282	A	7441	3	384	VIHL*AGAVIIGSRKSTNALAHFLRQG TPTPVILVLGIIETMNLLOPVALAERL TDNITAGHLLMHLIVSATLAILTNLTS TLIMFTVLLITLQIAVALMHAYVFAL LVCLYLDHDDAYDHGG
7382	21283	A	7442	15	277	GLAILPRLVPSNFWKVLQVWPPKMLG* QA
7383	21284	A	7443	21	694	NGCLNAHLASAEFDHSGVQLIEREEI CIFVEKINIOEKWKNGLIEIHLLEKI QPLKMKIAEKQKQICVTQKILPAKESL ADLAVLQIQFSQCTDRIKLEKQFVKED GENRARFLPGKDLTEKMIQKLDKLELQ LAKKEKLEKDFIYEQVSRLTDRCLSK TSGCKQDTLLETKKNNGYSRRKLNATEK MMALCA*LSMKQAPTELOKEVOGERRP
7384	21285	A	7444	141	428	DRSLLEAGDGRIAGDFFF*TGTFNVAQ AKVQWGIHSSLHP*PGLKQSSYNLNLG SYIHHWLRPHALFFFLKNRGSLECPGWG TGFRGTTFWNAK
7385	21286	A	7445	35	343	GYSITGCPKFLDEKIFDSGHEKERKINS LLF*KKKKKKKKKKKKKKKRGLLKK TSGGPKIKRGGIKNFPIKGGVKTSGE FFGKKPPFGGEKFWELP
7386	21287	A	7446	403	193	EYIKQGA*NNQPKLHARRRLTWKETP RCIHGCIAPIMNSDCLVDTSLIAQLPA ENGLGINVTISM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7387	21288	A	7447	411	110	LTDSLLNIIVR*EMSYIS*NSA*VYLY TFCYIYIYIYIRRIYSIYRC*YIYYG PAHVLVYSSSYLVYVYESHKYGYIMGL NILSYIYIYSYPSACS
7388	21289	A	7448	1	380	PTRFQKLKKNCNGVSGNDLCFFGGGQFL IWGFFFFFCILIEGGLNSKNYELKSLIK TYGAKKAEIETEN*KNRETLLEAAQL AIKVTNPANMLRTVEHDIYAMYHNPFLN KLNNCHKVAISCKQ
7389	21290	A	7449	200	437	VQSNNNKNNKRRRL*PGVVAHTCNFSTL GGQARRIS*AOELETGLNNLMRPNYNNK FINVLDDVHGVTSPVSQYKKVC
7390	21291	A	7450	405	3	PFRFFGFFFFFYPLKFFFFPKGFNFEGG FFPIFFPPKKKFFFKNSPGGFLLPPELG KIFFFLPPFKGPPRGFF*RAPLFFFFF FFFFFFFFFFFFFFFFFLQRIINF ARPGTPLSRAVPLRGALPPSA
7391	21292	A	7451	2	348	PRVRPRVRKYLQTKKCDLFLPS*GHSV SLRNTT*PDALKS*DTDSLLSPKLECHGV NTPNCNLRPLSLSDYPASLSREAWIAT RLRAWEIFVFLAQMRQDYCMNPGGGGCGN ELK
7392	21293	A	7452	1	168	LVDHGHAGLKLITSGDRPA*AYQSAGIT GVRPLGPPTYYFRTASFMTEICEFATV
7393	21294	A	7453	184	260	SSRGGLASRSSR*STLLGLPKWDYRC MPPLSANFFFFNF*I*MFCEW*RRSLGM LPLRLVNS*MQAILPLRLRLQGHFAGT QTFFSL
7394	21295	A	7454	405	64	FFFEFFNF*KKRI*DVFAKIFFKIFFFF SGLKIFWGGFGQNPQKQKFF*KIKSF FFLNFF*KNIFFVQGVFFLLNFFFR GAPLFFFEFFFEFFFEFFFEFFFEFF FFFFFFFFFFFFFFFF
7395	21296	A	7455	368	2	SQSFGPRMRENLRGPECHIKISRYRPAQ VHACHPSTLGGGRWIT*QGFPGKSTHL GLPKYWDYMEPELLLVYIQCFHFTFCN KAAIHCFKPEQLLYNKTSYFKESYKVK ALVACKPTRP
7396	21297	A	7456	2	183	TERDSVSKNKYIYIHTHTTHTTYICVGH VIYVYI*SLLLIYNIAYLIIHYVYILL IFKA
7397	21298	A	7457	281	127	YNFCIFM*RCGFNNVQSGQLKVLRRYS PASASQIAGITGVSCAQPVAYS
7398	21299	A	7458	2	194	TSVRKYF*YPTITDRIYGSTWVATGL HGLHVIIGSTFLTICLIRQLIFHTSYH HFGSEAAG*YWHFVEPARFLFYICYI** GSTWVATGLHGLHVIIGSTFLTICLIR QLIFHTSYHFGSEAAG
7399	21300	A	7459	22	319	GGSVTGAYHRILDDHRNQIFLA*GGSVT GAYHRILDDHRNQIFLALLISMLGLFY TLLQASKYFECPPETICDGIYGSFTFVAT GFHGLHVIIGSTFLTICWIRQLIHFTS RHFGLEAAA*YWHFVDV*LFYVSYI * *GSVGTAYHRILDDHRNQIFLALLISM LLGLYFTLLQASKYFECPPETICDGIYGS FTFVATGFHGLHVIIGSTFLTICWIRQL ILHFTSRHFGLEAA
7400	21301	A	7460	1	222	TILLGLYLLQA*EYFKATFTIYDGIY

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						GSTFFAATGPHGLHDIIGSAFLTICFIRQLIPHFTSEHHFGFEAAA*YHVFVDAT*LCMYVSIY**GSTFFAATGPHGLHDIIGSAFLTICFIRQLIPHFTSEHHFGFEAAA
7401	21302	A	7461	3	246	LNYSLFFHGEANLGTQVLTHPSTTAMYFVHYCQPP*ILYGTINT*PPVHHKNPIK KKKKKKKKKKKKKKKKKKKRGGGF
7402	21303	A	7462	2	155	SRRAALLPLP*ALQTTNPLIVMSSL LLIITLALSLAY*LOKGLD*AE
7403	21304	A	7463	1	136	PTRFAPSHLLYCKNIKKLFPSPGTANEAL IADIPLRCKKKKKKK**VLKASEE*N GCCHLHGMH*NSAVCTVFWLQIMSD* **KVNTQ*KKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKGGGNNK*KNKKLP PSGTANEAL IADIPLRCKKKKKPKV
7404	21305	A	7464	166	192	NIN*WNYHTVECVSDFKRKEILTHATT WMNLEDIMVSEISQSKDKYCMILHIEY KLYIHM
7405	21306	A	7465	416	55	LFFLRLGYFFLPLNRVFFFLSTLFFFFF VWGFFFFGRRFFPPPPQEVCFPIF*G IFFFFLFX*KNMFFFFFLWGPDPFFFL SGAPLPPFFFFFFFFFFFVFFFLR KANTKKMF
7406	21307	A	7466	295	84	IWGNVTLLOLVSLCFLFLH*GFCCCC CCLFLPLFVCLFVCMFLNLKPSIKCLLP FSLSLGCAEIPSSF
7407	21308	A	7467	142	258	PGTVARTCNFSTAGGGGRIP*GHEFKT NLANNVKLHLY
7408	21309	A	7468	3	192	PSEYPESPFTISDGIYGSTFFVATGPHG LHVIIGSTFLTICFIRQLIPHFTSKHHF GFEEAA*YHVFVDV*LFLYVSIY**GS TFFVATGPHGLHVIIGSTFLTICFIRQL I FHFTSKHHFGFEAAA
7409	21310	A	7469	2	110	GRVOKHHFGFEAAA*YHVFVDV*LFLY VSIY**GS
7410	21311	A	7470	380	8	TPQKKKKKKKAGGVPPPPPKKTTTPPP PFIYFIFFFFFIYFFFFFPQYMSF FVSHIMIQRHFLNF*ESSYSCISILQ*L FKFPFSLGLIKL
7411	21312	A	7471	1	107	PTRHHPGFEEAA*YHVFVDV*LFLYV SIY**GS
7412	21313	A	7472	2	360	VNTLLALLLIMTF*LPOLNGYIEKSTF YECGLDIPSPARVPFSIKLFLVAITFL L LLEIALLLPLP*ALQTTNPLIVMSSL LVVILALGLAYE*LOKGLD*AEWLHSL TQPTNNN
7413	21314	A	7473	423	167	VKVKHCFLPGVAPHAFNPSTLGGRGRI A*AQEFKTSLGNIVRPPSDTCNPIVLGL QA
7414	21315	A	7474	1	73	IKPE*YFLFAYTILRSVENKLGGV
7415	21316	A	7475	131	3	ISWVGAEWLTRVIPAL*EASGVSRGQE IETILANTVKPDAM
7416	21317	A	7476	2	103	PRVRSTGFSSIAHITRDVNYG*IIRYLH ANGAK
7417	21318	A	7477	2	325	NTLLALLLLIITF*LPOLIGYIEKSTPY ECGFDIPSPARVPFSIKFLVAITFLFL DLEIALLLPLP*ALQTTNPLIVMSSL L LIIILALSLAYE*LOKGLTERDT

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7418	21319	A	7478	423	170	FFSFFFFFFFFFFFFEIDKNVYLIM*C TNPOEKRNLLFCFLVMVSPVCITPHTYI CUCVCVIYIIYIYIYIYIYPFISSCCD
7419	21320	A	7479	433	50	RVVFFFTTPEKTKTFPPQETLYLFFFSPF L*NFFFPSPKPLFLFGGFAFNPPPKKVLF FLKFPGGFFSPPFKKKFFFFPRFFFA PDRFFF*GDPSFFFFFFFVFVFFFL TVKTGRFRGCQGI
7420	21321	A	7480	401	337	FFFFFGKFPFPQEPTVFPPPFKPIFF SLRLFLFWGGFAQQFPQPCK*VFSKFPFR WFFPPLERKKKFFFPFG*FLAPQGFFL KGPPPPFFFTTTTTTTFFRPILVGGR VGNPNPNTNYLPN
7421	21322	A	7481	1	84	KNFCLPTALLIHVSIPITISSIPPQT*
7422	21323	A	7482	562	412	LFSHHVSGTMHCTCNPSLTIG*GRIT*G LEFKCSLSNGTWBSHRVRKKKIA
7423	21324	A	7483	12	233	DIFHFTHSKIVGEAAAYWHFDVDURL FLYASII**GGLL
7424	21325	A	7484	385	56	GNEFTPDKENFFPVFLSTIFFFPDDKLK FF*EIPIFIPDPKPLFLPNFPVLFFEF FLWEFFTSFLWFHFFFTTTTTTTTT FFFFFFFP*KITEFYVNVNSFOHTK
7425	21326	A	7485	424	6	FFFFSEGSGLITREDIPAGALVDYGR* LVUUTV*TLFUGVYIVIEIARGNLRC DXRRXXLIHXEPSINLE*LYGCCPPPYH TEEPVPYIKS
7426	21327	A	7486	16	129	IASGLDIPLLLETSGSHSVTAQGVQH NDHSLOPLRTGLK*SSRSPRGSWDYRV LLCHPGWSAEA
7427	21328	A	7487	183	387	EKKIFFSPSRGYPGPFFFLKAPPHIFF FFFFFFFFFFFRRGGGDHNKFFFFF WGFLQNPLFPFFPRV*I*IFFFFFFFFF FFFFFFFLLGGGGGTIKIFFFFEGGF
7428	21329	A	7488	351	169	TASAFL*IRTYPRFRYDOLTHLL*K NFLDTLALLI*HVSIPITISSIPTOT TSGSCSAHLAFKP*AGMATFITKSJ* *CHTHTHTHHTHTHYMYITYHMHTY IF
7429	21330	A	7489	47	212	LYGCCPPYHTEEPVYI*EAFASKRKVL IVEEPSINLE*LYGCCPPYHTEEPVYI KSKRKRESNPPLVSSQPHGLHDFFKK KKKKKKKKKGGGGLKKPRGGPNLGTG GKNFFFFRGGCEKPPGGGWKKTLFLGG GLCTPDPRRE
7430	21331	A	7490	98	273	RSSLPARPTRAVILLIFMI*EAFASKRL VLIVEEPSINLE*LYGCCPPYHTEEPV YIKSYV
7431	21332	A	7491	70	405	KLDETWKKKKKKFXYSRSISLMMLLYLF S*SLSFFLLYSLLFLFLLSFYIYSLFLC FLCTKTATTEH
7432	21333	A	7492	22	208	TTLLSRK*NKLT*LTPLIFSLLSLGGL LPLPTG
7433	21334	A	7493	2	204	PRHF*IFVEMGSHYAQAQLKLVASSNL LAWASQSAGVTGVSHGLSLITSCL
7434	21335	A	7494	2	104	LGAPCGVF*KGPPFPSSSSSSYSSSSSS PS*QNI FNKIFLFCVPLETESVTQGVQ QWRDLGSLQLPFGGKRFFTITH
7435	21336	A	7495	291	160	FFFFFFFFFFFHHHHHHHHHHHHH
7436	21337	A	7496	422	180	
7437	21338	A	7497	244	296	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFFFFFFFFFFFFFFFFF GNF*FYK*LLGNRDGVLPPSSYL
7438	21339	A	7498	1	410	PTRPDQLIHL*KNFLPLTLALLI*HVS IPITISSIPEYT
7439	21340	A	7499	51	478	PQRYTLIMKICIPPGKGRFVPEMLAG NENTRCLIEERSYKYHYSLIKGLQOOC IFSSLLYKXNMICYCLMICYIYIPIFY DMYRQYSVLVYKLYNYVMLI*YIILYL FMCI*KYLYFIM*YKIFIYLYL*YK YIFVYILCVNYIYLYL*CNINITYLYTY IYININLY
7440	21341	A	7500	3	110	FTSKHHFGFEAAA*YMHFVDEV*LFLYV SIY**GS
7441	21342	A	7501	168	327	APCYKATVKT*Y*YKHYTEQWRSRK NPDINPYICQMII*FLQKSLHKI
7442	21343	A	7502	400	159	NNFSLRNLCGGFFGPKPFMGFCAGP *GFSFFLRNFFLDVFRGY*TFG*DF FYCPSNEVLGEPLMGKNKPGFP
7443	21344	A	7503	401	257	TSQKKKKKKKTPKKKKKNRKKPKKKR GTRGEPFKTGGGKKKKFKKKKKKGG PP*PQLVKGGRKKKKLWKKKGAF*K KKKKKKKNPKKKKKKPGKT*PKKKGGDPG GTF
7444	21345	A	7504	44	344	LLASLANLALPPTINLLGELSIVLTTF *SNITLLLTGLNILLVLYSLYIFTTQ WGSLLTHINNPKSFTRENTLMFIHLS ILLLSLNPDIITGSS
7445	21346	A	7505	286	252	I*FAFHVVGAGLEFLTSDLFASASQSA RITSVSQAWPVHNIYFSL
7446	21347	A	7506	3	213	RELPGLRFFLLSLLSSWD*WRMPSHPA TFCIFCRDEVLPCCPAGLLILLVNLKN CCCYHHHRYYYCY
7447	21348	A	7507	400	20	SLPQKRVSLRLKLSAVQLVMP*DRFSLC HPGWA*GQSGVTTASSLRAR*SSCLTW EYRSPFLPLADELFW*RRGLPT*PRVVS NS*GOVGLHGPSKMLKFSSLSPCARPL PFENRSTLNRVQS
7448	21349	A	7508	349	227	SDFLTSANFPASAKSFGITGVSHHTRP *PRFLKNVLIYSENEVYN*ASPRHVD*G GLELL*TL*FTHGLPKLNDYRREPPHPA LTKIFKGPYIQ
7449	21350	A	7509	371	21	FLVETGPHRVG*AGLEPLASSNLPASAS QTAGITGMSHCAPNPGLSKNTMLAVA TEQVGYWMPSPVFGHITARPEGKRLSDC LHSDTNVCVVCVCSGLIFVCFETGCRFA LQPG
7450	21351	A	7510	330	14	DKVCSVTQARVOWHDHSGLLFLSSSLRQ SSHLSLLSSWDHRRMPPGMANFFYF**R LRSHYVAQAGLKLASSNPPTLTQSGAG ITGVSHNTWPKALFVSTDLKH
7451	21352	A	7511	417	33	APPCGGGPKRIFGPSRKRGGKPPPPK FF*KNKPPKGGGKKSPPPKPNFPKKN LGPKKKSGFWRGAPRAPGGGVNFNP FKAGGEKFFSRGEINPPRGAGKKKGFL GKKNTKKTKKKDL
7452	21353	A	7512	81	296	CLREGASHAAQAQGLHWDHSSLHP*NP GLRGSSRLNLLSITWYRCVPPSLANFES CLLKIILGSPPPKKNL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7453	21354	A	7513	412	279	KKYTOGLGVVAHAYNPSTLGSQGRIRP* AQFETSLGNTGRCLH
7454	21355	A	7514	74	126	KI*DWVPKGAPLQGVF*NSTFRPRVRN RGPWP RP GP TP VKG * NKN * PAPRGSN P P F F F P G N P G P F K L R G W P G S S * G S F Q N C K K A Q A G * A P T * K P G P P P Q N K V
7455	21356	A	7515	332	20	GERQVGSYFFMNTERLFGMTKKF*KWIV SMVAQHSSSI SGVWVFRGQELAFPLSPD WQVDYESYTWKLDPGSEETQTLVREYF SWEGAFQHVGA F N G Q K I F K
7456	21357	A	7516	1	167	RTRGQRFTVLARIVLIS*HCDLPASASQ SAGITGVSHCTRGLSFLYTPAKHST
7457	21358	A	7517	2	223	GRMEENGSHYVA*AGLEFLGASDLP*A PQRAKILLLLGGHKPGLTLPLRLSSNSW PHVKNWRNPLKALGLRG
7458	21359	A	7518	151	476	SLGKFAVSFFSFLK*RRALAVLPLRCS NSWP*AVLLPWLPRVGIAGMSYHTQPDY HFQARAVAEILGLVSTQHSSVTGLFPVEN SFRAGHGPPRLQSQHFGRLRWADC
7459	21360	A	7519	3	134	CSFRLGAVAHICNVITLGGGRGRIA*AQ EFETCLDNIA R P C L Y
7460	21361	A	7520	14	219	APS IHGFGFLYTYITHTHTHVYMYI*V YIHTHIES IKCQPLTQSQNKANRIVF RTQFPMLTICYFMR
7461	21362	A	7521	134	334	KRHSC*TFPNCFFYLSLETRSHYVASTG LDLLASNNPPALASQARARTGMSHHAPP VLTRFKKGLF
7462	21363	A	7522	406	145	FLKTGFSFGFFVF*TPPPGFFPPPPPP IFGVPGGGFAPPLFFFFPOTKHFPPL NPPSPPPQRGFFRGFFLFPFAFLKTPP FPF
7463	21364	A	7523	3	382	HPQGGGRLTSL*NTSLRLKKKKKKKK KRGGPFKKNPWGAQI*PGKKKKNFLEK GAKKNHLNGFKKPYFWGGKLA KP KK N*TFGKKKKFLRGKGKKTPKPWLKKIF FSGFYLLKKIFPPGP
7464	21365	A	7524	319	106	GTRSCSVT*AGVOWHDHSSLQ*TPWLK RSSWLRNRNDYKHEPCLNNFYFFCRDG GLLCHPGWSQSPELK
7465	21366	A	7525	433	228	MQPYNNVNSSQLSLSSARQVTHVLT GNFFIK*ERWDLPLVPLRVLSKSWQVIF PPWPSKVLLQV
7466	21367	A	7526	26	351	CRSLVFLSLPKGLRFPVSLIHQVFSHFD FFFLTGNQTK*RK*TPFIPA*LFKTPA PKPGMVAHTCSPSYSGGLDORIA*AQEF RTSLGNKTNPISLGGRRKKKPPSGS
7467	21368	A	7527	438	62	QLSKIHRRPAGGRFFKSGGGFKPFCEVFG LPPFGKKANQPTKNNPPKKQKPSGGGLS PMGKPP*FPCSPMPDPSGVSFSRGGVA PAPKDYCPIV*AALI PSKKKKSKPG*V KKGKPNLYSTYNK
7468	21369	A	7528	3	132	FYLL*RRGFPVLPLRVLSNLQVILLFP PKVLN*AAHPH
7469	21370	A	7529	2	628	FFFLDGVNKLVLMMRGGLGANSREGRG PSQPMHGCQLEVRGRSGQGDHCTLG PMNRIYRGAPPTFAAPQAPKPFQPLL M*LPORPSSCLLPETPALSPLPSAEWGG FKLLTCTSETPPGSGSPSVGSANAQAAG

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						ATTIVARGHTPCTRGPLDTHAHSSSLRW AHTRPPKPLAHEGHTHTAHPTPGAW VGEPPFGQGWGRA
7470	21371	A	7530	63	205	GRTPRPRTRGVKIL*QFETHKTPGLPT LIALTLTLLPISPFILIL
7471	21372	A	7531	390	56	KTFFFPNLIATFEAKSVLPLLLFFPETG SRSSAOPGVWHQSSLPQPL*LGKSS CLGLSN*DYRCAPPCO*SPCLSLKCKW DYKREPPHAPAKESHMQSVLYLSLYA
7472	21373	A	7532	543	335	LAAYGGTCLQS*LESRLRWEDHLSPGVQ GCNELQLQHCSPANATE*DPVFKGEKKE RVLVVKFS
7473	21374	A	7533	3	145	WCDHGSLEPRSPGLKQSSCLLTPSNWDH SSEPLHTTSMWNF*IPKFLNLK
7474	21375	A	7534	386	106	SWTDEITMEI*ECVLNDSNPTPYQNLW DTEKVVLRKAFALNACMKKSERAQIRHT TCVHTHTHTHTHTHTGSKCLLRXYLLT IQOQNIRIN
7475	21376	A	7535	398	2	SLQPLPPRVKCFSSPSPPRNRWDVGAAP RGKGFPPFGKKEFPVVGQGF*PLPQGV LAPPPQKGRISGGSPPRPFPFFFKIR ISYPILAKQLKLCFLKKKKSIQAIKLY HHQKNPIKSSVFNESQRA
7476	21377	A	7536	2	344	HSKCPVAEVVTMAYIYRYSISSLLHIL ENIVHFFHFLY*GPNNLFFFYAGTRL IQRSW*PMII*VHVQIKREGQIFNK* IFCMIGRGG*ITCQGEFTSLVMVVKPC LY
7477	21378	A	7537	116	224	LHTHTHTHTHTHTHTHTFQNKLP*LFIP CGHIPRRY
7478	21379	A	7538	1	383	WHERTHSRITILFQSLTLLPLIAF**L LASLANLVLPPTINLIGELFVLVTTFS* SNITLLTGMINLNTALYSLY*FTTQ* GSLTHHNNIKPLPTRENTLWFIHLSPI LLLSLNDIITGFS
7479	21380	A	7539	31	332	DNYLSSVSSSGSNWRELLIASQIKWEE IVDRTPSHIRHTHTHTHTHTHTHTHTV LFRIGPHTHAREPRGHICGN*IRNOSP* KNPRTRGKNLRTPHW
7480	21381	A	7540	199	15	NNVOIK*QFETHKTPFFLPFLIALTLL LPISPFILIL
7481	21382	A	7541	337	157	AEIYVPLNSSLGNVRRLH*MESYSVQAQ VQWHDIGSVQPLPPGFKRFFCSLLSSW DSRLYFRCHD
7482	21383	A	7542	28	313	RARIGSDQCLAGTQVVENKSIQSGDFM WDFRS*SVTRVGVRNRNHGSL*PWIPG LR*SSGFLPNCWDYDRNEVWGKKEV TCPTVNLQSQ
7483	21384	A	7543	493	180	GGFGRGSLVPRDGGQGVFCSLPPPPSR VKQFFCLRPPRRWGREGSPRSYFFFP *EKRPFFFLGRVVLNPLGQGVGPWPFSQ RVGFPGLTPGPRASFFPNLI
7484	21385	A	7544	403	426	FF*KFFITHTLFFFFFFFFFFFFFFFF FFFFFFFFFLAPPDGGFFSFYQKIFL KFPQOPEKFFALPFGGGFFF*GKFPQFF CFLVFFFFFFFFLFLNGVSLYCPGRSRT GLKLSRRLASLRAGITGVSH
7485	21386	A	7545	3	335	RHYSYDPGYST*NILSSSESLISLTAA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7486	21387	A	7546	424	140	LLMVFI*EAFAYRRTGLIA*EPSMNL *LYGCPPPYHTFEEPGYIKSRLKRKESN PPKLVSSQPHGLHDFKKKIKRGGPF RRVKFVGGAGQPGPPFRGVLPKIPREK VFPPPG*NGPPGPAFKTPPKKKNTSS PPGNWAPPGLLXGPPPPPPPPPPPP FFFFFLNPLK
7487	21388	A	7547	2	348	FCHVAQSGGLKLASSDPTLASQSARIT GMSHHGGLK*GEFLGPSSNGALLLWEA TWLQSFMSASLFPVKPRPTFVYVFVAFV GYRDIYFTASSLIKVIQEGLYTMKCAP LTL
7488	21389	A	7548	2	90	RKQAYTHNTHTHTHTHTHT*KKTGIRAH KHTHTHTHTHTLTKAKQIEGK
7489	21390	A	7549	256	405	CELYSGKEMELVGLFIPTGTVRLTFY KKECSFFPHSQSRGHKLQPSILNEWHI RNPLGLTHPLLL*KTGVAEYRNSLVVH HPFFLSYAVSFLLQGSFAMLSKLSNS *VQARCLPQSPKVLGLKESPOERTVNS SIRGKKSWLYDLFSGGLQGLKLFIRK SVHSSIPRAEGLWCNCHY
7490	21391	A	7550	2	362	ILIMVTLALLLLYIT*LPQLNGYVERK STPYECQPD*ISARVPLCIKFLAAIT FLYELIELALLPL*ALQTNLPLIGM SSLLIIILALSLAYE*LQKGLD*AEIK EEOKTLOC
7491	21392	A	7551	1	317	TFDNSALLEFWDGGETEHSVSQAGVQ WHNLCSL*PQPPGFKQLILPQIVKENV SKISSQLLFSRVNNTNISPSEQITPESL QLARIGIFYAAKIHLTKGLRG
7492	21393	A	7552	479	183	YLFVHTTASHSNGACTGPTVGDIVSS TL*SMTEQVIMPLASAVSDGTVPVSRVA SRGSEQAESMVSEHIEILEHAGELVI ASPEGQLEVQTVIV
7493	21394	A	7553	454	105	KPFWGNKIRPPLFPGKRVPPFR*NPVR GSPPKK*FVFPVGRVLGTGVTPLSPFLK TTPLLNDPPLSQPPGGVKPENSPLYPGK KRFR*PKFPPCPANGTKRKPPLQKKKK RQVL
7494	21395	A	7554	439	1	LLKRCVRKDSPPPNQKIFFFILKKFVFF FAPY*VRKPYFLTAHFGKRPPQYIYFGP PPVFLIFCCFFPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP ERLLCARHCFRPPPEKTKNKIEAANFN SSGEER
7495	21396	A	7555	323	82	PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP VRSPLFIIVSV*LI*HVHRYSVYI EDDLVLTGSKILL
7496	21397	A	7556	194	412	KMYRTSLGLHVEAKKKKKKKKKKKKK KKKKKKKKKKKKKDSRGVV*KKFGGG HNTRGVKIIFFSLGG
7497	21398	A	7557	414	219	KGFKLLFPFPVF*FFLCPPDIFLKGF* GRKPPPPKNQGGPPPPPPPTPPPLPFF FFFFPPFF
7498	21399	A	7558	377	25	THVGGVFWGKFFSRRVFFFFYHLQIL SPPPQKRPPPKGTPEG*IFPLFKENIFF FF*DFFFAPPPPPPPPPPPPPPPPPPP

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						FFFFFFFFFFFFFFFFFLKVRTGV YCVPIAVILYR
7499	21400	A	7559	386	2	FFFFSGEIFFPPPGISGFFPPPL*NF FPLRLFLPLGGGAPFFPPPKGFFPKIP RGVFFPPLREKFFSPPP*IWAPPGFF LKGPLFFFFFFFFFFFYRKARTKP TCLMGDVSFKHFCI
7500	21401	A	7560	1	396	KTCHRLRLPTKKV*EKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKGGAS LKIPSGGQPLRPGGKNNPPPLGGEKK PGVFLKKHFLCGGHGFPKKPKNSFWG EKKNFWGGGKKKNIPGGKKIPSHKKK
7501	21402	A	7561	1	390	NYVFEFSDKLGAVATTNCPSTLGG*GL WIT*GQEFETSLGNMVKPYLYQYQKKK KKKKKKKKGGGPFKTLGGAQFNGGGE KKFFFLGGVKKPRGFLGKNPFLGGGK MGAPPPKIKALGEEKNF
7502	21403	A	7562	406	182	FVFFFXFXFXFXFXFXFXFXFXFXFX FFXXXXFFFFFVFCFFFFFFFF FFFFFFFFFFFFFFFF
7503	21404	A	7563	2	113	FHFTSKHHFGFEAAA*YHMFVDV* LFLYVSIY*GS
7504	21405	A	7564	313	97	SPTYCYIRNSAQSFSLIAKSFCSPHPT YHHDPHLEKSLTYCPQGS*PIIPVTC TYINRWPEATEEPQNK
7505	21406	A	7565	3	144	DAWVFVATGFHGLHVTIGSTFLTICFIR QLIFHFTSKHHFGFEAAA*YHMFVDG* LFLYVSIY*GSTFLTICFIRQLIFHFT SKHHFGFEAAA
7506	21407	A	7566	1	130	FIRQLIFHFTSKHHFGFEAAA*YHMFVD V* LFLYVSIY*GS
7507	21408	A	7567	434	1	PLNLKVIFFPRRKKKEPKYKCHIVGNLR NEMYSIQDNLSPRRR*RKRTCLIFP HKIKTSHSFDIKEH*NYVTLCKVLRR LSTNORG*IFLSTNONTILGRARWLP AIPALNEAEAGGS*GQETITLANKVKP RGRV
7508	21409	A	7568	441	86	NFSFREKGGEFVPPPLKIFFPPPPNF EGGGGPPSPQPKKVFFPKPRGFFPP PKKKNFPPPPQKIGPPSPF*TPPPF FFFFFFFFFFFFFFFFFFFFFEL MEVCLY
7509	21410	A	7569	1	155	PTRPDLRLSLFEAKSPNSRNTLHKPGVT I*EAFASKRVLIVEPSINLE*LYDYG FFYKIKEPVYFYSNQKKE
7510	21411	A	7570	434	1	SPTAEGGKNFFKKNPGRKTTPPKKKGINF FSPLTPKFFPPPRG*ILGGGGGPNCP PKGVFPKNPQGVFNTPPKKKKKFSPP GKNGGPPGVFLKGPPPPPPPPPPPP FFLRQSHTLRLPRLCSGA
7511	21412	A	7571	493	196	SSLDCS*SLQGS*FLTMLLAVDFVDV LY*V*RVLYVLQVVAITKHIVSGLNRR HSFLTAVKARKSKI*VPADLVPGVSLP SLFS
7512	21413	A	7572	1	239	RGLTILDAIKNICDS*RGVRIILFSEVW KGVPLTLDREFNVSEVTAHVET ARELELVDPDVTLEPDSHDT
7513	21414	A	7573	391	32	FFQFSPPGVGKGFCLNLFNNNGFRAGP

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						PPPGYFVLNKGVEFPGPGFELPSPS *VAPPASQKGGVSGVSPCPRVWVPFKK KKKLRGVEQRCTMHLLVYSIQVVPKPK KSSIGSL
7514	21415	A	7574	2	383	PRVRSTAFSSIAHITRDVNYG* IIRYLH ANGAKKKKKKKKKKKKKRGALKKKPG GGQKGGGKKKKFPFGGKKKKPGGIFE KKTFFGGGNGAHPPQKKTPGGKKKIL RGKGGKPLYPWGEK
7515	21416	A	7575	402	69	KIFFRNSPLWKISHPTPYRGFFPPFPF* NFFFLPGPYFFLGGCSHLGPPPKGFFQ KIPPLGLFSPFPKKIYLFPPRIFLAPP GVFLKAPPPFFFFPPPPPPPPPPFF
7516	21417	A	7576	1	119	LIFRFTSKHGFGEAAA*YWHFNVV*L FLVSIY*+GS
7517	21418	A	7577	219	69	NDISANTAIRKFWLKPCTTEGWLNT* LYIHLVEYYATLKVCGDLVVR
7518	21419	A	7578	3	287	HASALNGVYIEKSTPYRGGPDPISPARV PFFIKFLVAITFLLLELIALLLPLP* ALQTNLPLIVMPSLLLSIIIALRLAYE *LQKGL*AE
7519	21420	A	7579	10	125	ALQTNLPLVVMSSLLIIILT*ALQTT NLPLVVMSSLLIIILTILAYEGLOK LN*AE
7520	21421	A	7580	3	299	DAWRLLDPDF*VELPTEARIRIITTSQ DVLS*ADPTLGLKTDAPGRNGTFTT ATPQVYGGCSEICGANHSFPIALEL VPLKIFETGQVFTL
7521	21422	A	7581	3	116	AFASKRTGLGVEEPSLTLE*LGGGPPP* HTLEEPVNT
7522	21423	A	7582	398	2	RVPFAPKNSLQIFPPLFFWGSPPKFF TPPHFVFWGNFKENFFAFELRLPFP GEKIPLVFFFTD*NFVENFFFLSL FFGFFFFPNM*S*L*SPANFNV*VTH LFIWMVFFHPDEWFGPILW
7523	21424	A	7583	288	9	RGSKNLEKNSFPYKVNHNHNGSLPFLHL FFSPRGVGGFFFFFTETRSRSVIOAGVOW HDLSSPPGLK*SSHLISQSSWDY*RAPD HPANFVYF
7524	21425	A	7584	1	124	RDGGFTMLPRPILLTGLKQSSCISLPK* WDYRCEPLHLASC
7525	21426	A	7585	339	76	THFGHNGISVSPKKKKIPRGGGPPPLFP PIPRVGGGDSL*PRGGGFN*TKPAPFPS SWGKKKLPFSKKKKKKKKKISTPF SRIE
7526	21427	A	7586	205	87	SISLSLSLSHTHTHTHTHTLHSHRCV PQPIGLPISKWAKVELIT*R
7527	21428	A	7587	353	256	PHPSVTLTVTSQQQDPPAKRL*LAEG SDDC
7528	21429	A	7588	159	195	QICRRHVHINFLMSMGSIMITPFSFLF LNFL*SYVAQAGLKHLSQSDPASASQK AEIRGMSHNAWPHF*YFVELVHFIIYINK FVGIELFILTS
7529	21430	A	7589	76	205	RKKPEPEKTCFDNITGNTYPCLSYEH SD*YVNVRT*LCAER
7530	21431	A	7590	218	20	LSLYLASHLWLRPFHPLEWAPSKSSRL GTVASPCNFTLGGRGWNT*GQSETS LANAKPCFY

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7531	21432	A	7591	142	12	QIDYYLYLFI*RGKLTMLRLVNSNLH IILLPWPPKVLGLQM
7532	21433	A	7592	2	224	QITEALLITLLGHYFTLLQA*EYSKAP FTISDGIYGSTFFVTITGFHGLHGIIIGST FLTICYNPQLIFHTSEHKFGQLQAAP*Y WLFNVVARLFPVPSIY*GSLFYPPTSL RVLQCSLHHRFDRLRLNIFCHRLPRT RHWLWNPVHYLLQPPNLSLYLT
7533	21434	A	7593	1	323	HAYONTLVA*LVVWTF*LPVDSGYIKK FTPYEGGFEPKSAARVLFSIKVFLVAIT FLSLDQSALLPLP*AVOTTNLPLVM AALLLDIILALSLAYA*LLKGLE
7534	21435	A	7594	1	104	RACVCVCVCVCVCVCLLKMVCVCVCVCV CVFCAC*KMVCVCVCVCVCFCAC
7535	21436	A	7595	383	43	VFISETLCEHVASQTTTESLGLGTVAH TLNASTLRG*GRMIA*GQ*SKTRRGNDM SISSHSQTIACS PHLGRHQKNCMCVQ AAEAVLKGGVETDASFQIKIPINSLIN L
7536	21437	A	7596	2	331	WPPGTITPLNPLESPLNTTGGSLLA*GVS MT*AHSGLGENNRQVIALVITILLGL YFTLLRASEYFESPTISDGVDRSTFPV TTGFHGLHVIIGSTLISWIFIRQLCNF TSKHHFGKAVA*YWLNPXYLVHPPTN M
7537	21438	A	7597	384	23	LFKIKQYRFLPPPLKLIFFPPLKA*IF LGGFSHYFPKKKGFPKSPPW*IPPP YRKGHFCSHTPKNLAPRPF*KRPPHF IFP*RWGLAMLPRLFSNS*QAQVLLL QSEVLL
7538	21439	A	7598	401	189	RVLCPAGNS*TPGLKCPCLGL*KCWD YRRPCLIREYLFVYFLRQGLAMLP VLNSW*VTLLP*SP
7539	21440	A	7599	81	368	KCVIYFPLSYTLGRKAYDFFFLKELA FFPQGMQGNL*LKPPPLR*RDPSCL ALPRGGNGRGAAPPSPNPGFLGGNGVYP SGPGGFETDPLK
7540	21441	A	7600	264	25	AVEHPQLRLFCSH*NNIVEERLGLVAR TCNPCLPDKAAWIT*RHFPETSLANMV IFCLDIGSKSFLSMRFSRCLLWKL
7541	21442	A	7601	1	196	WEPSLVGETNVNSFNQKYNWPGAVAH YNAGTLGGGGGWIT*QOEILITLSKKVK PSTYFTNTR
7542	21443	A	7602	315	82	TCTQVFIALFITAKFKLICPLTDNWS RVVYVMTKHISAIKRAVIAHATMWKL ENIILSEIKQSQKATGCMISFI
7543	21444	A	7603	334	118	PKIKTEGGPPPKNAGGMYK*KKFILVL AAPHPPPGVFSVFSYFVFRRFFFF FFFFFFFFFFFFFFFF
7544	21445	A	7604	3	288	DAYTT*NLSSVGSFISLTAVILLIFMI *EASSSSSSPPGGLRPRAFPVRPPGAGL VF*VSVPPDLPCSLAGLQVLRFMELAR LAPHIRWIIQ
7545	21446	A	7605	354	33	EGRARYTRVFORPRFHLGIFAPQLGK KKKFSFKKKKKKNQLMGAVSHANNLS TKGG*GRGSRT*A*EFRTSKLGTGKN MVKIISTNFKNERGGALSOL
7546	21447	A	7606	401	161	YLVSHLLQILPPALFVVFVFF*DRVLL

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7547	21448	A	7607	354	50	CGPGWSAVVWSYCSLCLLGSNSSPCQSL PSSWDYRHLWRFLMPRGILCVVY SGAQDPAGQHGQTPFSDQKVPKKVYPWW CMVVPATQEA*LKKSLEPWRRLFLREA FFFVYLGWLSNGEPPLGGGGSVFLEAL EKSVMGSSSLGFGWVFFF
7548	21449	A	7608	370	115	TIRNICNSWEVKIRPFTGVWKKLIPATL MDDLEGFKTLVEEPTDDV*ITGELEVE PENVIEFLQSHDQTSTDEGLLLMDEQRW
7549	21450	A	7609	120	358	TTAVYLGHYQSP*ILNGTVNT*PPVVH KDPILFLTPTPCFHASSAMNLQLSHISC NSKATPHPLGYQQTYPPLTVHMT
7550	21451	A	7610	3	164	HE*ASIP*NTHT*HTHT*HTHT*HTFYK EBNLSHLWNISICFLGAHGKKKMN
7551	21452	A	7611	85	324	FRFFAFFFF*KKISFCFQAGGGGILPS LDPPPPGLKKFSGLTPPWSN*GPCPP GLIGVFLKKRGFPVLVREGPNLWT
7552	21453	A	7612	268	317	FLNCFNPGGGGCSQPKLGCPPPAWGAK *ASLSKKKKNNKK*LSYKAPSYGYGKG
7553	21454	A	7613	101	339	AVPLTMVKIHALWKRVRHKNKSL*LP CDPALSLVSMYPKEMKSVCLDKVCSPL ITGLPTIAGMWNPNRSMDSYG
7554	21455	A	7614	366	208	LELLTSGDLPASASQAGITGISHRAPR GTLFF*AVNGGGNGVFLFLRVNLGL
7555	21456	A	7615	30	328	NYCLDPHGETELGTHFTLHFTSTRAMVF EYCOAL*LL*GVINT*PTVLHNRSHI KNACLCLOARTVNLQISHINWKY*TP HPL*YQQTYPALFYI
7556	21457	A	7616	39	159	TPGLKQFFHLGLPRCDWYRHEPPRCPN MYLI*ISF*CV
7557	21458	A	7617	290	91	KMSPLIFPRDMASLCCPGWT*TPGLKQS SCFHLPKSDHRCSTSLHVAKTFLYLYFL KMFYYQNVNH
7558	21459	A	7618	37	246	TOELVYIYRYIDHTHTHTHTHTHTHS HTHYWIYTNKHTLKGPKLF*EKTGMGST PIISWKERLSLRS
7559	21460	A	7619	23	190	IPPQPCFPLLSLFT*IDMSNCMACVC VCVCVYVCVICDMVLLPFCCKLECSK
7560	21461	A	7620	367	2	FFSPKALIFLGGGGPFPFPPKSSFFSKI PPGGFFPLPGFLKPPPPPL*NPPLKKK NFFFFPPENWAPPRVFFKGPPPPFFFFF FFFFFFWSSRFLFPQFFFLNNKIGKK KIFRHLGAG
7561	21462	A	7621	6	25	SVILQSIITFIATNLLGLLPHSLTPTT QLSINLAMAIP*AGAEIIGFRSKIKNA LAHLFPQGTPTPLIPILVITETISLLIQ PIALAERLTANITAGHLLMLIGSTTLA ISTI*LLYYNP
7562	21463	A	7622	383	67	AFNLNGKFPFPPGFKRFFCPPPPPKKNGK NRGPPPRGKIFFFFFVKTFFHVGGPG F*ILTSQDPPGQQGGLGGFFFFQIGGT GDLNLSHKSMPMFTINTHNG
7563	21464	A	7623	372	35	TGGFWGVFFFFFKQGFPPKSTGSGNLGP KNPCGKGRVSPFPFPPNKGQGGPFP PKKFPFFFFFEITGFPFVALAGLEL PGSGNLPTSVSQSGAGIPGISTWPGVQF
7564	21465	A	7624	287	6	LSGVEVWDMINICLFPFKLPFCV*KWL

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						YQPVAVAHACNPSTLGGDRWIPGGQEF KTTCLSLPKRWAHRREPLYLAFCPFYNG IGCLLIIGF
7565	21466	A	7625	271	277	NRGKGKGTSLGLEIKENPFFGGGPPFWANP PP*GLKFWGGVGPKRPPPKRVFFQNSQ GTSFPLPPVLKSGGLVLKKAPOKKNKI TFOPKKEGPPRGSLKRAPPPPPPPFFFS LRKSSVIEK
7566	21467	A	7626	2	269	LLGELSILVC*FPKHTTFLVLTGLSLIF TGLYSILYILTTQWQSLTHIILNKLFL TPKNTLMFIHLYPILLSINPDITKKKK KGGAF
7567	21468	A	7627	397	164	FPFPKKVFFGKNPKKKEPPRVE*TPFP PPFFFLPPKKKKFFSPDP*TWPPPGIF *KPPPLFFFFFFFFFFF
7568	21469	A	7628	3	324	DGNVSTLYLGATGSHGLHIDMGSAITTY WYIROLILHFTSKIHGFFAAA*YWHFV DVD*LFLCGSIY*GSPGGPKFSRGGKG IAPVHNGDD
7569	21470	A	7629	2	246	SLGLTTL*KNISVLLTGLKILVTGLYS VYIFATQWQSLTHINKIKP*LTRENT LMFIHLCPILLSLNPDISYPGTIS
7570	21471	A	7630	112	290	LISGKGQWQMLRPLVLTFTDSFSK*K NPSTLGEQCGRIT*GOELETSLGNIVRP HLY
7571	21472	A	7631	248	2	KVPASGRKPEPHWYFVHAPVGCGRIPAT AINTQKWKYQGFPPALSPRLCSGAISAH CYFGPPGSDSPASPS*LAGTTGTRP
7572	21473	A	7632	383	106	GWGQCFKPAIPALERPNPQECFRPGVLN QP*PQNKSPFFFFFFFKKKKYIYIMVY HAYNPSYSG*GGRIT*AQKFKTSLNNT VRPHLYKK
7573	21474	A	7633	435	133	YACLGLPKCWDNRHEPPGLANFCIFSKN RGFPISDRVINSWPRVG*PKPPKMG FOTLVQASGLPLILFLTKGPPFFSQHE EQDWTSSQHRFPKRGK
7574	21475	A	7634	1	209	NAYRIVILCQKLFPLLSGKNMFKKTRCW LGMVAHACSPST*LG*GGRIA*AQEGFT SLGSLIRPCHCKK
7575	21476	A	7635	117	495	STSFIDKVLRRHSFLFSLFFETKCSL TQTGVQWHDGSL*PPPPRFK*FSLGLP LSSWDYRHAPPRPASFFVFLVEMREHHV GOAGLELLTSGDPPASQASAGITGMH HALAHLVFSSGKS
7576	21477	A	7636	1	241	LPSSSDSPTSASQVAGITGMCHAGLEFL FLAF*LINF*FFFGNSFFVPGAGGH GIGG*LNPPPPGLKRFSLTLWGG
7577	21478	A	7637	3	93	EAEAGESLEFGDRGCSKLRSCHYTPANQ QSVTLVSKKTKNTKTSEVPFVGLNLLY KVSINILIFKEIFYQAPLILV*DNPDSS TLSSALQPGQSKTVSNKTKQKTVS*PG NRV
7578	21479	A	7638	46	228	GIPHIQPSKSVFNHVGEGTVAHTRNPN TLEY*GGSIT*GHEFTSLGNIVRLPPP SLQSI
7579	21480	A	7639	1212	1023	KNHSENIKKM*YICTMEY*AIRNEIM AFAAT*MKLETTILSEVTQEWKTKYCMF SLVSGS

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7580	21481	A	7640	479	318	AEFLNLGGGCESEPR*HKCTPAWATRAK PHLKRKKK
7581	21482	A	7641	470	172	RNIRPRENOYVPVFMVAFFFLAKNN*QPK CPSSEAMNKLRCIHTTAVLHSEEEQPI TDTNNSDLRSIAPWSRSQTRAAAHRI PWHSGKGKTPSTENA
7582	21483	A	7642	2	201	AGAPPPANLPPFCRLISDC*ASNQDSVG VGPSEPYATVRKYLELLQMHMDMCTY RFSIRIVLNL
7583	21484	A	7643	521	385	GGSPLETH*YTSQGGGIPYTDLTGSHPS OGRIQEAPKLTHL
7584	21485	A	7644	331	3	DLVPRKGGGGKKTTPRIKKFPFGEDFF FFTPHYFVVFVVVFWGGAFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFF*DYVIS F*EERFNKPYRCQSTLVQIGHTSNL
7585	21486	A	7645	88	367	HCSFLLKGGKKKKKKKKKKKKKKKKKK KKKKTKKNEYKNLGGAPP*KP PSGALY KYRRENFIPIPSFERVSKYPPDLCKKNL FWGGLNIPS
7586	21487	A	7646	378	37	FFFPXFFFFSPPXFFFLFXFF*XXFFF XXSFFSLPLPLXPPPPPLFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFNI*TI VL
7587	21488	A	7647	34	293	TGIPGVISAIFMI*EAFVSKRKLVLGKK PSINLE*LYGCPPPHTFEEPVYIKSTQ KRKESNPFKLSSGSGPHLHDFFEKKKI TK
7588	21489	A	7648	22	106	KNFLPLTLTL*KNFLPLTLTLI*YGS IPITISSPPOT
7589	21490	A	7649	1	231	FDRTTSKDISK*WVLVSKKKKKKQKKKK KKKKKKKKKKKGPPPKTGGAPKNP GEEKIIPFLLGGGKKNWGF
7590	21491	A	7650	79	286	VVSRLVSLRNCITITCS*AKKKKKKK KKKKKKKKKKKGGAFLKIPWGGPIPPG GGKFFFFPGGYY
7591	21492	A	7651	57	375	SGKSEFHVRPQWFGTGADACNPSTLGG GRWIT*QGEFETSQGGPISTKKKKKKR GALLKSDLGGPNLPGFNLKVFSGRGI LKPTWEFWEGTIFLGEKIGPN
7592	21493	A	7652	3	357	LAFLLALSKITHASIPVSPSPKSPRS KGTKKKKKKKKKKRGGPLKKTLLGSPK INGGKKKKIFFPKGGEKTPGGLLEKL FLGGGKMGPNPKKIKPLGEKKNF*GEK GEKPP
7593	21494	A	7653	113	378	MGAFNLGPFLLMGGGNPSGNHVLGA GSYLPGGKTPPKKQKGGPPDL*GRGG QCSPGTKPGGGGKTLGAPPTKSLPGF LQKK
7594	21495	A	7654	341	147	NFFFSLKPPIFFGGGFCPIFFPPKKSFSS KIPPVVFFSPPP*EKIFFPPPLNPAFP RVFFKGPP
7595	21496	A	7655	395	3	FFFFFFFFFFFFFRGSE*FVLFPVSPAP SLRG
7596	21497	A	7656	2	162	ESKGYTHTHTHIYTHIYTHYTTPREH *PKGADVAMLIINLFFKPRCVALL
7597	21498	A	7657	333	28	LEFFNFSSYLFSS*RVGSPRPPPPP LKKAV*KFFLFDIFLFFFIIFGLGFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFLEHILRLMFVTFSSHR
7598	21499	A	7658	1	137	HSSLDGRVRLCLKKKKKKKKKKKKKKKK KKKKKKKKKKKKGGGLP*EKKKKKKKKK KKKKKKKKKKGGGLP
7599	21500	A	7659	236	32	LFLKFLYP*EIFI*F*FPLTFYFPR LKLFPPFFFFFFFFFF*KNFIK NIYFFFLPYLYKFFIYIKTFLFLKI
7600	21501	A	7660	301	65	KAPPKTFWFFFFFFFFFF*FUSYFFFF FLFFFFFFFFFFFFFFFFFFFWKS LAAT*FLRGFTF*LAYILKTT
7601	21502	A	7661	70	273	KHSPPHKPASD*NTETTKKKKKKKKKK KKKKKKKKKKKKKKGGGALINKPW GPIHRGGEKFFPSFLRRD
7602	21503	A	7662	1	353	ILINTLLALLLITITFFGLPOLSGCLQK STPYEGGSDPISPARGRFSLKGLQAMT FL*ELEIAL*PLP*ALCTTNLPIDM GCLLLNIILCLSLAY*LP*GLDCSRYH SQRIQ
7603	21504	A	7663	1	131	FIRQLIFHFTSKHHFGPEAAA*YMHFVD VA*LFYVSIY**GS
7604	21505	A	7664	2	192	PLSQSLY*LAADLLILIT*IGGQVSY FTTIQGVASVLYFTTILILPTISLIEN KILKWAY
7605	21506	A	7665	356	2	TFFFLSSPGGSCGSPTPARPKNPPPWG GGLPLFSRRGALPKNFWGGYVFFFLF *KKPPFFPPPGQSPVTSKDVVPLRM PPPRPHVRPLGLPKKFSPPRWKQVKK TKKRAA
7606	21507	A	7666	312	2	GFFFFFFFFFFF*DRVLLLPRLCENG VISAH
7607	21508	A	7667	1	233	FWLSSNAEFDANSANCELEVQRMIDQD SFPTYHYFDMYVCIIY**RSLAVSGLV SNSWPAIQLQPPQSLGLQE
7608	21509	A	7668	174	295	IFFLFCGEHSLAVLRVLNLSWTQAIL PLPP*TLGLQ
7609	21510	A	7669	183	330	NKFLVMSVAMAHACNDRTHRGGWIT* CEEFTTLANVMNVKPCLV
7610	21511	A	7670	3	319	TSNTLLALLLITIT*FLPOLNGYTEKST PYEGSFDPIPARV*PYIKFFVAITPL LPDLIALLLPL*AVOTTNPLIVMSS LLLIIILPLALAYE*LQGLD
7611	21512	A	7671	1	313	ARGERERERERERERERERESGGGGP TQTDCKGGRNT*RGREIYRESDRPP FLPTTYRVNLQRPVGLRRKAGADKTFCL ILTLLARDYVWPDYMKRADHM
7612	21513	A	7672	3	91	TRRERERDR*REEREREREI*PREKNSQ S
7613	21514	A	7673	1	115	DELANLFTI*KAGFPVLPRLVLNSWLQV ILLWPPRLN
7614	21515	A	7674	3	232	TRRERERERERERERERERERERE RYRE*DREREREREDCVWGGVVISLR AVALSGAPAVGRQTERISR
7615	21516	A	7675	1	234	ARGERERERERERERERERERERE REIERERERLQREERERERGRVWHA PIERG*PKQGGFWKEERVKEPLGLKL
7616	21517	A	7676	1	262	ARGERERERERERERERERERERE RERERERERERERARAAPNL*ERWAH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7617	21518	A	7677	214	2	TPPAPGVSLSWRETRGGPPWCKKEGGW GRLGHPPPSILRAKGG
7618	21519	A	7678	3	341	QOASVAQAGVKWPDCLSLQSMPPRFK*F SCLSLSSWDYGP PPPCAGLHWRNRVT LALQGLPTTSLALV
7619	21520	A	7679	1	357	HERHELEELIKTLFFFFFEKKHNLCKP GGKKRGPIWFLKKFFSPQKKPPPPPPF LREIGAMAPQGGGLI* NKTPFRPRGQ GGKFPPTPGKPNPPPPKGNFFL*GNP QPPGSPTPPPQKVI PPFEGHQA
7620	21521	A	7680	365	1	GTRINTLALLLIIT*PQLTGYIYK STPYECGDFDISPARVPSIKFVLVAIT FLLDLEIALLLPLP*ALQTNLPLIDM SSLILIITLTLAYE*LQGLD*TDYF SVGGGAN
7621	21522	A	7681	387	3	PDASQ*HCTNGQSNRLINLLIKALLTTA KIWIQPKCPVDARIKIMO*IPRMEHPS AIKKEILPSVATWMSLEDTPVSRISQAQ KDKYHTVSCMWNLRMLNABEPGRVVP GVGQGAARA
7622	21523	A	7682	107	290	FFFKKEFCPRKKAKK*NMWPGNLGPRG* KNPPPPFPQKRGKGGPPGGEILGLF* KKGFPFPMRGSGKLWPLGFSNLNPKRG CKGFPDPPPOKRGKGGPPKGLFFFFF FFLRQSLLTSLRLLV
7623	21524	A	7683	1	348	ELNKRWGLGAVAHACNBPST*ELNKRWG LGAVAHACNBPSTLGG*GRNIT*ALEFKI NLDNKARSHLKKIKHQOQKNSGLDA
7624	21525	A	7684	364	77	GTRERKPTLWVYHREMERDCSCVPGS SGISESRVWVQGVMEVYPAL IYLCLEPK YLVISEFSAPFRIWGLSVVAHTCNPS NLGGGGGRIT*SQEFKTNLANIVRPHLF FFLF
7625	21526	A	7685	3	24	GGPSYFPRLLALGGGGGPGFPFLPRGNFS FFNFVKKGVFFPGVFPFLPPGVLPFP PPFWAPG*PRPFNFFLAGDGFPPFFFLG GGFFVPVAGGV
7626	21527	A	7686	1	125	HEETITQVKREFVE*KKIFANPTFNKGL TSEIYKQLNRKPKNNPI*KQSSK
7627	21528	A	7687	459	298	GTRFGMPGTYSNYPDTYTA*KITSSIGS FISKTAQPGPWE
7628	21529	A	7688	374	248	LSLPSSWNHMCALPHASFFL*RGGLAL LPLRLVSKSAQVMLLPWPSKVLGLQV
7629	21530	A	7689	284	163	FPHNNHVEIVRPLSPRYPIISHVICTY RSRW*ASEGSQKK
7630	21531	A	7690	83	255	GTVAHTCNLSLTRGGGWIT*GQEIDTS PAWPPKVLGLQA
7631	21532	A	7691	3	193	KVDYVSIKSEFF*DRVSLYHPS*GTVAR S*LTTTPNPGIKQSTCPTVPSSWDYRHV LPLPTRTIFSVPTQSLATILI*ITLNL INLGIHFL
7632	21533	A	7692	1	364	HERLDPADFSFNFFSDVGLAMFPRRLV NS*HQVILLWPLTVLDYRHELLRPAG FYLANPT
						NKFSFFP*LFVLYHLLFFGGLFLFFLI KLGSLLPINFSSKSVL*ETNWIYFSLV FTDCPCFIPIISFGFSLIYFIAVEPLK FIGFILSFI*ITVFYQQAQWLTVPVIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7633	21534	A	7693	370	151	WVAEVRGSL GKKYSVASFGKLPWPQGFKTAPEPPFF FFLK*RCGFTMLPRLVLPWPQGILPPQ PPKVLGLQVLRHHIWLK
7634	21535	A	7694	3	373	WFGYTLNQAYAKIHFTIIFIGANLTFFP QHFGLSGMPRRYSDDYPDAYTT*NLSS AGSFISITAVILITPMI*EAFASKRKVL IVEEPPSQAGITGVSHCARAEYLFIDRR DGLSLCNPWT
7635	21536	A	7695	406	394	KFF*KKLFEPFPFFLELACLFFFLPPI KGLPKYIAPGIKPPPPKKEKFSSLKV LFSPPYFFPIPPPIFFFFFFFFF FFFFFFFPPPPPPPPPPPPPPFRFEG ECNRL*W*FYFFFKESDHCIP
7636	21537	A	7696	2	334	ILINNTLWALLLLITTFWVPLKGYIKK STPYECGFDPISPARVPSIKFLAAIT FLLFDLEIALLLPLP*ALQTTNPLIVM ASLLLIILALSAYE*LQGLD*AE
7637	21538	A	7697	2	95	LNLTIIYIILTTTAPLNLNLSSTTLTLL SRT*NKLT*LTIIYIILTTTAPLNLNLS STTLTLLSRT
7638	21539	A	7698	423	326	RQCLTMLPRLVNS*SCVILLWPLKVL GSQA
7639	21540	A	7699	400	32	PHKEYESYFFSPNQOFFFFFPHR*NFY VGVLKQPPKKKFFFLPTPERFFPFL *KKNIFFFD*YFFPLVIFL*PDLFF FFPFFPFFPFFPFFPFFPFFPFFPFF FFSSNSPFY
7640	21541	A	7700	125	407	FINFSSTFVVKPTTCNMQKHTPIARTKD LCITITFFFFLEKNFLFVQVGGGGILG *LKILLRG*KQFSCFTLGRWTTNGIIP PPKNFLKKFF
7641	21542	A	7701	50	225	PNNVMRSCWLGKVAHVCNPSTLGGGR RLA*AQEFETS*VTQ*DEVSVIKRKKKN FK
7642	21543	A	7702	2	146	EIALLLPLP*ALQTTNPLIVMSSLLLI IILALSAYE*LQGLD*AE
7643	21544	A	7703	1	93	ILINTLALLLLITMGLPQPKGYIKK STP*ECGDFDIPARVPSIKFLIATIT FLLFDLEIALLLPLP*ALQTTNPLIVM ASLLLIILALSAYE*LQGLD*ALLL LIMTMGLPQPKGYIKKSTP
7644	21545	A	7704	2	112	GRVGKHHGFEAAA*VWHFVDVG*LFILY VSIY*GS
7645	21546	A	7705	1	325	TAGQFLPKLSILLSYNPAITFLGYPYKI LKTIVYMKTCIWMFIALFIVVOTWKQO SKLWYIQTIKYSVLK*NELSSYNTSK KLRCILLRERSQYKPPYFLIPTM
7646	21547	A	7706	2	169	SRSRAGTLAI*TNLFCPTMIFTLLIVL TILEIAGALIQAYFTLVLSLYHDST
7647	21548	A	7707	263	346	MLINVLPLGLFVGVILSKESPVSQDGGV QWNLFSMQPPPTGFK*FSCLEA*ASIN LSPHEQYRLALSFLKLT
7648	21549	A	7708	343	163	PKEF*RGGFHVGGAGFKLLRSNGNPF SASQNGKITGVNPLAQTNNSIPMPAD
7649	21550	A	7709	459	144	FWPGASSHAFDPTTLGGGRGRIA*AHFF KTSLGNIVRPPSDTCNPKVLGLLA
7650	21551	A	7710	2	83	NFLPLTLALLI*YVSIPTITSSIPPTQ

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7651	21552	A	7711	19	181	YVYHFKACT*MFISSLFIITKNWKOPIF SSYGE*VNKT*YIHTMEYLLFNKRKK
7652	21553	A	7712	392	49	SDIFNSDIFSHY*CSVF*SYLAYNRVLS FL*LPLEFIYSYP*IDHAFCHFLHPVSS FWLDFFLFIFSFYFFSYFFSYFYF*FYF *FIFNFIFNLFILFYF*SFSSFKCLKF PC
7653	21554	A	7713	334	208	FFP*EWVLTTLPRVLNPGAPAILLLWP PKVLGFTGVSHIKI
7654	21555	A	7714	2	408	WNGMEWGLKWNRLERYGMQWNGLEWNR TE*TRMVWNAMETRIELNGLEWNGMEC NGMHLNGLEWNGMERNGTDPWNGTDP WNGTDPWNGTEWNGMEWNEVDSNGMEW NGIDNSNGWTRMEWNGMESTRV
7655	21556	A	7715	362	223	VWWMFPIPTLWEAEVGG*LEPRSSKPA WATQDAIFPKKQKHQP
7656	21557	A	7716	2	335	LVTINTLLALLLIIT*LPQLNGYIE KSTPYEGCFDPSARVPFSKIFLVAIY TFLFDELEALLPL*ALQTNTLPLIA MSSLLLIILALLSLAYE*LQKGLD*AE
7657	21558	A	7717	2	142	SITL*LPQLNGYIEKTTFFVECGFPEICP ARVPLSLKQFPLEAITFLFDELEALLPL LP*ALQTDDLPLIVMTSSLIIILTILSL AYE*LQKGS*AYMPRRPRFVHKILLRS YVLLII
7658	21559	A	7718	6	92	FFEEAAA*YWHFVNVV*LFLYVSY**GS
7659	21560	A	7719	417	164	PLEPLISGRGLPQIAFPFKGSPKPSR WFFFPFP*KKKNYPPDPKILDPGGFF* NPDPFFFFFFFPIFFFYFFKTALPL
7660	21561	A	7720	25	401	THNS*DNWD*PIPHA*P*TSYVKKKKK KKKKKKKKKKKKGGGLKKFRGGPKY TGGGKIIFFFMGKKKKPLGDFLKNKFF LGGNGLKHPPKLSLQKKKNKPKGRGG KKTPLCRGGKKS
7661	21562	A	7721	388	2	APPFFFFFFFPIFFFYFPLGVGSFK*N SKVPWISNFKLILRVFICSLXKGINPF LEKCFYMPFFVAFIIRLNFSLOAKFLL LNFALLPPEPIFFPPPPFPQIEDFW HPYIEQVYQSLFSLSL
7662	21563	A	7722	389	71	PFLPHQKQVFFPPPPKIPFFFSRVFFF WGGWAQKPPPPKPFLLKTPGFFLPPP *KKKFFFSPPRFLPPGPPFPKPPPNF FFFFFFFPIFFFFFLN
7663	21564	A	7723	77	220	TRRGGWYLMFATPAILEA*AGGLLEP KSLWTPWNRSISPKKK
7664	21565	A	7724	16	258	ISSVFKRSFAMFLVLNSWERVVLP PRPE*LGLQCATTTTFNFDEFLRLP LKEDV*TRDQREILVYVFLFYGGA
7665	21566	A	7725	353	111	ITFGARPRFVKAGGOGANSRLKPFEPG NKWSFSPSPSKKWEGR*P*PRPPFFFF PIIREGVSLCCQGSQIDGLQSS
7666	21567	A	7726	2	185	MSMGHTRISSAWTKKPELVSVEDDFKLI WEISGGKLEAITDLDPKGDDEDDLLELS *MIDT
7667	21568	A	7727	346	143	SOQFLYLSFLLLLLY*FLFFKMSHS VQDRVQWRHLSLSLPLPRFRQPSRLT LPSWEAEVGG
7668	21569	A	7728	411	221	NLRPFGSSYSFASAS*TAGIPGARHHTQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						LIFAF LAEILRN LAKLYLIPRKNPIYYL PNCYINI
7669	21570	A	7729	2	303	AAASTNNMLLFFLRHRLVVEVLGHMVGLI FTFFKKLENQAGRRGSHL*FQHFGQRORWE DHLARSRVQDHPEQHSKTSSSLQKNKMSI ESNLLNHLKLFSTGRM
7670	21571	A	7730	67	65	SICEYCFVSSVFLKALFESVMOAFSLG CVSCOS*AFLOHLYFKKLYFLY*AGLTM LSRLVLNTWPOVIHLDPWPKVLGL*AF C GNEA
7671	21572	A	7731	354	238	QSILDDVAMVLD*QAEFVIMKMRLLIY VHEAKKIGLVK
7672	21573	A	7732	33	186	RGALAVLSRLILTPGLKSSCLDLPKGW DYRWEPPRPGCF*LMVLVLSF
7673	21574	A	7733	1	181	VNAGADCSSIGGVFPLQHKKCHGKDYP RGITTLERSYVEETHELVSKSK*PLRA QINL
7674	21575	A	7734	336	80	HKLKEPPGVFPVFPFKNLGEGGPKPKFF FKKAFSPILSFFFGKIFKIPRFRGENFA P*NFGKNS*KPRFSPPPKKKGFFFF F
7675	21576	A	7735	2	163	TPVSTGTVPVTLT*VPSPIIFPVSEKRA GCLHLCNFTCTELRLTSLTIRS
7676	21577	A	7736	87	258	KAPSVCLFSAALLMLLMSARTSVCTVRF LSPS*AVISPVCTCTYTSRWEATEDSK
7677	21578	A	7737	1	103	LDSKGIYMTLQPSKLEPKLEANVEIREH MLENSSRP*RDLYDAAAFKARTKARSKC RDKRAHVGEFF
7678	21579	A	7738	193	300	GGLPPPPPPFFFLKKRGFPWVTRGGGN PPPLEMGGPTPPKGWNYGGGPPP*FHPF GGVGPPISKGGGLGPPRVTOGKPLFFKK KKKRGGGGKPPYS PFLGGVKOKKGVNP GGGSKPKPPPPPPPGGKKKPKFLKK KKK
7679	21580	A	7739	150	17	GRVAQVWMLMHAPAL*KAAGRSLEPR SNTDQGWHLPISTK
7680	21581	A	7740	1	358	SEPRPPPPPPPPPKKKFLKNPPPPPK NPQKNPPPKTKKSPPTTPKKKPIGT PPOTPKKNC*KKNNPENKGLNYP NKNPHAPKPEPKQREKPLVPTKKKK BSPKKKK
7681	21582	A	7741	235	147	F*FPLGDEISLCCPGWSLTPGLEQASCP GLPRRWNYRCEPPHSVKTI
7682	21583	A	7742	131	12	AASTYGO*FKICGAILRLMPIVIEPI KILQIGVPFTL
7683	21584	A	7743	1	184	NOYPWCFNCHMSMGESKTLNRSQGVAH TCNPSTLGGQGRIT*A*GSKSSIGDKV RPHLY
7684	21585	A	7744	347	202	SLFVETGYHYVD*AYLELLASGSPFASA SQSGFISVSLCTQPMFOFE
7685	21586	A	7745	138	263	KKRKTYIHTKTCM*MTAALFIRVRKKR QSKCHSADEWINK*YIKICLSIHQLND IWIATSF
7686	21587	A	7746	358	169	AAVAERTONTKTEDLVGLGWIKKVIY WPGVVAHVNCNPITLGGRGGWIT*QGEIE TSLPTRR
7687	21588	A	7747	78	346	AIOMLRNQVKIRLPKSPVEIIPFKVIVP FOVKIRKSONNELLFQESCLFATSTG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/155,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SVRPLSPS*AIISPTCTYTSRWPEVTE KSQKK
7688	21589	A	7748	222	98	KKKARHGLGAVAHACNPSTLGGQGGRIT *VQEANIVRTCLY
7689	21590	A	7749	314	52	LNNVDLQFFLGPRKKKKRNNDSLSFVSA EEVRLMYCFNKLAAILHYF*FSNKFIVFV *KFGHLLDENMGSKFDNIGMNAMANKDN ASK
7690	21591	A	7750	371	216	YHTHTHTHTHTHTQIPSLPLNLEGPGVY LLSCGSLHLKNLW*KCMRKERKK
7691	21592	A	7751	3	238	FLIQTFGFGHVSQAGWELLR*GNLPAFA QSAGITGMSYLCVAESLYLLPFLKILC SLLTLSPYDTWKVALLCSYTV
7692	21593	A	7752	2	247	NSDIFDIYITQYIFLYLYIYITQYIYLI *VFLIIFKFTLK*EFIFISLSISFRLA FIVYRDVILLFLFFFS*NFVGDLSIS
7693	21594	A	7753	359	2	TLKIRPLLYLPLFFFFFF*KKKIFFFPP GGGKGV*SGFYLMGRGTFSLFKRFLLF YPPKEGGLRGSPPPPSFFFFFKRGFP FLARGV*KKGPGGTPLPWLPKSLGLRG
7694	21595	A	7754	3	174	CSVIQAGGQCGHSSLOP*IFGNIQSSY LSFPSSNDYRHATMPS*FLFFIETKMLQ
7695	21596	A	7755	292	219	IWPLSHVHNSPLTHSPSQVDQGLFTLL PCLSGMYMVQFPLAEMFFISLLEHAC LSLCEGSAQKPLMLWELSYLPLMLQLP LCL*LCVCISGQVCRCLMCLGVCVCMH VCVSVCCPTHLOAQTGGC
7696	21597	A	7756	2	195	VALNADGATDTSNDYGAEMPLGIERGL DRIWEMPELNLRPNEFDCMTD*PCIQHA PSVSCGLA
7697	21598	A	7757	4	280	DHIVDMITPSPFRTTIAVE*DLNLYIVI RGHITSILKPNKNLKLWYIYTIYYSAL KQNEILIHATIWLNENMQDEINQTKD IYCTISLI
7698	21599	A	7758	352	107	FLTRASRGHNETIVTSWPGAVAHVCNP SSLGRRRWIT*GQEFKTSLANMVITFF ISKNSNRFSLQFPFISLRPTHYKVL
7699	21600	A	7759	92	4	RPSPRRGGWTGA*GQEFKTSLGNMVKFCL Y
7700	21601	A	7760	92	4	RPRRRRGGWTGA*GQEFKTSLGNMVKFCL Y
7701	21602	A	7761	328	124	PLFSFLFFPFFPFFPFFSRRRDVLPCC PGWS*TPGLKLSSSLCLPKCWNKYHEPL HTAHNF
7702	21603	A	7762	1	167	VDSTDKRPGAVAHNPNPSTVSGSQGQIT *GKFNPSLANTVKLFKKKKRKRKALF
7703	21604	A	7763	309	226	RPRRLTLSPRL*CSGATSAHCKRLRLPG
7704	21605	A	7764	349	7	QVCFELFFVCFSSIFMTNTE*QGLKVTS GISSNVY*FLLIWLIGKITQYDIGRCFS EYGSPEQHNIGIVRNASSRLGVVAHTCN PITLGG*GGWIT*GEGFETSLANMGKPL LY
7705	21606	A	7765	43	339	FFFFLFFFFFIIFLLSFFF*DHFFVS LLFISNFVFLPPIFTVFGAHLFICLL FFPICMELNLFPPNPNYFYFPFLFFYL LFFFF*FEMHLFL
7706	21607	A	7766	352	102	HTSCLTIKSSLSKKNISCVSSSISFFF* FLIEIGSR*VVOAGQLLGSTDPPASA

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7707	21608	A	7767	346	90	SQSRITGLSHHAQLSSTSLVENVZW TPFSSFFSPFPFFPFFSIFPFFFFFSNR DRVLVCLYLGWS*TPCLK*SSQGLPKCW DFRCGPPCLTSTAFYISITVNFSPSNCY S
7708	21609	A	7768	278	87	AASTGVGPSEPSAGYYLLVCRLLRSLEK CSIRVGVT*FSRCHLSPLSLTRKGNLSLT PCASVR
7709	21610	A	7769	5	272	AVYHPINESCVLIGNKDSCLLY*LFERK VKKKKKKKKKKKKKKKKKHYE*NTFPPG VARKINFLCICQKVDAGGGLTGGGPP IFEFLL
7710	21611	A	7770	198	33	QRPSQRQCRAMLGVVAHAYNPG*LAG*D RRTT*GQEFKTSGLNIVRPPLYEKPM
7711	21612	A	7771	97	410	A*WLPVPVPIIWEVKVRLLEPGSLRPS WATWKP
7712	21613	A	7772	5	415	ILCVLHFVGTTPFVHL*YMHFLPLTLA LLI*YVSIPTITSSIPPYT
7713	21614	A	7773	1	342	VVRVTSHGSG*AAAYAT*YILSAGSFF PLTEELLI*FMKRAEPT*KR*VLIIHEP SINLD*LYGCPPTPYHTFFDPVYLNKRR RRDSHPPKLASRLPHVLDHFFKKKGGGR RF
7714	21615	A	7774	398	122	SPPPPPSPSPSFFLPPSPSFFFLFLFL FFFFFFFFFFFPPFFFFFCRD*VSLC CPA*SQTPGLK*YSYHGLPKFWNYWHEP PCLAYFL
7715	21616	A	7775	1	336	FNFLLIITIEMESRSVSAHCKLSLFGSS NSSASASRVAGSRGAHHTWLFFFFFFF F*KKKGAPPGGGGLLTKKKNPFPAP QRGGINGGTPRPONGGGKFPWGEKKKF
7716	21617	A	7776	1456	1232	FAIESHCVTQAGVQWCNLASLPSPTEF K*FSCGLPSSWDYRCVPPHPANFYIFS RDRVSPCWPNGWSKTPTDLK
7717	21618	A	7777	400	2	NTEFPYGPPIISLLGM*PEMETYIPRPK CTQMFLVFLPTIAK*KKPKRS*LING* ILVYPLMEYYSATKRFDMHTKNVDAI GHIILSERQM*KTHIVYSIHRASCTAE VRIKVS*KKRAATWIKSILLA
7718	21619	A	7778	360	218	PVLNF*NL*L*RWHLNMLPPDPSNSWQ VILSLWPRVLG*QRGGRVEQARGANG MSKCPBGDCLCWAGA
7719	21620	A	7779	1	372	FEVRSCEVAHAGVQWHDHRCFFFLGSSD DPSVASCSIRITGASHCTQG*L*LLTK VL*VSAFCLSVNTLRLTSLKSDTFLGS RSKLNLSGESLQYISPSRHFQILLCFR FLPRLVLVKKK
7720	21621	A	7780	372	219	ATSLLSYFKLPPOPPOSSATTIISO* STSRQDLPPAKRLELTEGSDDP
7721	21622	A	7781	358	145	IKNIHDSWEDVKISLTLTV*KELIPLVLT DNSEGLKTSM*EVTAEVVEIARELELEV EPKDVLVQFHDITNR
7722	21623	A	7782	317	146	GRVDCKCPFYRFOMLLVRLSMVAHVCPN STLGGRGWIP*GQEFKASVSRMPRPHL Y
7723	21624	A	7783	13	186	DRVSITQTSWAHFPTSAS*VAWTTGMHH HTWLNPFVFFVEMGFHHVQGVGIRLPLLS WK

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7724	21625	A	7784	339	221	KNDLAWLRLVSNWLGQSSYLSL*NCW DYGSFPLCPAL
7725	21626	A	7785	355	3	FGNSGRVDLFFFFFFDLRVSLCCPGCSA VTNLEVHISALQPTQPLGKPSHLSLLS SWDYRRVPHPS*GLF*KG*YSITQLR FLNLHLESGRLSLPKFVASTVIRITQS GLGK
7726	21627	A	7786	1	201	QQFSHVFRLLFCFSQCEPPSSHQFG VCTRNTKVSQAW*CVVPFANREAE TGE SLEPGRRSTRP
7727	21628	A	7787	270	1	RPRRHLVFCVLMGKPCPLGPHLTITLTP YTLTTPSPTRSLGPPECK*SFHLSFPSS WDYRRFQRLANFCRGRILLCYPDWSSS PGLKQS
7728	21629	A	7788	229	2	DGWVRINWAGPGTVAHAYNISNLGGRGR RIT*GQEFKTSLTNMEKPLYSHEVRS LRPARPTWRNPISNTKTM
7729	21630	A	7789	118	263	CSKSYWPDVAVHTCNFSTLGGQDGWIA *AQEFKTSLGNIA RPPISVF
7730	21631	A	7790	246	359	TFIFSETRSHTVQAGV*WHDHSGLP* PWAQVILSC
7731	21632	A	7791	70	102	AA*SRLTATSLSRVQALPLFPQPEQLGG QGGRIS
7732	21633	A	7792	7	312	PLDFQLRLHNSYCEBKGVPDFSEIYEIC IVLICK*RKPLNQKKKKKKKGLI* KKKKNSQKKWDFPWLPPNPDETNSLFL PKEFLWLKTKPPFPLTLT
7733	21634	A	7793	1	341	IRFE*YLLFAYTILRSVFNKLGVLALL LSLILALIPILHISKRSIIFRPLRS LY*LLAADLLILT*IGGQPARYPFTIIG QVASVLYFTTILILIPTLSLENKVLWW A
7734	21635	A	7794	1	143	YGSTFFVATGFHGLHWIGSTFTLCIFC IROLIHFHTSKHHGFEEAA*YWHFVDVV *LFLVYSI*GSTFFVATGFHGLHWII GSTFTLTICFIRQLIHFHTSKHHGFEEA A
7735	21636	A	7795	2	257	KWAIIEFTKNSLIPTIATITLLNL YFYLRILYSTSITLLPISNNVKIK*QFE HTKPTPFLPTLIALTLLLPISFFILII L
7736	21637	A	7796	22	326	RDASDCSFQNLFPVLWVEK*MVFLLTKK KKKKKKKKKKKKKKKGGGPFKKNSWG AKIIPGKKKIIFFFLEGQKKLWGFFKK KPLFWGKKRPNPPKN
7737	21638	A	7797	506	281	RGAN*NRSGCGKRERERERERERERE RERERERERERESRFPKRQRETEIQ TSLTSLAPPPTCVF
7738	21639	A	7798	435	336	MRSNIHFSTHTHTHTHTHT*ILKQH TFSK
7739	21640	A	7799	411	106	RNPFFLFSFPLQRGGFFFIYWGPFRRF PPPPL*KTFFPKLIGAPPKKKPPFPFG EKMVS*PPPPFFFFFLRRPFLFSP GGGVGHFRGPPPPPGV
7740	21641	A	7800	2	296	FVPSIANWCFFLVSF*TGGSNYFFVHR SYSQAGVDLIFIRLANTISNLSFI*RG GLAMLPRIVLETRAQTILHSWPKVLGL QWATVPSFQLKN

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7741	21642	A	7801	344	105	PGFFFFPPGKRGFPKPPFLGTGPFPP PPLF*NPAP*FFWAPKKKIFSPPPGK KIFLLGKPPPLFFFFFFFFFFF
7742	21643	A	7802	68	216	VHTIAKIWKQPCQPSMD*TKNMRLYT VE*YSVLKEREILLYGHYAM
7743	21644	A	7803	407	3	GFH*FPLFSGYTLLDQYIAKHIFTIIFI GVNLAFPPQHFLGLSQMPRRYSIDYDAY PT*NLSSVGSPIELTAVILLIEMI*EA FASKKVLIVPEPSINLEWLYGCPPPYH TTEAAVYIKSRQKKESNPMY
7744	21645	A	7804	2	156	THRTIILSGGL*TLLELIA*LLASL ANKKKKKKRGCGPKKFPWAKI
7745	21646	A	7805	2	309	THRTIILSGGL*TLLELIA*LLASL ANKKKKKKGGAPLKKIPGAKIKRGME IKNFSQGGKCKTORGIPGKKPYLGGGQ NWEKLPKKFKGLKGGKNF
7746	21647	A	7806	110	362	TLSDLERLLMKAVSHFLMDLLEK*CV LKNQSSKKKKKKKKKKKKKKKKKKK KKKKKGGPLLKNSWCGPNFPGGEKIFF FFRGGF
7747	21648	A	7807	295	108	KQRGVFFFFEMESRSVVGARVQWCNL SSL*PPLGFGKQFSCLRIVYRKDSL KPRLLP
7748	21649	A	7808	2	142	GSTFFVATGFHGLHVIIGSTFLTICFIR QLIFHTSKHHFGFEAAA*YHVDVU* LFLVSIY*GSTFFVATGFHGLHVIIG STFLTICFIRQLIFHTSKHHFGFEAAA
7749	21650	A	7809	390	2	PASLLHCG*ISDCASNE*GSGVLGPSE PGAGYNLLVCHLLRPLEKCSIRVGVTFR SRCLLSPPLDRKGNLSLTPCTSOVRQCL ALLQLTLGALHPVSCTHCPTISGEMNPV SQLEMQKSPICVTHAG
7750	21651	A	7810	1	157	FLHFGQAALLETLSGDPFASAS* GSHRAQLVCTFTITIVFLKNSSY
7751	21652	A	7811	368	44	QNFFPPKKRLFPQPPPLFFLVPSFKGEG FFFFLRGFFFSASQALL*FTTFIFFF FFFSFFFLYFSSIDSGDTHDLLL GVSXWTSRLPWIAHNNHAKVGVG
7752	21653	A	7812	400	80	PQNSPSPPGIGGFFFPPL*NFFFSPKA FFFLGCFSPFFPPPKSEFFKIDPGGFF SPPLKKKIFFPPFFLAPRFFFKAPP PFFFFFFFFFFFKYFRHI
7753	21654	A	7813	119	230	SEEFETSLRCIVPSL*KKKKKKKKKKK KKKKKKKKKKKK
7754	21655	A	7814	3	412	HEQHL*LLLP*PLAIT*VISTLAETN RTPDFLAEGETELDSGFNIEYAAGFAL LFIGEYTDIIIRNTLTITFLGTYYDAL SPELYTTYTVTKTLTLLTSLFL*MRGY RFRYDQLIHL*KNFLPLSLALLI
7755	21656	A	7815	1	183	LRLELSEFSTRERERERERERERERD TRIDIYIVSQRRKKYIV*IRRNIFVYHA EFSKR
7756	21657	A	7816	484	97	QPRTPDLK*FACGLGPKCWYRHKFPCL ASDGNHS*SSPGLLVSSASVSPSGHMS PSQQTSPWVSEESLLGRVPGFLYFPV DAPGPGAWLAHVQAVLKLGSDDPPVL PSQSAGFAGLSNCAFW
7757	21658	A	7817	2	219	ADRLRNS*EA*EREREREREREREPY

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7758	21659	A	7818	190	292	PFSHIYTDNRH*MRHERTLFLWGSGE VRDAAPVWSHIPNTAL NSHLIFPWTGFFMS*CTYNLVLPGEK KFYSHA
7759	21660	A	7819	498	139	RRAATPAPAAAEPPPLQRP*PFSEPPD TQRDARGRRRGEDPONSFFHPNDRQPS RALCSTPRMHLWIGPAFFMTLSVSG AVIPRNGPGGVSSGCPCLQLLCCQAGS STIRKIPS
7760	21661	A	7820	489	330	ELGFLHVPQAGLELLS*SNPPASASLPT SWDYRHDHRTGHHGPIYDSKMCIF
7761	21662	A	7821	490	260	FFLXXNFXFXFFFXFXFXFXFXFXFXFX FFXXFXFXFXFFFXFXFXFFFXFFFX FFFXFXFXFXFFFXFFFXFFFXFFFX FFFXFXFXFXFFFXFFFXFFFXFFFX
7762	21663	A	7822	493	482	VGOAGLKRLLTSGDLPASASQSAVITGVS HRARPIMYFRYVQ*AKGSHV*RWY
7763	21664	A	7823	456	121	ASFFPIQYQGLGGTTPQEGGCG*GPI KMGYKRRPGGPHGGSKRPPTQ*KKSIFY NVLVFLYLRDKGLAIPTLVSNWAQVIL PPWPKVLGLQTRVTVPAGONILKENMFF
7764	21665	A	7824	294	457	LCIGFVILISYPFNIMENWYCRPGTVAHT CNPSTLGG*GROITRSRDRHPPQHG
7765	21666	A	7825	26	235	SVWNSQTGNKVFRTISW*IDQMRCIH LMEYSAIKRNEVLINATTTWLNINTIK LSKRSQTLKSWIL
7766	21667	A	7826	30	303	SYVGVVEFGSSGPTLPSWPHQTPRTYL NSVASAINLTQCPH*PEKIKKKKKKKK KKKKKKKKKKKKGGAPKKKG*KTP KTPGGF
7767	21668	A	7827	464	21	REPPHPAPADILILHFWLEL*ELISVV LNTRCVVICDDTPRKLTQCPMPRLLLQT EPL*VLFSNLGSGFSLSKS*MLVNF KGTDSRSLSFLVAVFCLFL*RWGLAMLH RLVLNCPQVILPPPPKLLGLQVEATT HEFHGTE
7768	21669	A	7828	372	205	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF
7769	21670	A	7829	463	313	DIYPERRNSKINSFAATWMLKELILK* LKNRKNIVCTHL
7770	21671	A	7830	449	266	VQCMRFLHVQAGL*LLPSGDPRASQVQ SAWITGVSHHAQRSIFFKRNNDCCRPD NTECT
7771	21672	A	7831	480	148	IELRLSHGAAEFHRPREWYIGFVKLKER DFYPRIIYPAKILRHEGEMKTFDPKQT LRHFINTRPVLQEMLKVKHQSEIKGC** ATNNHLKVKKKNSLW
7772	21673	A	7832	23	131	QRGNSKGYLHLMQEEIRKLEEEKNQL EGEIIHFYKMAASEALQTLSTDTDKD KHGKKQ*FL
7773	21674	A	7833	16	339	NTDTLGLSLMAFCRDGLAMLPRFLNITGL KRSSCPDLPNCWDYRHGPPYLAFLVLLK *TSLILLPYHKHRTCVFNVLTCTNFCG GVCPGMEILLCKVGYLSLKHHT
7774	21675	A	7834	355	70	KKTIRGSGSVLGFPPKGLFFFFFF FFFFFFFFFFFFFFFFFLQFLICQQL S*STEXTVHSKYLSFPFHCLIFCFPIL LCSTFCNGAHY
7775	21676	A	7835	494	282	PENGMIGGGACSEPR**HCTPAWAKER

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						DSVSNAKTIQNKKNLGN*HSISTAKAKN IIIS*YKSELKKM
7776	21677	A	7836	305	185	LVETCLTVRPLSPS*AIISPVICTYTF RWPEVTEESQKK
7777	21678	A	7837	179	191	LGCRKYLFLYINGGLKCLYIKCVCVCVCI YIGVYIGMCVYICITYILMAS*NQVTSF LSFFYVFLNLYR*IPVKVITVLNLRMTG LP
7778	21679	A	7838	466	343	LGRLRQENHLPPEGRGCSEPRSPCTPA WETEDAVSKINK*INK
7779	21680	A	7839	451	89	LRDT*SGVICLPQAWAVGAPPPASL PPCSLI.SDCCASWORSVGVQSPGGG YNLLVRRFLSLSEKRSIRVGVNFRSRCH LSPLSLTRKGNLTPCASFVRQCLALLR LAHGARTH
7780	21681	A	7840	442	164	AHTNGFSQCIRKSVTPDLMEEMKKAAH AI*ENPYEKRPKKEVKNNRNCPCMKSL AQKKHQA*KKASSLRAEQAAES
7781	21682	A	7841	494	359	ICMLPRVLNLS*POVILLPWPVKVLGLQ A
7782	21683	A	7842	577	224	IFFFFFNKILFRFPGNLNMGDTWVSPTPP LQG*TNFPQPQSQEVGLQKAPPPGLIL VFLSRQGFPPQLGRVGFHFPFPGDPPRP FKKIWSHPGGKSPPKKKKKKEIAEVLG AFRLR
7783	21684	A	7843	404	56	HTLSNVCCSSYLNLDFSLRGRGLIMLF RLALNSWAQEILLPPPE*LQLRLRQ ENLLSPGVQGPQGHNETPTS
7784	21685	A	7844	1	323	INTLLALLLIITTF*LPQGIGYINNSTP YEGGFDPSTARVPFCIKFFLEAITFL FDLRIALLPLP*ALQTNPLPIAMASL LLIIILALSLAYE*LOKGLD*AE
7785	21686	A	7845	419	159	FLFFFFFKXYVLSGCIY*YCNLFSS* QYFFFYVMAFRILFTFLFLHFYNYMF* CTYFYLSC*FEYICSHIIHYFIYFLHL ENF
7786	21687	A	7846	475	124	FFFFFPQPQKGGPPPPKNNFFFFFTRI FFQVFFFPQKNEFF*KTGKVFFF PEF*KIFFFPFGVFFFPVFFLSPPP SSSFFFFFFFFFFF
7787	21688	A	7847	6	189	FLFKRQQA LIDTVSPVALAGVQCNHSSPOP*PPS LKRSSRLALPRFWDYRCAPLCKAHSFNS NHEK
7788	21689	A	7848	20	249	KINFIVELTCSNTVHTFYVYGFDKCIL PTTOLFFFL*ETGFHSVARLECSGVIMA HCSLDILGSSWRPANFLNL
7789	21690	A	7849	101	398	LFQKKKKKKKKKKKKGGPLKKKPGGGK NKGGEKKKIFFLKGGEKKNPRGNFKKKT FPGGKKGEKPPKKKKSPKKKK*RGK GGKKSILCWVEKNLG
7790	21691	A	7850	87	226	GSLSPIMLVLPFLIHL*KNFLPLTLAL LI*YVSIPITISSIPPQT
7791	21692	A	7851	2	440	GATIRRLH*FFLFSGYTLHQTAKRHF TIIIFIGNLTFPQHFLGLSGMPRRYSD YDAYTT*NILSSVGSFISLTAAVLTDL MS*EAFASKRKVLVEEPSIDLERLYGC PPPYHTFEPPYLIISRPRKESNPAKLV

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						SSQFHG
7792	21693	A	7852	1	80	SSLLLTITIALSLAYE*LQKGLD*AE
7793	21694	A	7853	5	135	ATFLYFS*K*SLSLMLPRLVLNSWTQAIL PWWTLLKVLGCTFFDPL
7794	21695	A	7854	38	419	FUMVBLHSSGLGQVRPVLKKKKKKKDPNE GGSPKPNKQKQIFA*NGKPPFFFPPIP KKWGGPPGGGASPL*SHPSGGPGGPNKK VKISKPPCCPGOTPVFTKTFTT*PWGP IPEKGRKTVCPRTH
7795	21696	A	7855	398	61	FFSPFRPGGGFFPPFPKFFSPPTIFF GGGVNFFPPDKMVFLLKISPVVFPEL IRKKIFNLSPGFSWSPGQFF*GPDPKF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFF
7796	21697	A	7856	1	121	LDASGRLPSPKPKIKKNYNRP*EPK*T KICSLHSLPQOS
7797	21698	A	7857	1	332	TPPIARPAENSARGAEGRRR*ITIALQVC NKKWPPTKLCHIKKKKKKKKKKKKKKK KKKKKKKKKKLWGGGGGKNFFKGGKK KLGKGGFKKGRKKKK
7798	21699	A	7858	3	191	SPRHLLTRAAGIRHGGQTLGLLLTSGNLP ASAS*SAGITGMSHRIGPRMLDLLTLVS WKOHGL
7799	21700	A	7859	503	62	FFFFNLCCLSGLRHLKLPFQPLHL*N GGMVLSITLSIKSPSLRPSLSYSL**P REKIKWGGQVRWFMPINRPTLGGGGGG IA*SQEFKSSLDNMVRYPLSEPP
7800	21701	A	7860	355	86	YIKG*QMVNNGASQAGMTGYGMPRLIL
7801	21702	A	7861	336	225	PQLAGPVKTVRKVYKKEKARVPEEKK FKAFASFRKGRANRVPFIRAKKAKEAA KQDV*KKPPIPLAGGSPTRPPSQAHLF QNPDPNGNP
7802	21703	A	7862	465	170	GGFPFKTHFFGGERGGKYHRGKKKPPGH QRVNPSPKKKKKNWGRGNPFTLLCG GQAKKPPQPGRGCEP*KVPPNNSVLGK KKNFFPKKKKKKK
7803	21704	A	7863	495	275	RSFFFFFFFFFFFFFFFFFLVARK*YYFL ATKKKKKKKKKKKKKKKK
7804	21705	A	7864	493	70	PLTASISLPVNRYIAPIHRVVKIK*KS Y*KYLA*CLAQSKCPKSVCSHLGSP*LH FVPPPNPAEAMWTARQC*CIKRLGKGT LCVAHTYNPSCSG*GRIV*AOEFKAS LGNSEPLILKKERKESQAWLIPPIIPA F
7805	21706	A	7865	67	385	VARTIGMQHHAWLIFIFIIPVETGSHY VAQTSLEFLASSDPFTSPQSTWITGVS YSWS*PGIAHTCNPSALGDRGERIT*GQ EFKRS LGNI VRCLYKNNKNNK
7806	21707	A	7866	454	0	LSFFFFPLGDRVTLCCPG*SAVARSQLT VALNSWAQAAILPQLHKIVPPCLANF*N FF*QRITYMLHRLVLNSWAQVILQWPPT CPTAAQA
7807	21708	A		1619	698	PATSSSSSSSSSSSSAAAAAATAAL PPCRPPLRPQPLPAHEVATLAPWRG*K PSFTSSGKRWLTSPQTSKSCASCL*SM RASSPSSG*SKKGPLPEAAASVAACA VCWRVRAPIYVAATTAYTMAVGMHAF WEVINTWRMMSQAIRPLQWTWNSVTA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7808	21709	A	7868	52	187	S LDFN*RRCLTKLPRLVLNSWAQVILPPW PPKLLGLQV
7809	21710	A	7869	33	373	AGVQRDLGLLQPPPPGKFRFSCSLSPS GWDYRHAPPHLANFVVLVEMGFHHVQGA GLKLP*GDPPTLAYQSAGITGMSHRAR PGISVFLKLSFDPPFKLIIFRPGAETMP S
7810	21711	A	7870	100	119	VVFVEIVFPBGLLSPSCFHLGCFRIHLK AEF*FFVEGTGSMPLPRLVNSWAQVILPP WPPVVL*LOA
7811	21712	A	7871	471	446	LLWLFRVLNSWAQVILPPQPKVLGL* AYI
7812	21713	A	7872	449	33	FSFFFFFGLKKDLFFSPRGGGGGANS FPPPNPGKKGSAPPPLPKSV*NPAAP TGVFFFCGGGA
7813	21714	A	7873	334	41	PCPSLFFFFFLRQSLTLWPLRSCSGVIS AHCNCLPSSWDYK*HCPYLATAGPLL SQSELSYVTL*LOESRPLCPVDFMTFL PSLCFQSPNSTTL
7814	21715	A	7874	342	716	STGIFLPLVCF*DGVSITLAQAGVQWPDLG SLQSPSPRLK*FSCLSLASSWDCRHVP LLANYLYP*REGFTVAMMVFS*PCD PPTASQASAGITGVSHCAHPGMFFLNWP LKSCPSESAAV
7815	21716	A	7875	454	215	PPPARCH*PP*TLVHAEFKSHYSLI SSTQGHKHCGRDQQLPRKTRDCLSLVY LLTFPSLLSYDPAKLSARNTQE
7816	21717	A	7876	492	176	PCGGRGAGGNWGPWPHLRASASSRWAN ALQPHTRSSQAPAGTGPQ*GAQHLGQ LLCSISHQALAAPPGRAQDLQAMPPEP SPRPPLPMAAQ
7817	21718	A	7877	281	439	TWSIDL*HMAVLFFFSFLFAFLSFL SFLSFLFAFLFL*VPSFSLPQRSL
7818	21719	A	7878	507	338	LLRLK*EGHLSPPGRGCSRPLHHCIP HWATE*EPSPKTKN*N*S*MMKMKIN
7819	21720	A	7879	55	298	PCCLANFLKPL*PQSLMGLSLFNSW PQAVPLPRDPKKNQLLFFQCSQCLCP QHLCCKOHTFKILFDIEKHFERLEH
7820	21721	A	7880	145	292	YFGGQTVYIFCDRDRISLC*FVLLTSLV SNSWFAIILSQPPKVLGLOA
7821	21722	A	7881	3	203	LSLFLRLECSGTFTH*SFRLGSHRSP TSAS*IAKTMGRHHAQLRFFFPVPGV CVCVCGCVV
7822	21723	A	7882	324	211	AWMLMPVIPTL*EAKNGSLEARSLEFV WAHNETPFLF
7823	21724	A	7883	2	124	QHFGRLRQVDHLRLGVHQVQRQGHETPS LLK*INVYIYMT
7824	21725	A	7884	367	141	KCWDRRREPPLAAGLEFLNFCPEIVT EPCCPALAYF*NFL*RWSLATLPLRLVLN SWPQAILPRWPPKALGLQE
7825	21726	A	7885	471	215	RGMCVSHIFLPCVARYNITSARESLLKE FTECTERKHTHTRATHARATHHTHTHT HTHTHTRV*NSRSQPYCRVHACSAYLIG G
7826	21727	A	7886	462	204	RHSS*LGLEKCDWRYRHPHLLACTSSF* RKSDISLSDDELGTCKHKWVQVXSRAG SVGRDPCSGHTILAGFQOLGA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, ∅=possible nucleotide insertion)
7827	21728	A	7887	409	152	PVELALERPNQDPLRPGVLDQP*QNNK ISFFFFPPFKKKKKYIYICMVVHAXNPSY SGG*GGRIT*AGKFKTSLNNTVRHLYK K
7828	21729	A	7888	1	152	GVHVCCDCKICVCLCVGVGVHCLCVCV SK*VHMCRRGTIFGNISWEGD
7829	21730	A	7889	101	399	EIINIVFFFFPLPLLLFFFPWGRFKKQ LNPEFLTNSWKKHKTIGGKNPMG*KK AITNPQKKGRKRSFS*NAQPTQGGKNG QNSQSKAVGALTAH
7830	21731	A	7890	478	142	RFSKKKKRGVLNFKKKAFFSKPKPVF KKKKLLKNPFFKAKKQFFKPTPTPLFR EKFPFGPPKKKKRPPGLFKNN*KGPPW PREKKRVKKKKKKVSHYNNHMPISVH
7831	21732	A	7891	497	320	PFWKFEFEWFSF*LHKYPPYVCVVCV VCVVCVDFDRFFPKPAPSPQSHFGINLS FLI
7832	21733	A	7892	217	23	IPPFKKFF*EMGSHAVT*ARVVQWVHNA SLQPETCGLKGFSLHLLPNSWDCRSVPS SSARRQSH
7833	21734	A	7893	652	470	SSSSSSSSSSSSSSSSSSSSSQFERK TRSAPOVBGGKPNFCSLEAPPGLSLFS CLNF*RSWDPPGP*PHATPKTRAGDGL LCATHRRARHCTPGLRFPFLFLL
7834	21735	A	7894	25	178	GLLFFWRDGLVILHRLVNFVSSDSP ISASQSDYRCDDPCPACPLIFW*LLKH SF*FFWRDGLVILHRLVNFVSSDSP ISASQSDYRCDDPCPACPLIFW
7835	21736	A	7895	104	451	ILSFNTTWEAEDMLSEISGQTQDTRYC MILLVESKVNLRPGMMAHANPSTLGG *GERIS*GQEFETSIVNIARHYFYKRF KIKSKFKKIVRKQSKNVRRWLEARNK GRYG
7836	21737	A	7896	510	335	SCIVSLHRSWDLNHWVPPFLANF*IFRKG GVLPCCPGWQIYTFQIQIFPLSITPVAF SG
7837	21738	A	7897	37	260	AGNSQNGGGGACSPWRHCTPA*ATER ESVSKNKQTKFLCSVPYFESTHFTNE ATGAWGEVKVALGHAASW
7838	21739	A	7898	35	456	THTCGGIRKKLTNRKNQK*SQOKPSAP KEPEVKNQKKTNNKKKKKTPTQIQPT KKPFRNPNLRVFTFVITQNKPTTRGRK TFQVKLFPNPNCLGNKPTLLPRGLQ KKKKKIPFFYSHPPPLAQKKKATPWQNG LGFT
7839	21740	A	7899	494	149	PARLLSLHSYEVKSVLPKEEGLNFFVQ SVAHTPTSCIGLEEI*LLD
7840	21741	A	7900	494	114	GAEGGPLSKKKKKLLPDYHTGPMISL YLWPFSLNGHTLTLMCAHTHTHTHTN H*LSRVGLPVLKPGQYQANGNRWSP*YN IKE*PKTRVMPVTPOLRNDGPMLTFWC SSRNSFMHVLGKL
7841	21742	A	7901	19	454	VMCNSSVSLHTHTHTHTHTHTHTRSW VGHMPLVLSQEAAGRLGGSSLRQ RAMIVPLHSSLGNAAPCV*HTGSCCVS QAGVQWHNHSSELYPQTPGQSSLSLL SR*DYRHVPHPFASCVCVRVCVVCVVCV CVYDGRGITPH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7842	21743	A	7902	3	393	DAWDPLNPLVNLVSPKRNSSLDTRKKP CRESKKFNTHSRPKSSHQLRKRSSSTPT T*KIPNI*LNSSTPSRAKKRKKKKPKKK KK*KNSQKKKKPMRRTKKKGGGLKKI LGGAKPFGGRKEKIFFF
7843	21744	A	7903	424	139	LFFFFFFF*G*GVFIFCYVGQVGL*LL TSGDLHISASQSAIRGVSHHAPPLSLI VFIISQCVGLNHTVHLQYIQCSFVHHF LINOEKDIIK
7844	21745	A	7904	1	181	SO*LY*LLAANLFLIT*IGGQGPSYPT IIGQASGLYLTITLIIPTICLIESKI LKWA
7845	21746	A	7905	3	281	HAYAHASATFFVSTCGHGLHDHMSAPL TMCPIRQLIFHFTSKHFGFOAAA*YWH FVDVV*FLYVSIY**GAVLKEPWGGS
7846	21747	A	7906	1	84	PTRPLTMLPRLVSTPGLKQSSQLSLPKC *DYRCEFACTAYS*LTMLPRLVSTPGL KQSSQLSLPKC
7847	21748	A	7907	3	392	DPDNYTLANPLITLPHIKPE*YPLFAYT ILRSVPNKLGGRLALLSILILAIPIIL HISKQSQIIFRPLSQSLY*LLAADLFL T*IGGGRPSYFFILIGQVAVLYFTTIL ILIPTISLIGDRILKWA
7848	21749	A	7908	2	231	GCVEKGLSHC*WECKLVOPLWKTVMGF LKEKIDLPDPAIPLGGIYPEKNFTL GPLHSGVRSRRLKPGYSRV
7849	21750	A	7909	529	297	KIFIGAPVFCPPHFFFLIDPF*GVEKI FFSFVULLPFGFFFLFLGLFFFFKLF FFFFF*FKIDFFSKKGVGK
7850	21751	A	7910	410	61	FNNQAMQVVPFFPFLKIFFF*RV*FLE GGWSNLSPPPK*GPSKPPTRVL*GPP* GRN*NGFPG*NWAPHRF*RAAPFFFF C*DRVLLPRLVNS*AQVHPWPVKVL GLQA
7851	21752	A	7911	512	314	ANFC*LFIEFGPHIGQAGLELLTSNP PALASQIAGTGVNLRFGQDFSSYSEN PLVYGLSYIA
7852	21753	A	7912	1	264	SSTTTLLSRT*NLK*LTPLIPSTLLS LRGLPPLTGFLPKWAKKKKKKKKKKK KRGGGGKKPKKGGGGETSSKDTFFPK KGGP
7853	21754	A	7913	416	129	FFFFFFFAPPKIKTPPEFFKREYIY* ALSVOGSUCKALYIHFRISSOYPC*LG FFFFFFFFFFFFFLKGLDLLSAYCVPG SVQALHTLSH
7854	21755	A	7914	397	34	IFSNLFFPQKMKTFPPFPPLKLYFFSET ALFFFLVFFPFPFPKPIFFFNPNPKFF FYPS*KKKFFFIIPVYFLAPPFFFF*AP PFFFFFFFFFFFFFFFFFFFFFFFFF FSVSKQPLFCLKI
7855	21756	A	7915	396	86	IFLSPRK*GFFSPPFP*KFFSPKPLIF FGGFFPKFPKPKNFQNPFGVFFYP FKKKKFFPPLNFGPPRVF*RPDPFF FFFFFFFFFFFFFFFFYLVWC
7856	21757	A	7916	351	112	SFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFPI*KYFVIYISLSLIPFCKFLK GRECDIHFCDIQHSYKYLGHFKCSTND RQMNK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7857	21758	A	7917	445	2	PPPPPPPPPPPPPPFLSVF*LHYAEGIG ASPCYIMLGYNSSFPCCGTIS IAPGENF YRLYFISHASADAWDRFLDRYRGGIN
7858	21759	A	7918	2	407	PPPPQVYENIWRITFFEGGGLHIFFEQK RFCFYKTYTNYIKTLPIKKKNIPSLAHI KMPVPSRIY*TPPLPFFFFFFFFLFFFF FFFFFFFFFFFFFFFFFF
7859	21760	A	7919	107	11	KMWYITLECYSAKKKKKEILLPDTTLI NLKDIMLSKISQHRKTHT*FKT
7860	21761	A	7920	1	70	FFFF*AAESCSRIKCSGTTIAQCNPELP GLSDPPTSAT*VAGTKGVCHHTQLRIF IV*LSGRILLQDQVQVHNHNSV
7861	21762	A	7921	123	260	GICARKEFGAVAHAYKLSTLGG*GGWIT *GQELETSLVNMVPCPL
7862	21763	A	7922	184	399	LHLMLRVLKKKKKGGGLYRSPRGAKVN PALQRDLSDLIGSRILSNLIGFGKAPHS WGG*APFAATGLHGLHVIIGSTFLTIGF IRQLIFHFTSKHHFGFKADD*YHNFVDV A*LFLYDSIY**GSRILSNLIGFGKAPH SWGGTKWDNPPDPMKSS
7863	21764	A	7923	2	407	GRVGM*EAFASKRKVLIVEEPSINLE* LYGCPPHLHTSNKKPPHTKKQKKKKK KKKKKKKKKKKKKGGGLKKLWGGPK NTGGKKKNFFFFWGGKKKNLGLFKKNL FWGGKIGITPPPOKKNPIGEKKF
7864	21765	A	7924	1	398	PTRPPTPTSSSRAPPPPPPPPPPPPPPP FFFFFFFFPPPPPPPPPPPPPPPPPPPP FFFFFFFFPPPPPPPPPPPPPPPPPPPP FFFFFFFVSAALFPKKKNFFFF*FFRG *GFYFFPPLYPFI CGGGGVFFPPPPFAGH NIFFPPIPKKNGIFKTLRGKGG
7865	21766	A	7925	2	335	NLTFFPQHFLGLSGMPRRYSIDDAYTT *NILSSVGSFISLTAGILIFMI*EAFAS KRKVLIVEEPSINLE*LYGCPPIVHTF EEPISKKKKKKKKKKKKKKKKKKKKK
7866	21767	A	7926	1	328	RTRGRTRGESNPSLRITQNSPCHLSHPIL KKKKKKKKKKKKKKKKKKKGGPLKKNPF GAKI*PGPKKNLFFKGLKKTPLGNFE KKPFFGGGKKRKPPOKKKTLKEKKKF
7867	21768	A	7927	27	226	LSR*KM*NKSHIYSFEKKKKKKKKKKKK KKKKKKKKKKKKKQKKNRPKNNGSEN GHPSKIFNL
7868	21769	A	7928	398	2	GGGGCPGGRGR*NPCHKGRDPHPK KKFPRRRKNRGGGGRKSPQKKKAPQ KKPGRGFKRAPQKKKTTPPRKKGPP KNFKGAPPPPPPPPPPPPPPPPPPPPP FFLGILARTTTTTNDKNHR
7869	21770	A	7929	3	156	HASAHASAPV*SVLMTAVLLLSLVLV LAAGVTILLADRLNLTFFDPA
7870	21771	A	7930	405	249	ASAHASAPLV*SVLITAVLLVLSLVLV AAGITILLDRNLNTFFDPA
7871	21772	A	7931	921	699	DHPQHSSEITLSQMKMTMSQCGAHL*S QVLRRLREDCLSPGSSQSCSEL*SHICT LACIE*DLVQKKKF
7872	21773	A	7932	423	259	HLDSLQPLPGPKSSYLCLPSSWDYR CEPLRPAQRGILMAQSRLLTSKNG
7873	21774	A	7933	395	35	PRVKRFSCFWLPKSGRPRAPWQVECF PFC*NGGSPFLPGGSWTLAPNYSPPPA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, =possible nucleotide insertion)
						QNGLVQALRFPGPPTFFFLIFFTKAPWS WPFPGGKKKKLSPKQHSERHLHHKYIR LLSQHGM
7874	21775	A	7934	1	118	NF*IFCRDNGALSPQLNSWPOVILP PQPPKVLGLQA
7875	21776	A	7935	322	383	KKRTGLIKISTLCFVKNTFKTKKQAPE RKKKVPILFYSYKRPVKIYKLLFPFCRK KIKKIPPGPFTSFCLSLPSSWDYRHP PPCPVNFCCIYNKNGVSPG*PG
7876	21777	A	7936	3	131	GPHRVGGVQL*LLTLGDPPASASQAGI AGLSHRSQPLTWL
7877	21778	A	7937	334	146	HPQGLNT*NMVSSSGAKHSRSLSPKFW WDCRQEPCCPVMFLKRGINHALYSPSR KLLHFL
7878	21779	A	7938	2	371	SEFGAGYNLLVGRF*SPSEKCSIGVGV RFSRCLSLFSLTSGKNSLTPCASRVQ CLALLWLQGVHLPLSCHLALPSEMNV PVPQMEMQKSPFICTADAGSCRPFLFL GHLGSSPQSKL
7879	21780	A	7939	2	95	RLNLGGGCGCEP*SCHCTPAWVTKRNSI SKK
7880	21781	A	7940	1	191	PTRPSTQPLGK*FHSLSLFKSWDYRCEP PCLAVILSTPCNMSMPNIFAAYS*F GLYSSRW
7881	21782	A	7941	127	383	SKDCVRIVLLRAQAKAGSYRTVMNCRPG AVAHTCNHSTLGRGGRIA*GHEFTSL GNIVILPLYKKNKKKRGARLREPNLT P
7882	21783	A	7942	235	3	KNILPGYFCFLREKPPPGLESFLSKK KKKKKLARHGVAPI.LGRMR*EDRLRPGV QGCNELWNCCTPANATEQNP
7883	21784	A	7943	3	225	EHGSLYPPTPLGKSSYLSLSR*DYR* AAPCPANFFIFNPL*REDTLMLRLVSN SWTQAVLLPPKVLGLLV
7884	21785	A	7944	2	232	TLLPDNLSOTIYNNKKKKKKKKKKKK KRGGPFKKKKF*TRGGGKKNFFRAPKI FFGGVRLKGGGKKPGEPTN
7885	21786	A	7945	394	41	WCRWLETWAGGSGAVPPPPPPPHSSSS WDLALQSGGASSPSPGAVAHACNPSTL GGQGGMIT*VQEFETSLANMMKPHLFSK KGPVTAVAHAPAKAHAMNCTPTMHMTOH VLHVL
7886	21787	A	7946	405	100	FFFSPPRSSSLEFLSSFFFFFFFFFFFF FFFFFSTGLPVYWSPTH*SLPVPRIFFF SYLWQTEVETMLGTE
7887	21788	A	7947	391	212	KEMQIMPMR*HLTPVPMVITKSKKAC WQCEBKTLAHWNKKCGTAETGKLAG F
7888	21789	A	7948	106	301	LQLPITQLVHSHYFMKRIYRLGVAVH TYNPSTLGGQGRIA*GVKFTSLSNTA ROKKKKKK
7889	21790	A	7949	342	208	GLGAGHTYNPSTLDN*GGNITSGQEPD TSLANVMKHVVQGGF
7890	21791	A	7950	391	21	RQGFMPPLRLISNS*FKGSAHSLPKCW EYRSEPPSLATWYVTLRHFCSLTLLGQ GRSKFHKWESRLBGLAKVSSLRSSYC SSLRLILGLEILLSPLLFLETGSGSVSQ AGVQPLCPGLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7891	21792	A	7951	146	355	EMRQTQNEIVTKSSNETVFCNKIIIS LGVAHACNPDL*GQGRIT*AMEF*T SLDNIARPCLYOK
7892	21793	A	7952	289	327	KGTFPLPERLKWKQPPFFFFFLKRESLF LP*FWKQCGRPPLFFFFFLRDSVSLLP RLVSHSWP*VILLQPPPKVLRLLQA
7893	21794	A	7953	861	586	DRVRSVAQARLQWHDGLSLQPPPFGE*Q FSCLSLLSSWDYRMTWTFVVF*WRWG TCVAQAGLDLSSDNPPALASQSARIIG ESCCVLLK
7894	21795	A	7954	402	52	PRKVIS*PHDLPASASQAGITGVSHR TRPSFNFSYIETAITETKSLQSPGMIN *SLPSGMVGFKPHSFHISANFCEALAVQ QTLGEVPGHAPLSPPRQEPVPCPKVKCL KTALK
7895	21796	A	7955	259	3	YNTKVLSPFILL*TFLKHLWLGAVARAF NPSTLGGGGRIA*GQFKTSLGNIERC RLYKNLKLFLSEGLFLMAWRGAKRVTR G
7896	21797	A	7956	171	386	LPRLFLSLVFTTIEKSRPGMVAHTCNLS TLEG*SGWIT*AOEFETSLGNMAKLSLP KIQESASLITRSQNK
7897	21798	A	7957	397	283	PQPLPFGLRQFSCLSLSPKC*DYRRDSAR PAKKNPTFNK
7898	21799	A	7958	169	324	GTHRVEMCSQWLGVVAHADCPSPGLGQV RKIT*AOEFETSLGNIGRPCLYLK
7899	21800	A	7959	290	397	DCSSCCSPLKGR*RG*AQWLPVPIPALW EAEAGGS
7900	21801	A	7960	496	298	LSKRTGSYLVAQSVVYWLFTGTIMVHDSL KLLCSSSPVVSAS*VAGTTGAHRCEVL TTFQPDVYRL
7901	21802	A	7961	404	174	PQPKQGSFF*KKKKKKKEIDHILSHKAN LMKC*RIKII*TMLSQNEIKLEIIIKR QLLKETFLPMKKYTIKRLS
7902	21803	A	7962	25	99	PGLFLSS*HQVILLPWPFKVLGLQL
7903	21804	A	7963	436	106	GGGKSPPPGNGWAPPNGPEPLFF*KKKK XNPGGGCGRFPFPPPGGRKKGVYPCGG GFYLTNFPFPPPPWGGKKKFFFKKKKK KKKKGRICAIYIILFITSINFKKAFI
7904	21805	A	7964	212	395	ERERKERDRGEREREREEREGRRKHG GR*GGREGGRHPRGAEDDPDRAGRATDK RTGAL
7905	21806	A	7965	344	345	FSDCYKRSSCASWTWTRLAHHPPARP GAAPSPKRKWDVFAVNRNPPSRRHPCAT PRPAPGATGRPSRVKSTAFQTMLTPQR DHLPLPIPLSQPPSP*PAPLVNR
7906	21807	A	7966	397	298	RQFTMLPRLVLNRSRTQVI*LPWFPTVLG SLSIF
7907	21808	A	7967	92	268	IKMSLCPNFFFFFKQNVGPRAGAYPCN PTILGGQGRKIT*GDQLKTLVNMKGHF FY
7908	21809	A	7968	257	107	RTHTHTHTHTHTHTHTHTHTHTHCENSRT TKNIANNCS*LESQRNNGKCTYAKF
7909	21810	A	7969	413	12	PPFPPLLTWECFFPQIL*FVGHSAAPL FK*LKIIPRPPFPFPFGIGIAPP*PKIFF PPGFSLPFPVKLPPEGEKILFPFPKKKKY PPFPQGS*SF*PPFPFPFPFPFSTSAK KSKNQLFI FSPFPFNPKYNT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7910	21811	A	7970	399	212	TGVWNSHSLQSGTPGLKRLFLILLIS IWDYGCMPYLSFKN*FCTKGSGCYAE ADNVIL
7911	21812	A	7971	584	424	RPRRENRLNPGGGCGSEPRSYCTPAWV TE*NSVSNRNKNTQNPFI FSCCKQFD
7912	21813	A	7972	105	1	PSMPQLSHL*NGILGRVRLTPVIFALW EATGRS
7913	21814	A	7973	363	28	SSSLGGHPQLWFHTLKLRLPVTVSVA*NK LCKDIEKKLFFTIALHNKFLRKLTRDV KILFNNK*IKKEGNEF*NILCLWIERI NINKVPYPSKVMYRSNTLP IEVAVFKSQ
7914	21815	A	7974	404	250	FFFFW*R*GFTMLPRLVLSNWTQIHP ALASQAGITGMSHHAQPLSIIIF
7915	21816	A	7975	2	60	FSCCLGPFPCWDYRHAPHNLNFCRQGV LY*PQVILHLPQLPKVLGL*ACTITPG
7916	21817	A	7976	325	81	KTHSLLEGFGFLLQPLLPSPIPHAP TPHLIFLLLLFCF*FFK*RGKQGLTTL PKLISNSYSQVTLTPQPKVVLGFOA
7917	21818	A	7977	406	282	QWRDLGSLQPTTPNFK*FSSLSLPSNWE TKAGRSREPGGGD
7918	21819	A	7978	382	221	DCIISASYLQKNFFFLGDKVLLCHPGW SAVA*S*LTVTSKRVHFYSSEISLY
7919	21820	A	7979	423	29	FLW*RRGFTSLPRLVSNFVAQGCLEWL PKVLGLQA
7920	21821	A	7980	3	238	SLAFFVETGSHFVA*AGLELLSSSNSPA LASQSAEITGVSHDTQPE*GYSHM*POY PYQLRFNSDITI LS NVLFVPMF
7921	21822	A	7981	324	128	WLSVSPYTFELSLVGYEFVHDVI*TL IFVYVVVSLFCFLWFLLCMVFVVFVC CCFLSVFCI
7922	21823	A	7982	1	86	NLTMLPRLVSNWAQAICLSWPPKVLGL *AQAICLSWPPKVLGL
7923	21824	A	7983	1	137	RANFCIFVETEFCHVAQAGLELLGSG DPPTASQAQAGTGMSH*D*PANFCIFF VETEFCHVAQAGLELLGSGDPPTASQSG AGTTGMSH
7924	21825	A	7984	2	277	PRVRSQVRVYQVY*NLQHVHPDSTNL GIYLTDLPHVWNNMYKVFAAUSVETIA KV*NPCLTRRQCNKLP IHAMEYVYTIK KNEDGRA
7925	21826	A	7985	211	42	GPCKWPRGPGENLGGFFFFFRRDRLD TMLPRLALNS*VHAILPPQPRKVPGLWV
7926	21827	A	7986	409	183	LLRLK*SSHLSPKWNDRCEPPCPAIF FKRKQILKESFPGENTCCHLNSLEVLIK NKRRTCYNFPNTLAVLKNM
7927	21828	A	7987	2	194	RFFFTQSRLLQFPFQPK*SSHLSQLSS WDYRHVPCLANFFLFWYFLOGGGAFL LKLKFLFK
7928	21829	A	7988	483	209	SSPSLGNFCIFSSGGVSECFWGFQTFD LVNIWPPGPPSLVFFFFRDEGLSMLLR LTINFA*QVILLPQLPE*LGLQADRQVP LYPAEVF
7929	21830	A	7989	164	29	KFWFWLGTVAHANCPNLSILGSGGRIA*A QELPESLGNENGRPCLYK
7930	21831	A	7990	3	474	PTRAPLRAPFETIVQSEEFKSHHGFEEA AA*YHFPVDV*LFLVYSIY**GSPPPP PKILIKNGAETKKFFF
7931	21832	A	7991	469	323	VETGLHHVAQDGLPTSGDSPASASON

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
7932	21833	A	7992	469	13	IGITGVSHHA*PDFTFLEOF KGDIVSSSDSSPSCGGLFVPGAS*LLCL FTQALAMVGARRPFSMLPCSLISDCCAS NERGSGVMGSPKPGVGYSLLVCRWLRLPL EKRTIKVGVTRFSRCRLSQLPLARKGNS LTPCVFVVRHRCFGSHSVGCTHCPAPAVR QAPVK
7933	21834	A	7993	15	439	IASGRFFSIRKFFLVAITFLFDLEIALLL LPLP*ALQTTNLPFLIVMSLLLIILAL SLAYE*LQKGLD*TEPNKKKKKKKKKQOE KKKKKKKKKKKKKKKKKKKKKKKKKKKK GGNNMFFFFFWGGEKKTGGFLGENLFLG GGK
7934	21835	A	7994	392	186	YFYIINNFFKKKIFI**IIFFLKKKFL *YSPKKVFLFF*IFFFFPSSSLFFP SSSSPPFFPPPPPPPPPPPPPPPPPP
7935	21836	A	7995	11	386	TWEVEVAUS*DHATIALQFGQOE*NAISK KKMTGRMFIEVSFIIASSWKQKCS*TG E*MKSLWYTHIIEYYLTIKENKVLHEV SRLTLIDTGRERSKTEYTLNPIYTNL RIAKLGGCCGSHL
7936	21837	A	7996	3	186	DSECF*RGSCSTQAGVQWCDRGL*PQ SPQLKRSCSFLPHKMDHDEPLHPAGV AVLN
7937	21838	A	7997	316	649	RDRSFFFEBSRSVAQAGVQWHDLSLQ ALSSGFMPFSCSLPSSWDYRHPPPCPA NFLYFLVEMGFQHQVQNGLDLTS*STR LGLPKWLGITGVSHMHAPQDGGFHVG
7938	21839	A	7998	468	336	RRGFTMLARMVSI*PSDMPASASQSG TTGVNHHIRIHRSL
7939	21840	A	7999	464	283	TLCGGIRPTNIMKGNLLYSKIGLVNVL LPKNPRRNQNNV*PNTWALQPSHVDI
7940	21841	A	8000	46	487	RQRLSLQKFLFFVQCFARHGGVYRG RQASLSCGGLHPVRVSQLCLPT*VSAM AAAPHPASLLPCLISDCCASSEQGSVG VGFSKPGAGYNLLVCHLLRLLEKRSIRV GVSQFSRCHLSWLPLARKGNSRTFCTFR VRKCLAL
7941	21842	A	8001	295	1	TQFWGTRKRLPLKRRKKNSGDREWRWLC NSVTILNATTMYTSEWLPGTVVTHCNP KTSGG*GGEIA*QBFKASLGNTA*SWL YKKILKISPLWQT
7942	21843	A	8002	144	317	ELFYLKEMV*RPGPVAYACFPSTLDGRG GRIT*AQEPRTDLGNITARPVCYLRKKK RG
7943	21844	A	8003	69	291	HCVWTMIFIVIKYFYNPNQNNSMRYYS HFMDKETDVQSD*MT*RLGAVAHACNP STLGGRIA*GQEFKTS
7944	21845	A	8004	3	176	IVAHSSLTGLKQFSCFLSS*VYRNM LPLRANT*FFGNRVSLSCQGS*TLAS LGGSSSSPASACQVAKSTGTCYHANLII DELVGTSCRLAKAGHLCCL
7945	21846	A	8005	419	178	NPPPKKLLSSSSSSSLPHLWGTGPF PPPPP*NPPPEFNFGAPKKKKKLSPPRA EKLVPFGPPPPPPPPPPPPPPPPPP
7946	21847	A	8006	429	225	QPLPFRFK*FFCLSPRR*GHRHRPBP FNFFFF*YFLRWSFVLVAQAGVQCMDLS IYLNFWLLDF

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7947	21848	A	8007	756	224	PPRHQFQHVFPFLLHFSTFSPAPFKSHA AAPNSNPPQAHAPPAPAPRAHSPSPPP RGATPFPFPPFSPFLAAVGRAPIFPREP LLPSSSSSPFPF*IGEPGPFSPFPLLKT RPPK*N*GPKKGFPPFPKKNWFL*K GPPFPFPPFFLRQSFTLVAQAGVHKT RLHLKKKSN
7948	21849	A	8008	170	559	SSHLSQSSNDYRSQWMAHTCNPSMLGG QDGRLT*AQKFOTSLGNTVRCHFYFKKY PKNKIFFYSPFINTNPKKKKKGGAVLK NQSLRPRAGKVLVPLWGHILQFRGPRPK NGGTGKPGGLPNLLAPR
7949	21850	A	8009	1	662	RTRRTSRWYMPVLPLSLSHWGAGESLGP *KMWVD*APIAPLHSTLGDKMTLPDIKK KNGETVANTSPSLSTTAKPAKFLKAKKD QLMRDLFLPKTPKKFQMSTGLDARSKRW LKIWRRHGIWPLKNIGPTEDVQASAHG GVEENMTSDIEPAJGHDRPTEDVQVS AHGGVEENITSDIEISEAKDHHLVEDL SESLSVCLDEDMTIGSQWKPICLS
7950	21851	A	8010	377	2	NFFFFFPFWGFFFFFLGPGFFKFFVF*IF PFFFPFRNPFF*FPLGVPLFFKK*IFFF PFSIRFCFFPKKFFFLILFFFP*PFFP FFVYVDFPFFSFLYIYFFFYVSLFFT VLIISLIYHFAPA
7951	21852	A	8011	1	363	PTKPLF**RGCFMTLPRLLNSWPQVIC PPRPKVLGLQT
7952	21853	A	8012	278	39	FXXXFFLSPPXFLIFPFFFFFFFFFNFFF FFFFPFFFFFFFFFFFFFFFFFFFFF FH*DQ*FSNFDTPFTFLISNII
7953	21854	A	8013	79	412	MNECLLKGKGGFFPEQCENLGLC*FL KVP*DSIDLGAHAYNFSTLEGGQER ST*AQEFKTRLGNTPCLYQKTHKK TKKKHPHGLCGWANGPTLYLGGVGTKIT
7954	21855	A	8014	277	19	FGNIHNFLLIGSRSVTQAGGQWCHHSL *POTPVLKQSSHLSPSSWEIEAAVSQV RITALQGRQSKTLPNGNSQVLRADARR SI
7955	21856	A	8015	1	130	ARIVSIS*PCDLPASASQAGITGISHH TQLAHNTLKASPTLF
7956	21857	A	8016	4	417	RLMPPLHIANPLFF*RHGFTYVAVQGLKL LGSNDPSASTSQSGITDVSHCTQPHLL KSSHSTFPLKTLDSMATNCSWDKVHYLF TACRALLPCPLPSACFPSSLQVPSVFTC CVPATLITLPLPRLAFEHVTLCPFL
7957	21858	A	8017	388	158	CUTWASNCINWICPFLS*INSHLCNEYI VLI*GEIYNVCISITLYCIYMCVCYIISV CVCVCIVH*TPYLIHKCLI
7958	21859	A	8018	154	382	GIKRFGAVAHNCNFTLGG*GKWIG*AQ EFTSPGNMVKPQIYLKKKKKKGGAVLK DPSLRPRAGKIVIFVWGPLI
7959	21860	A	8019	396	237	FFFFFW*G*GFTMLPRLVNSWSAQVTH LFWPPKALGOVRTWVGPLRLANF
7960	21861	A	8020	412	168	GNLLGSPLPNGVCKNKPTLF*KKK*SL AVLPKLVSNFWP*MILPWPFPKI*GVQA RAPPPQILKKKSSHFNHNSVNSL
7961	21862	A	8021	1	124	TRFLHVSQAGL*LLTSGDLPASASQSD YFIISPAKILFL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
7962	21863	A	8022	3	200	HLSPYFFFKDRVALCHPGWSAVVQ*PI VTSIFWSSC*KLTSVRRWRPFWLTR*N PVSTKNTKN
7963	21864	A	8023	3	132	FLFFQF*FMRGLMLPMLGMNSWA*V ILLPQPEWLGLQA
7964	21865	A	8024	3	187	VGGAGLEPTSGDLPASASQSASEITRMS HRAQTK*DFIGSFSEFS
7965	21866	A	8025	405	231	SDKWIKKMYIHTTYY*ALKRKEILTH ATTWLNLENILLSEISQSPKHRYVIFL T
7966	21867	A	8026	175	382	GKRIFFYPPOEGGKTPPQTGFLFFFF LKKK*PGGIGGARFSPLGGVGRKNSFT LKGGAAILNKGPPSLPPGKRWAPPQKK KKKGQAWMLMPVIALNEAEAGRS
7967	21868	A	8027	83	374	GDQVWMLHACNPSTLGGQCGRITWDRE FETSLANIFFPISLTKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKASSGGVS*K KNFSPRAGKEIFF
7968	21869	A	8028	382	148	SPHCSLDLVGLQSSSHLSLPST*DHRCV PPRLAIFSFALFFWEATTTTKATMLP RLVNS*AQAILLPQPLKVLRL
7969	21870	A	8029	88	208	SGSV*ENNPISAWNLQSTIPATQAEV GLLEPRSSSA
7970	21871	A	8030	1	283	NKSRKKAIQWTEKMKETEMKMLNQL PNSEHAMIOMMKIEMKGRMKIKF*DK ESKDDRKDEREDRDEDEPTPERPTS RDDSDDEDRDEGKNEDEKRDSDSDDE ADEDTQDDVDYDMDAHKADEDDDEDE EVAEQMTKKKKKKKKKKKKK*KDKRK DEREDRDEDEPTPERTSRDDSDDE DRDEGKNEDEKRDSDSDDEADEDTQD DYDMDAHKADEDDDEDEDEVAE
7971	21872	A	8031	2	139	LQTLFLIAF*LLASLANLALPPTINL LGELSAQFAVIGMILY
7972	21873	A	8032	80	324	YLHFYFVR*KLGLDTVAHTYNPSTLG DPERRIA*A*EFKSLGNMVKPCIKYKKK KKKKKKKKKKKKKKKKKKKKKK
7973	21874	A	8033	299	158	GNQPGASHTCNPSTLVGGGRII*AOE FKASLGNMVKHYLQKHKN
7974	21875	A	8034	416	60	AQWLTSIIPPL*EAEVGGFFEPRLSPA WATE
7975	21876	A	8035	398	271	FYFL*DEVSLPLRLVSNSTPAILPPWP PKVPLRHEPPRA
7976	21877	A	8036	385	151	FLYFL*RLGLTLLPLQVSNISSDDPT* ASESAGITGVSNHAHLRICILTRPGNS SH*NVRRAGLODTQSALIPPG
7977	21878	A	8037	3	406	PASAS*VAGITGTHHHAQLIFVLVETG FLFFFWAVLFFKTKNGPPGGLFFFA APPALGGGDFGGQGTSPKGLVGLGT RGGAAPKPLGAKKEPSHLLGGGAQNL KPRGQKGGFYFYFLARDFLLG
7978	21879	A	8038	428	20	LANO*WKPPSNPWETKISPKKKKGGPGQ GFFPLTPPLWEAPKARKLGSFWLGR*NP LFQPKKKFFGGGPPFPYSLPKLSPK NGVTPDEVPESHKPKFPSPDPLQK*TP FPOKKKPKRLKGMFLHGSTPQSL
7979	21880	A	8039	3	194	QNKISQVWYTFVILATWEAGGESVPE GRQLRW*AKTAPLHYSQDEKYLKASVDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						YCLTSCI
7980	21881	A	8040	415	96	LEPLKYFPLDANKICNDSWEEVKIST LTGVKKLIPLMDNFEAFKTSMEKVTA DVVEIGELELEVEPADVTELLQSCAKLE GMRSCFLWMSKESGFLRWIYSW
7981	21882	A	8041	413	254	PGFKQFSCLEPFKR*DYRHKPPCPASKY FKINYLRLNIVRSLLTLN
7982	21883	A	8042	409	102	GFFPPGPPFF*FPFPGVFPFPPPPNFW *GFGPPPPPLE*FFRGGPKKIHFPPFF LWDPPLFFFFPFWPKKTPPKKARSLKIF FFLGGKKIPNPPFFFFF
7983	21884	A	8043	414	153	GRGWATNFYFLILK*FFPIFKKFFFF HLFFFFFFFFFFFPPPPFFFKVIF LFTLVLTCPQTSREAEFDPKVCVSLK ML
7984	21885	A	8044	401	292	NYLPPQ*KKKYPQGGFRKPIKSPPPC PPPPPPPPFPPLNIPPPQKGKFPKP KYFFNPPLPPLFLLKPPPLFF*GPKK KNLIFHPSPSKKICPKFRGPP*FFFFF F
7985	21886	A	8045	370	14	TPPPTKTPFFFLYPPPWREKRGFF*KA NMSPPVKKKIPLPPYIL*KGGRYL AKLSNLKGSYLSFCPPPLPSLPLSL FERWGLTILPKVLNSNAQMIPLPLK VLGLKV
7986	21887	A	8046	395	268	PPFFFF*ETGSCSIVQGVQLFTGTILV LISVGLTCSISDL
7987	21888	A	8047	379	98	GPAENSPPLGSEETPLGYPGKPRFF*K NKKINPARGPGPVVPPPPQG*AGKRPLP PRRSGOLTQNGPPPPPGGKKKPPFKKK KKKREPAIC
7988	21889	A	8048	369	177	ENTRGGFTEFFFFFK*NLARLSRLC HGTISAHCNFRLLGSSDSLPLTSDNDIGQ INKSLFA
7989	21890	A	8049	1	128	ALGLVAHAYNPSTLGSQKQKIA*GREFG TSLGHRAPCLYKK
7990	21891	A	8050	166	163	PVHGGEQTTQDKLCL*STHLGLPKC*BY RREPPCOASKLVPTGILADSKHSCQTM DSCFSNOLYKQR
7991	21892	A	8051	402	245	YFKSVCOAQWLNTYNPSTLGG*DGWITC GOEFLPLPWSGITGASHHAQPHF
7992	21893	A	8052	404	268	QQLWRLRORDCINLSCGGCSEPRSCYCT PA*ATEPDPVSNKQINK
7993	21894	A	8053	1	154	GFLRVGQAGLELTLRLDPLTASHSAGI AGVIYRAWPGEAYLESG*WLRFT
7994	21895	A	8054	406	150	PKKKKNPCPPPEVKFDSLKRAPLFFFFL EESCFVTQAGLECSGAILAHNCNLCVGS SDSPLSL*RWVGNSHFIFTSLLSVSPRS N
7995	21896	A	8055	1	125	TAVILIFMI*EAFASKRRLVIVEPSI NLE*LYGCPPPTH
7996	21897	A	8056	400	260	HMSPHLAFFFSFLFL*RLDMLPRLVSNS WPQALQLLLPQVLGLQV
7997	21898	A	8057	396	263	FLQPGTVAHACNPSTFRGLIT*AQEFK TSLGNKVRPCLYKQY
7998	21899	A	8058	402	211	FSCWCTKPKAAG*FPAPNGPPLFNNPP GAGTNFGPPRSGGPGSPPPPWGPGRPR CPNGIFFC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
7999	21900	A	8059	1	279	VLLYHFGNSAVVGSWLMQ*TPSNADIWR IARGFKRSSHFSLLSSWDHRHVTCLAN FFLIL*IWGLAMLSRLPLRLRKPVLDD *APSPCGLI
8000	21901	A	8060	408	315	SLTMLPRIVFNS*QAAILLPWPPKVLGL QV
8001	21902	A	8061	198	2	RIQHVESNCHLEVEGGNAQWLTPSTLGG RGRMIS*AQEFETRLGNTVRPCFYKNLK SQPGMVVRI
8002	21903	A	8062	3	294	GLSPTAHPIAFTSQPLFSGLSVCRFL WAMCEQCCHLPPIRCPPIIGPECALYT TSCLLHQLKKREG*KKKKKKKKKKKK KKKIF*WGGGKK
8003	21904	A	8063	197	184	IHDLFPPF*GRVSLCCPGWSAAAQSRIT AL*PGLKETFFYL*IRRSWDHKAAPLP APP*LPWVTIITPSTHEVSAVCSLLY VKSEQCQ
8004	21905	A	8064	3	373	TSGSLAKRPADCLSAQPTTPSSLCGCS PVRVCITVPRCTHARAHTHTHTHTHTH SNHG*APGAILYQELQKGVSHVFEKEK SDPEA*TKGG*HVTNPHGRQRSQEGE HRIQVGRCCSG
8005	21906	A	8065	532	106	ENKPIHNLSINKYIGKILRDKALLYCPG WRVWQS*LFVANSWAPAILLCPGFLS TWQYKRVPPQVLKIFSKKKKNKPTNIIR PKCHTRNGDIYKRGKVGFLCSYCPFALL LLLSLLLLLLLLFSFSTRDSAGACCS LP
8006	21907	A	8066	411	130	PHAOILFLRR*SLTVFVRVNSWFOAI LPPWPPKVLGPOARMVSPKLVLESIL RIPTSVIFFPLNLCSNKLAEIKEGCSA AFLFNQRFAN
8007	21908	A	8067	3	32	DAWADAWGSLTDEWEKIWIYIHAMQYYS SFEKREIL*YVRTCMNLEDTMVSEIRQS QRDDYCMIPHI*GTRGVH
8008	21909	A	8068	410	116	STFNITQWPGTVAHTYNPNTLEGQAGRI T*GOELETSLGNIIRPNFLFCQACPGQ GLSTVRMCGSLHYFVLPRLPLKCLDNR KSPFYHPVILPCYE
8009	21910	A	8069	158	289	DLCSLRNIVRPOLYKK*KISQVRKKKK KKKKKKKKKKKKKKKKKK
8010	21911	A	8070	388	1	APTTPCFLKPPFVLGGPPFGKAFQKFP GGGFFPSISQPKPPPNPNSLISGKVR PSPQSPIMVFPAG*RPDPPLMWG*KI KIPLPPPPFKTPPALSPPFFFAEFRS CWPGWNAVMRSLSATS
8011	21912	A	8071	15	336	KLDKRYDRTGSGTTHASGYLIEPLVAE ASYELIISLAPFFERRGLALLPRLEGS GVIVAHCTLLKLGSGPPASAS*VAGTA GMNHHGEHPOLFEKNSGFF
8012	21913	A	8072	396	274	PHLHTWESSL*EQGLAMLSRLVNSWPQ VILSPWPKVVVL
8013	21914	A	8073	189	54	NKPLGPMVQACNPTPLGGQGWIP*A PEFKISLGNLAKPCFY
8014	21915	A	8074	3	257	HAFVLLFETRSCLSRLSSGAMIAVCR LELLSGDPLTASQVAGTKGM*DDAWL RQVNSNWPQVILRLSHPHMFLFQSLT LE
8015	21916	A	8075	1	119	TLFATWEAGAGGLEPKSLRV*CVETAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
8016	21917	A	8076	232	266	VNSSRTFAWAA LFYCSGQWCLGLPTIQGVQWHDHGS LQP RLPGLNQSSCLSLPKWDYGREP*YLA* YQARYHGS LARQNVPNIRPGIMVHARSP STLGG
8017	21918	A	8077	390	143	LGGFLVFCPPAKKGFPPNPINLGTPTRF PPPP*KAPEINFGGPKKKKIPSPPPG VKFDLKRPPFFFFFFFIIRLV
8018	21919	A	8078	424	144	LKNYIFPTEL*NRDRVSLCCERVLNFW AQEILLWPFPKVLGLGA
8019	21920	A	8079	182	45	VHKAGWVAHYHFTSLRGRGWIT*GQE FETSLASLDNMVMPRLC
8020	21921	A	8080	405	163	YFLEEMGFHADQGLELLTIGDFPGGM SHCTWNLNLVNILOKHPHRNIQNV*PH ISGFPVKLTGEGHNNHMHSTQKHS
8021	21922	A	8081	39	240	QSKTVSKKKKKITPCYRVVS*SGPGKVS SHLGLPKGMWYRREPPHASTFSQSFPV KDHFCSGVSS
8022	21923	A	8082	2	263	DCCVSS*GSVGVLSGEPAGYNNLVFR LLRPLEKRSIRVGGSRFSRYLWSWLELA RKGNSTPTCSTQVRQCPTLLGLHPLCD KPO
8023	21924	A	8083	1	248	SVGVGPSEPGA*YNLLVCCLLRPLEQHS IRGGVQSFSKYRQSWLPLARKGNSPT* ASCGMRGPALLWLTLLGLHPLSNKFO
8024	21925	A	8084	3	255	HLSEFSSWDYKRMPPHLANFFFFLGGK GVLP*GQTGLEL*N*KNPPA*PFKAGV KGVTHRPKP*NGGKGRPEKDTPGGFFL
8025	21926	A	8085	409	145	LRGPYKKNFSQAPGRKRTGSFKKAPFF FFFF*QSLCCPVLSTGVIIAHCLE LLTSSDPASSASRVAGTTGACHCS*VLQ TFTF
8026	21927	A	8086	199	26	GFFPPFNKTEIF*RPDFLNFVFLVEMN LTSLSRLVSNPWAQAVLLPWPFKALGPQ A
8027	21928	A	8087	222	3	SVGITGVSHRVLYWFLTKLGLGRGAHSC NNSALGRCGWIT*ACEFETSLGSGVARH HLYKKYKNYPVAVRL
8028	21929	A	8088	415	197	TILCFVHQNSVFSSNPELSL*IFIF*D RVSCFHGWSAVVQSWLVFPILCATVK YFTCCQYIIMIFALNS
8029	21930	A	8089	297	71	FIFPENKNPEVVAHACNTLRGRGRIT* GQEFKSLNSNIARPHLVKTKQNTLSK YIOVLGFQTLTQIDLANY
8030	21931	A	8090	185	415	PFGLKQSPHLLTSS*DYKHTPPCRVNF FFFLCGFGFFPKAGPNLGN*RNFLAPS KRAGNAGINNLAGPIFFRFFKK
8031	21932	A	8091	2	125	RKQASKKERKE*KK*KKKKERKKERK KKERKEKERKEEP
8032	21933	A	8092	8	412	RGPQGTTLTCTFDLSYSSSLSHWSQLC VAFPLEECIFPHKPLCPACFFFPSCWG LAILPKREYRGKIGVGNLLELL*NNPP SGTSKIAEPALFHHTHARPFNWIKT FPYIAQTGF*LRSPNSPTLEV
8033	21934	A	8093	249	143	NIFAA*TWMLRTTILSEVTGG*KYKQHM FSLICGS
8034	21935	A	8094	3	280	PERWDYRHEPPGPASFT*LLLFVFNLR KGLYVGQRGRQLLASSSLPAPASLSAGI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, =possible nucleotide insertion)
						YRSHCTFAWTVTRPCY*INK*INGKDT IRQNLKKM
8035	21936	A	8095	404	16	QMFGCLFFLPSSKEVFFPPPIFFFYRESF FLHFHFLDPROY*LYFIKKNIPLPSPF IFFLFIKRVSPYIFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFWGSMEL LSKAHQICISSHSGS
8036	21937	A	8096	358	200	KSYFIFSLIIFSHYFFLLFLKHLLATY CFLIDCTLFFSFCPCCLFVLLSGRFP RSLC*TFH*RLYFSFPPIFNQKLF*LS ICFCCIYLFYLYFYFETVFCSCCLGWS MMA*FNGMFKDRI
8037	21938	A	8097	2	132	KEKKERKE*KKRKKERKEKKERKKR EGORKEGKEGKNSST
8038	21939	A	8098	48	331	PGTWACLGGEILKQWTKGRGRAGSH RTSWIEPLETVFLELEAGRLSPGKNI SRLGAVAHICIASLGGGRQIT*GQEF DTSLADFCST
8039	21940	A	8099	7	373	NGRLRRGFAMLARLVNLF*PRDPPT*AS QSAGITGMSHHARPTIESPIHCWCKM E*PLCKLILYFHLFIFKROKLGVHWHCH SLQPPFPLGLQSRSLTPPSGWYRRGP PCPANI*LLI
8040	21941	A	8100	116	432	YLRNLFYQRCQAFSPALINLMCSAL*ESH TVAQAGVQWNLGSLPLPPRFKRFESCL SLPSSNIFAPLSPYFFRNSFTNISPSSEI GPOITDPLPIKKIKVSVNVE
8041	21942	A	8101	361	138	FNLLGRKKKNFGGLKEGESRRPPNPGPQ FFFFFLFFFFFSG*RMGLTMLPRLVLNS NAQVILLPWPKSLGLEV
8042	21943	A	8102	1	199	PTRPFFVLMEMFFYHIGQTALELLTSGN LPASASQAGITGVSDR*LA*YLFHFHE LFCYFALLLI
8043	21944	A	8103	412	46	KGGSPFFPPPKIKRGKPPNPGDPFFPF SPFFFRGF*GSPFFPK*KVLLVGLPKPK PPFFPLGWNPPPPVGGFSPPQSLQFF FKKVGWVFFFLFFFFFSPFFLFFS ETESHIIAQ
8044	21945	A	8104	192	2	EETELSFYTIKYLYLPRNQKVKRL*RRL GPVAHACTPSPLGGQREWITRSGVQDQ GQDGETP
8045	21946	A	8105	373	183	GGPF*FOYLILPLDNFFFLSFPFSQD FFFLSSFFFFFFFIINIFYFF
8046	21947	A	8106	373	281	SFKTAPPPFFFFFW*RLSLTMLPRMVNS SWAQVLLPQPPKVLRL*ATORKKHFRQ EQI
8047	21948	A	8107	3	114	FLIFVHIGPNYVAQAGLELLSSDDPAL ASQCAGITGMNHARPYLL*TLNIP YDPEIFLLGIYPR*MKTYVHTKACT*FF ITPLFVIAKTWKQPK*PSVLGLQA
8048	21949	A	8108	416	243	PGVFFPPFF*NPFFETIFWAPKKKKYF PPPLNFVFFKGPPPPPPPPPPPPPP L
8049	21950	A	8109	2	211	SVTQAGVQWNLGSLPLPPRFKRFESCL LA*CWDCGHEPWLALVTTSKHTSCSL LCIPTATFLGLVT
8050	21951	A	8110	172	28	HVVCFITSPFGPYFL*RQGLTKSPRLVF

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8051	21952	A	8111	2	225	NSWV*VILLWPVKVLGLQA QKSAKNFYHLSIYLSIYLSIYPSIYHLS IYLSIYLSIYSSY*VILEQKWNISKY CL*CTIQTNCL*QLKE*VIRLIPKL*YK IKLPTCNSVHLNWFNLCNLSWLYKYLAM *ARKLVCPA*FVVYNSNKLILITIKRIGH
8052	21953	A	8112	392	221	FFPKRESPPDKVNPFPPIFGGGKTKKK TLANN*PPPKKEKPPVFFKKEDPF*NI VGNFKTSPKI*AVCP*NVFKKKKGAK KKSSFKNF
8053	21954	A	8113	369	112	IFPSTIYYEXHFFPPPLPFT*PPPLFF PFLKKKKKFFPPPPXXXXFFFKXXXXFF FFFFFFFFFFFPPPPFFFLAF*HVSF
8054	21955	A	8114	418	248	KYVLTPGV*NLILLNGPPPPPPPPFF* RVSPCCPRLP*TPRLTQSSCLSLPRSWD HRCMPLRLVTF*FTFLKSHQSLRLTLTY TLAGTTLG
8055	21956	A	8115	229	78	SFKGAAPFFFFF*RONLMSPLVUSNS RPQAVLPWPPKVLGLHRGGWIT
8056	21957	A	8116	356	66	PLFPFFFYIKNKKKKFFPPFYFFFPFP PKGYSHKIDFFFI IKFPSSSSSFPFP FALSSFFPPPPPPFFPPFFFA*PVPF FLYKIPMLYPQL
8057	21958	A	8117	212	81	ERLSHCSNLNLPSSNPPASAS*VAGTSG THQLVMVHAGSPRF
8058	21959	A	8118	367	2	GVPFFPPSPAKKGVFHPHFFFLSPRFP PPPPFFPLWFYFWGP*KKY*FPHRPGY EFFFF*GGPHPPPPPPPPPPPPPPFF FFFYAEGIGVSPCYIMLGYNFSSFPFGT ISPRVPRV
8059	21960	A	8119	38	215	FFKSAPHHTRLIFNFFFFLEKTGSHYVA QAGVELLG*SSPTTSAFEGITGLFLS FKN
8060	21961	A	8120	266	2	POIFLFIETRSHTI*QGVOMCDHSSL QOPNGLKQSSLS*DYRHTLTAP*FC FL*RCGLAMFFMLVLSNPPQAVLKHP CCMC
8061	21962	A	8121	3	332	DAWADAWHVPCCPANFVFLV*TGFLHI GQAGLELPTLSDPPASASQSVPIYFLET ESHSPAWETERDSVQKKKRGGRFKGS NFTSAGLORFIFPMGP*PKLISRAGV
8062	21963	A	8122	378	66	LFIFLPIREVFPCIPG*NNAPPGVLYN GRPPFFFLLETVPLHAGQAGLELGSDD LPVSASQSVGITGMSHRVQPKLRFVNI SPFFEIFCEIMLLVPLAQF
8063	21964	A	8123	2	316	ISMLLALLRLITIFRLPOLNGYVEEPTF YECGFNPISPGRAPLFIHFLVDITFL FDVQIALLLPL*ALQTGNLPLIVMPSL LLIIILALRLDYERLQNGSD
8064	21965	A	8124	331	14	ITSILLYITF*LPQLNGYI*KSTPYEC GFDIPSPARVPFSIKFFLVAITFLFDL ETALLPLP*ALQTTN*PLIGMSSLILI IILALSAYE*LOKGLD*AE
8065	21966	A	8125	2	228	IITTF*LPQLNGYIEKSTPYECGFDPI PARVPFSIKFFLVAITFLFDLEIALL PLP*ALQTTNPLIVMSSL
8066	21967	A	8126	451	200	KA*WNRFAILNVTKYTCESQEVRIKPTF

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8067	21968	A	8127	2	396	AGVWKLI PAHTDDFVHFKTSVQEVATD VAKIASLLELEVESDUTE* LQSODKT LIVINTLLALLLIITTF*LPOLSGYTE KSTPYECGFDPISPARVPFSIKFFLVAI TFLLSDLEIALLPLP*ALQTTNPLIG MSSLLII IILASLAYE*LOKGLD*TES GWEKLVKKEKADKLKGGRP
8068	21969	A	8128	1	350	GTRGLQTLPLLIAF*LLASLANLALPP TINLLGELSVLVTTFS*SNITLLTLGLN ILVTALYSLYITFTTQ*GSLTHHINIK PSFTRENTLMFIHLSPIILLSLNPDIT GFSS
8069	21970	A	8129	375	1	LTCFSEHRPPPRANFFFSRKTRAPFFLP GGFQIPGPNFAPPFPNGGPIGLDPO PGLNFF*KSFFDPDKFFLFPPI* N SGVFLPRNPVFKTPNLFPPSPFFPGD GVLLCHPGRLPRA
8070	21971	A	8130	32	211	GIRHGFAMLPRLVLNSWPQATLLPWPPK LLG*QAGVELLASSNPALASQTAGMTG VSTRPVLLPTGLTHCLDACLGSSSL
8071	21972	A	8131	396	5	KYRGQPPFPKFFFF*DGFSLCCPGW SQISCPK*SSCLREG*DYRHEPPHMTLS SSV*CSGQKRCINCLGCVVAHACNL SPLGQRRTIWGKKFETSLDNIVKNRLKK KKKKIYQGGGDHPCITFN
8072	21973	A	8132	347	34	KAGPVI PRGQVFFFFFPDGLLLCFP GWRVAVKS*VTATSNWSAQAITGMLPPC PANF*KIS*QOSISMFPRLVNSWPQVI LPPQPK*LGHLVCLVPSLA
8073	21974	A	8133	102	270	DYRRTPHLANFFVFL*ROILTVPMLV SNSWVAIILLQDFFSVQLKMGFLSVP
8074	21975	A	8134	338	47	FLSTQKRESSPLHTHTHTHTSHLLTH HHGRGQERGRKR*GG*WRTGTHSPHGP HCVRLRKSRPSGELGAAQGGCSLIQPKI EDPGSGSGPREVP
8075	21976	A	8135	68	467	SLLNRI PFCLCINSFDCVFLGLLFEAG FCSVAQAGVWVYEHGSLOP*PRGLK*SF HLSLPKFWDYRNEP PPHPPSCFKALNFK DYCDSGTVPCPFMKLSMLFIHALTESF VLFTVMSKLITTKHLTI ISNV
8076	21977	A	8136	500	355	FHHVQGAGIQLLTSGDPPA*ASQSASIT GVSHRAPQTSFLNKLPSLR
8077	21978	A	8137	58	222	TYGYEGRGSVAGLSLSL*SATTDSLDY DYLQNWGPRFKKLADLYGSKDTFDDDS
8078	21979	A	8138	345	196	KGDQAQWL RPGMVAHCTNLSTLEGGGR IT*AQKFETSLSNTLRPPISFK
8079	21980	A	8139	500	355	FHHVQGAGIQLLTSGDPPA*ASQSASIT GVSHRAPQTSFLNKLPSLR
8080	21981	A	8140	3	231	HASADAWGRNEWPCAVAHANNPTTSGG* GGWIA*AQEFETSLCKIVKPHLSKKK KKKINSPGWSSPCTPLF
8081	21982	A	8141	416	26	ARTFPNNSFWQGGGFFPPRPLEGGPG VIP*CGQVQARPAPEERLFPKPKQIV GGGGEPPLPPPRAPGPKRPFEGGFG R*PKPRPCPGWGAQGGVSKKKKRNNE DSKIPLGKYPVGINMA
8082	21983	A	8142	413	35	RGAGGGGSPFGPRYPSQHLHARTPTT FARSRGSFPGRGSGWRGGLG*SREPR

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						LPFLPPRALPRSGASSGPLDGGACGGPR RERWAPLGGIRADARGCRAVTSPEPYRL PGAGAAARRR
8083	21984	A	8143	166	368	ENILWAAMVVLDDCHPSTLGG*GGRIT*G QEFKTNLANIERPHLFFFFFRKDSLFPA FRAEGGGPILF
8084	21985	A	8144	1700	621	DLRDHSVLQGGFACLRGCEPILSHSEG SKIGSRESEGEHRPEADPPSEVGSRR RS*QDS*GPGPGNGQDTKPLSHAAPN WTPDPAAVAAGGTSLLPPRGCGDI*RG SHTARSGARVGSANAHARGGSGFSRHSG SHGCLRNQSPRLGKAGALCGSANVSGL* GSGLTSRGRRRERLMPGVARGR*GN PRRGRGKHGIPASGLPGRCHLGIKMST LQPRTRAPEELFVPOESSGSTEKMLVS FHGSSLRNEATPRYSQCEAGNGRWOQS LSLERWPPWTHPLGTPTPLMPVAVARCC ILPGLWPLLSPSPGSASPVSGPGCLSL WPNAFKKDDFPVRQDTSWRSVS
8085	21986	A	8145	390	38	NTTTFNIIYFFYFFFLFIYFFFFFF FFFFFFFIILFIYLLVFGVWVLGL GLALALLAKLFLVNSLCRRYRG*SLIYY AWL*FFIFPLRIYYICARFQPLSPILYL GKWFG
8086	21987	A	8146	20	187	KLTTSTGRNFGRPTRPNF*VF*RDGDLI MLPRLVNSWPLVNLFPWPKILGLQM
8087	21988	A	8147	417	64	VRRPVRPRVRPRIKKKKKKKKKKKK KKKKKKWGGF*DFWNGEGKPPQLQKNDP LLFWGFFLKSPFFFCGGLFPWGGPFFP PPFNFLGVGGKKKTFRLLCGPFSAPFGG EKN
8088	21989	A	8148	351	187	RLGTFFYLSNLRPFYLSITHGPIPYIGRL TSONPLLLDLT*LEKLLPKKSTYN
8089	21990	A	8149	465	60	PHFWGNPKKNSGFPFAKKKKYIFLPG *KQVAKGVFWVGKKKQFQGGK*KG GOLFYPVLSQVLGGGQNHGPPGKAGFGE NFFPFGGGLGMAISRNLRTPLFLAGGGE DPKKNFKPPPKITLGAQVKKK
8090	21991	A	8150	1	175	WDYRHVPVPLANVFFVIFRGDKVSLCCP V*GPTTELKRSSCLGFP*GWDYRREPPH LA
8091	21992	A	8151	59	35	RWNSRPRRPGKLKPTSGDLPASAGSAV ITDVSHHAWPETFFR*RA
8092	21993	A	8152	269	159	ARVEVSKYIYIHTHTHTHTHTHTHT HTYTTKKLPS*LFQVCKMEKFGRLVVO
8093	21994	A	8153	1	256	EGPEPRFFFFFFFFFFFFFF*TLKI RFPIWRQKTHNPDKGLHQDISQVLSLQ ITNHFRHYFCTNFTCIQERDINQSLF F
8094	21995	A	8154	252	41	LIIPLVICIVFVLQFKIFSVISLNKGL FRNHFFIF*RWGLTMLPRIVSNSKAQV ILPPWPKVLGLQV
8095	21996	A	8155	21	443	HELSLI*FISTLAETNRTFPDVLGDESE LVSGFSIEYAAGPPALFFIGEYTNIIII NTLTFTIPLGTTDYDALSPELYTTFYVTK TLTLTCLVL*IRTAYPRFRYDOLIHLL* KNFLPTLTALLI*YVSIPITLTISSIPGT LLHLMKHFNLEIQKA*TRINLKRISR
8096	21997	A	8156	2	205	

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						HVI INLSKAKHKG*ILKAVREKMLIMYK KPLVKLQVISN
8097	21998	A	8157	2	205	LLHLMKHFNLEIQKQA*TRINLKRSTSR HVI INLSKAKHKG*ILKAVREKMLIMYK KPLVKLQVISN
8098	21999	A	8158	2	222	VYTWGTGKARVPPGPF*LPVMTPTRLHK FYNEPIRDANESASAEETNPQSSIIHPQ DEQNGDIRRTDKVTIHO
8099	22000	A	8159	1	297	GFFHHVQSGSLLELLTSGDPLASTS*SAGI TGMSHHAWPLNCSYGDGFSWLKCPCLTV ACWEEGWRKLLMNEGREGRAHQLESV INFYIKDSMTKRRYK
8100	22001	A	8160	138	437	NEYDHPSTIKERRDFIVCVFFFFSKRS LTVGTTGGPSYLEPFLGNKEFSCLTFL GSWDNGGATTRLG*FVFFRKKGVSPCG PGWS*TPDLRKTTPSA
8101	22002	A	8161	330	148	QQSKTPFFFFFPPKKKKKIYICMVVHAY NPSYSGG*GGRIT*AQFKTSLNNTVRP HLYKK
8102	22003	A	8162	391	255	RPAPADF*FFFFYRLGLAVLPRLVNWSW PQATLLPQPLRVLGLQI
8103	22004	A	8163	131	3	HKVSLCYPG*SALMQS*LTVASNSWAQA ILOP*PPE*LGLQA
8104	22005	A	8164	97	440	NRGSLCPGGGRGALSHPTARSRSGSPG TPQKTGNNGPGPTTPVNLEFFEKRGFTT VGCGGLKLR*RSPPPSAPQKAGITGGS RRPGPIQKKFLKTLGETKWMKLIKTY LK
8105	22006	A	8165	541	295	FSQOKKKIFISTNLSHQESKIYICKEME SHSVIRLLESGAIMNHCSLKLPSDDP PASVS*SAGIIGVSOHLANYTPFKKIF
8106	22007	A	8166	440	259	PPCKFFFFFVFKTGPRHVV*AGRLLD SSDPPPLAQSVETLGMSPSARPMFGVF HSLR
8107	22008	A	8167	23	405	FRICHLRLVHLVVFIFSTTDNHLST AMFLYSNDVVIAQNVSGPFLGIIFRTFF FFFLKGEFFFAPOVGQGGNGL*LNPP PGLKGFSGLTTPPGGSGGGPPNKNPFW IFKKGSGTLWPRII
8108	22009	A	8168	23	388	PYFSCALPRHPPPTTNLGFHLGMGAPWG QPSVAHHTLLFFFFFLKRDFCFVPRVEK LWLEESSLNPPLLGLKFSCLTLWRTGN NGGPPPPPVIFCF*KKGGVYWPVGPGGE TPALKETPGL
8109	22010	A	8169	612	498	NIHFSLSFSHTHRMHMTHTHTHAHTYI RTP*DNVPQ
8110	22011	A	8170	2	288	VNLTFPFFHFLGLSGMPRRYSYDPDAYT T*NILSSVGSFISLTAVILIIFMI*EAF ASKRKVLIVEPSINLR*LYIKKKKKKK KKKKKKKKKK
8111			8171	381	101	QKSLQCPNSIATILEEVQVIFLGSPLYH QRNEMRLTKWLRGLGAVAHACNPSTLGG MGGWIA*AOELETSGDPPPSNRQLFTG EHNNDNKLI
8112	22013	A	8172	136	360	TKRHFGLLK*TKKHFGLLKKKKKKKK KKKKKKKKKKGGGAFKKKFFPRGGOK IFFFGAPKNKFGGGLTKGGGKKPGVT KK

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8113	22014	A	8173	358	58	EKVSVFLLKKKCSGILLPCRLTLPGSTDSPASVCRMPAIAIGPRRHA*LVLVETGFCVGRAGLQPLTASDPPTSASPGAAIADGVSTQCSMVPRIVQ
8114	22015	A	8174	254	370	GLTVLPGLVSNWSAQVILLSWPPE*LRPQAYATGAGFL
8115	22016	A	8175	48	269	FYVILCLDRVLLCCLGWS*TLGLKLSYLSSLSSWDLQHVPPPHSASCLTF*VKACFFLLKYLKRLKIYAKIM
8116	22017	A	8176	1	338	PTRPINTLLALLLIITTF*LPQLNGYIEKSTPYECGFDPDISPARVFPSIKFFLVAIITFLFDLEIALLLPL*ALQTTNPLPIAMSSLLLIILALGLAYE*LOKGD*AEF
8117	22018	A	8177	426	130	QSLDDPGNWTLSLQK*KNPFF*GGAVFPQRLGGENPPQGSKEQKRPPAPQGG*PRQPPSPKKGNADSEFSIFNLQALLCKQYCVLHALPNKILF
8118	22019	A	8178	396	244	KIHLLYICMCYIYTVVISRHYLLR*HTHAHTYTHTHTHTHTHTPKNTKYTLW
8119	22020	A	8179	2	119	TRPGNWPGVVAHFYDSTLGA*GELIT*GQEFETSSSLY
8120	22021	A	8180	2	80	FLPLTALLI*HVSITPTISSIPPT
8121	22022	A	8181	438	333	SLPGLRLHYNCNLKSGKGCN*PKSCPCFPANGTK
8122	22023	A	8182	393	19	IFFFFFFFFSPPAKFFFIKFKRRPPPLMGVGF*SPPPGFGKTPPPQKVGFSRVFPPPPPKKFFFGGGKYFFKEPPPPPPPII*KGGAKISPPPPPGKKKNPFFLKGKKKKTPIFFFFPPKKIKN
8123	22024	A	8183	24	269	GSQVVLGFCFRDRLVLLCHFGWSAVM*S*LTIVASTSWA*RILHCSLLGSWEYRHTPCL*NRNPQLTVKWRVKDHNKKSHR
8124	22025	A	8184	154	361	WHNEDPLQPTHGLKRSSHGLSPSTWHYRHVPPRLANFLNLSFRQGLAMLPSTVCSHLVFLS*HIYMTFGYLS*SVCSHLNLF*W*WHNEDPLQPTHGLKRSSHGLSPSIWHYRHVPPRLANFLNLSFRQGLAMLPSTVCSHLVFLSETLGFK
8125	22026	A	8185	228	337	RPGMVAHACIPGILGGRGWIT*GEKFBETSLAMVVK
8126	22027	A	8186	314	127	DTQPKNEGEEGEEQELWLGMTAHAYTPSTLQ*GGRIA*VQEFETCLGSLARPPSLQKNFKN
8127	22028	A	8187	10	420	TQAEVAVNNDHATALQGRGQSETSPSEKKKKKRGPPRWGENFFPTPGGF*KGDNKKTGFPPFKRGDPPPKNWTWPFQKRGAPPEPPPLGGLGREPLGGFVGKGVETPPDDPIFKONNPPEKKPHRGFNFFAF
8128	22029	A	8188	398	1	LKKKRBPOTPFSPKIQF*KFFPPPPFKKSPFKNLLKKRAPGGIFFFFPVGLGKNPSPL*MGSPPPPLFNPNK*KKPLLLKGPGF*WPFQKKKPPFFFFFWRQGTFLPRHTPSCLVNFCIFCRDGI
8129	22030	A	8189	30	153	ANYVRREDHVSLSGG*GCGKFWLCHGTAPWVTEENPKGKIK
8130	22031	A	8190	206	45	HPSQNSLSKN*ERVSVCPPGWSAVAGSQLTAASTSQAVILLQPPPE*LGQA
8131	22032	A	8191	3	228	TCVCLVCVYICDVCGVCVYIDYIQ

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						TVRYIHTYIDITTHI*TVIHTYIDITHMW VCVYIYIYIRCMGVRT
8132	22033	A	8192	41	416	ICRVKETAISPELLTHSLVELS*PCL TAQ*RNAIDPLAKHLTAVLYNLIHSGGF WSSLKSHFIFLAL*YYL**FI*SN*RRD LAVLPRLVNSNWPQVILPQPQPKVLEIR YEPSSLALILFFN
8133	22034	A	8193	2	183	KRLSTWQKQVEGEGFQCMVGVPSVAHA CVSSLEGGQKIA*GQEFETILSNIVR PHLY
8134	22035	A	8194	2	465	AGVQWHDLSLQSPPPGFK*FSSLSLPS SWDYRSAPPADFCIFRRDWAGMGVGC GFHRVARAGLELLTSGDPPASAPGAGI AGMSHRTQRQDNFASWRRGGPQMSPS PSCFLQNTFSLKPSWVAPYDHASALGG GEYGGPPSPQPHLE
8135	22036	A	8195	397	149	LICLTDLPFIRFLSLLLALVTFVNTKVKV KDLIKLGVVAHTCNLNLGG*GGRIA*A HEFETSLGNIVRAVIVPCCFSVILSR
8136	22037	A	8196	355	95	KKIMPTLCKLPS*YRCETITQLSLQSS CDHRHMPHPHTNPF*QHLMSLRSLVLN SRQAVLPHGPPKVLGLQAPATAPGLLS LF
8137	22038	A	8197	382	112	KTDGKGGSSPPPPPPFFFKSFAFSFR GEKKAPLKSQRLGCPKPKDPPPPGSG* TQDKGPPPPGQPIFFFFFLKGVCLFSRG GSKTFI
8138	22039	A	8198	32	361	ASRIGFILQEFPLVRVMTNPSAGADGY NFLEKQKGTERTSCSVAQAGQWCHRNIL L*P*TSSELKQSSCLSSSWDYRMVFL LGQVITLLIGKRLSVYPRDVSLC
8139	22040	A	8199	1	314	INTLLALLLITTF*LPQLSGYIEKSTP YBCGDDPISPARVFSIKFLLAATFLL FDLKNALLPLP*ALQTTNPLIGMPSL LLITIALSLAYE*LOGLY
8140	22041	A	8200	3	109	FTSKHHGFEAAA*YKHFVDVW*LFLYV SIY**GS
8141	22042	A	8201	3	216	DAWAAVGHHTRLIF*YVEIGSLCVSQ AGLEILSDPPSSASQAGIRGMSHGA GOEHLFHRPIGKIK
8142	22043	A	8202	1	267	RIHTGEKPYKCEEGTGFKGSPSTLTTHK FFVYCREVAVLLKNCYSHLYP*IIYNG SEADKREMLCICIFHPLAEQENVENK RKYNP
8143	22044	A	8203	422	92	PLVFALPPKIGFAPTPSSPPPPFFLFF FGPPVPPPPFFNPPPPFFSPPPKKFF PSPPPRGKIFPF*TPPPPPPPPPPPFF FFFFFELFLYLLILC
8144	22045	A	8204	445	260	VCSPPLEFIWVAPGSPPLPKNPPPNFF FGAPKKNFFPPPPA*NPFFLKGPPLFF FFFFF
8145	22046	A	8205	103	248	GPGVVAHACNPSSLG*GOWIA*AHSEFK TSLSNVRIPIAKKKKGGPF
8146	22047	A	8206	407	197	QLIFKFL*EQASHYVAQAGLELLGSGNP PASTSQSVKVTGMSHGANLLAPTLRST LNYSLSVLLLP
8147	22048	A	8207	1	142	SCSVAQARV*FRLGSLQPPPPPPFFPS CTPAWETVRLHLRKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, X=Tyrosine, Y=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
8148	22049	A	8208	2	370	PEVFDYFN*FKNL*LHKTCQ*L*AALF VITKTWNGCPLTGEWINKLEYIHTMDY LAIKINELANHKMM*RTLKICLLSERS* SRKATYIMISIRHPRKRGKTIEIVONSS CQGLGERQGL
8149	22050	A	8209	363	108	KKPRVEACLSPGVGRERAKRR*KRERE RERERERERENEL*KLSLADLCIKNG*RE EFKFKRYVKRYAKILRVSGRKQYGNV
8150	22051	A	8210	386	254	LNPGGVCSEPRCLCPCTPAWIR*DSVS EKGGKKRKGPENSLATNF*ALSCNLDY LRCMLKMQQRKRETEVRFPQLHHN LTLGFV*LIYQRE*RTGWVAKYMLY TFS*PGSFPLRKCVHEVFGVSPACSPL FPLIHNLHAKAC
8151	22052	A	8211	3	131	AHLFIANFTEYFKPTVTITYCSKKIKBFK MLLLIDSAFSPYPRALMENYKGMNVFPMH DNLTFLWPMQ*VIFTS*SVYLR*FC TIAAIDSDSSDGGQSNLKIF*KGFTTL DAIKNICDS*EL
8152	22053	A	8212	86	286	WSIWECTVISQLPHKPKTSFKNTYSWS GVMAYTNLSTLGSQDDQIT*GOEFETS LANMVKSCLY
8153	22054	A	8213	393	344	SFPFSLPSKMGFKNLVPSGVLFFFLNK GFRYFGGGFKILSNYPPLASQKGGI SGISPWPRALVFF*WRNLGPN*RTIVSP NYGLK
8154	22055	A	8214	3	313	QGLVLNHSGLLQF*PGLRRSSCSFLP CSWEHRCTPPHLANFLILCVCVCVCTE GSHFVAQAGLELLGSSDPPLISQKSWD YKV*AIIPRAKQNYLMLEY
8155	22056	A	8215	165	348	RFCPLFPEDLLTFSREGPGTMAHACNLS TLGGGGGGIA*GQSFETTLGNIVRPHLY FYLKK
8156	22057	A	8216	379	218	VFLVETGFLHVQAGLKLPSTGDPFASA SVSAGITGVSQKCRF*YNVFIFQKSSLL NALPFCSLTMLLGNLPSFMFTPKFPTCS
8157	22058	A	8217	32	276	RYLPIAALFTIAKI*KQPKSSLLDKMI KKLWCITMEYYSALKVILTVTTWMNL VGFIPGIDNHQKAKYMSLIGI
8158	22059	A	8218	171	2	KGVFLGRLEFFLDNWLCLFENSTVQ SRLSATAS*IQAILPQPEELGLCLP
8159	22060	A	8219	530	73	TKPTVGSNSRSYINQFYFESTLTFGSL MRLTIYHFFFLVYNPRVMWTPAM*L LILFYSSSIDLLAKQPCLDNGFSFH AC*TNATLLFPYSI*VLGLSPHLIFPV CFSFYFL*R*GLTPPMLVLSSNPQVIL PPQPKVLGLQA
8160	22061	A	8220	350	135	FFFFSQTGVAQRNV*RDHNSLQ*PPG LRQSSCLTLPKCWDYRCKPLCLASNIYF KDKVYTSPTVHTQY
8161	22062	A	8221	185	331	PGMVAHAYNPNTLGG*GGKLT*AQEFET SLGNINSVPKKRRKRKEMM
8162	22063	A	8222	73	232	YCSFKFITLTCLSWLGTVAHTCNPSTVE GGGGRIT*GWEFTSLGNIVRSCLY
8163	22064	A	8223	418	211	AMPSELLTYLLTIFCRKKKIKFYNGEFT MLS*LVLSNWTQVILPPWPAKVLVLPRL ALFYSLLVLPFS
8164	22065	A	8224	227	33	ELFSTTQAGVQWHDHGSQPOPGMSLY

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						CH*CLRFSWRFAEKPGWCSSLRFMEL SWGASDAF
8165	22066	A	8225	244	287	TDSFTSAFRSAGITISHTLFCST* I FCRAGLAMLPRVLVNSWPQVILPSQPP KALGSA
8166	22067	A	8226	53	235	NNKWQGVVAHTCNPTLLGG*GEWIT*GQ EPETSANMAKIPPLVMFAFCPEETDNK SHTK
8167	22068	A	8227	275	25	GVLMPNFKFCI*QNSPFMLPGVULNSWI PAILPQPKVGLQANTILYKYWGKE MWHKEICGTHDVLVSKLLTTRFKRHL
8168	22069	A	8228	386	211	QLKLPLKGNKLRPP**KEFFFFFQRO GLTILPRLVSSSWHQMFPPQPPVELGL QA
8169	22070	A	8229	1	117	VFILFYF*DGLAMLPRLATNSWAQAILL PSAPKVQGLQA
8170	22071	A	8230	356	26	WHVHGSQGF*PPGLKQSCFSLPSSWDE RCAPHPINIFYQICRDRVYKRWANMVIS PNPLVLISQSGAGITSKIPCSEISTIF IFSHQLLVGRVYPMMLVLQLGKTCI
8171	22072	A	8231	3	188	FFSLRPA*IFFYIYFFFLKNKVLCHPG WTQLLDPNWTAAGLQSSHLSSLSSLN FRGSA
8172	22073	A	8232	2	253	KLDYINGCINLAQKCLCLFGSLFFOR* GLTLLRLFMNSWPQAILL*PLTVLGL QATMLGSQVPVFDLGLITLCRCRPGKLE
8173	22074	A	8233	373	65	PEKAGSCLELAFGLQMCPPWASTLPAA LTDGGLATVENHVSQFLKSHTHTHTH THHTCTRTLLVFL*EALTTTPLLRSI CKHRESACSLSTWPLCC
8174	22075	A	8234	390	46	RVFKEG*NPELVKAPAPPLFFGGV*GRS PKKHPQCGGGGPPCPGPPFLTPFPF IFLRPPPPFFRGGLPPPPPKTFF FFFWKGGKFLPQKKKKKFFQSISTRVS IHK
8175	22076	A	8235	387	216	QKLGVLVPPGRVIFVFFVFFFC*GGGL TMLPRLVNSWPAILLPPQPKVGLQV RFFFTTPQCFQFTLSF*RRGLAVLPR LVLNWPQAILPQPPPELLGLQAHPTTL GPVFSYCVRA
8176	22077	A	8236	1	201	SVGGGGLTMLPSWSQTPGLK*SSHLSLI KCWDYRPEPPLAHFSLNLQLYCHTKL S
8177	22078	A	8237	399	229	SHTLPHSSNFYSYF*RGFAMLPRLVLN SWARAVCLPQSPKVLGLHA
8178	22079	A	8238	192	335	GRDRVLLFCPGWSQTLGLKSSCLGLPK HWDYRHEPFAENIKFCVWPTLYFYWP ALVQINLP*QLQGTCEVCVACM
8179	22080	A	8239	442	254	VLKLFCCSHRGFTMLPRLVNSGLK*SS HLGLPNCWD*RCFVHPASLCLLTSTFW PPTLCNIHK
8180	22081	A	8240	381	180	NAIPFYITKCNFSTLGG*GG*IT*GQE FENCLANMVKPLY
8181	22082	A	8241	388	260	GFITLVRLVNS*PLDPPALASQAGIT GVSHCAQLIYVQSRSLQLLW
8182	22083	A	8242	1	145	GLTVSQAGVQWCDHSSL*SQTLGLKQSS SLSLPSSWDYKCPQHQAQDRFLMEFFQ M
8183	22084	A	8243	1	173	

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8184	22085	A	8244	202	327	TLFTIFFF*RG*LAVALPRLVLNSWFQV ILLWPPRVGLGHV
8185	22086	A	8245	42	289	KEKRSITLFIFFCRDGVLLWLPRLDLS WPKTIFPPWPPK*LAQAHTTIPRGGS IILICIDVKRERKQYAKSKNPEGT
8186	22087	A	8246	592	485	NIVSQAGVQWNNLGLSLPLGLKRFSC LSLLSS*DYRHVPPCPANFCISVETRFC HVGQAGLELLASNNPPAPASQSTGITGV SPCTPRVYVLLNIIANGPS*RAETLV NLATNQEDADSSLAGLGSCHCF
8187	22088	A	8247	307	12	MCSPVFPKOKNPLFLNFFKKEFLFFFP GGRQCHGFGLAPPLGLNKLFLVLPFG NGDTGKPPARCNFFFFFGIFSRDFV SPC*PGNSLIDDP
8188	22089	A	8248	392	237	HYGQASLAPLTSGDLPSAKPGSAEVTGV SHRAWPTVLI*SF*KFNVV
8189	22090	A	8249	153	386	FFFGWKEKSLFFPPPLKGFPPPTLL GGGD*KRPDPGPFKFGKNGVSLWE GWF*TSNLGNLPSPPKRVGIT
8190	22091	A	8250	387	166	IETILDATKNIHDSWEEVKISTLTRVK N*IPTPMDFNGFGFKTSLEEVADVMGIA RELEVPEHVIELLHDS
8191	22092	A	8251	405	266	LFAIVKR*NHPKCLLIYARINKMWHIST GWNIIISLISGKMFPSYMLTWMNLEIVM LSEISHSQKVT*YMVPLA*GHLEKNCL PIKQOTPIPSSSSP
8192	22093	A	8252	379	201	PGANYACNPSTLGRSGWIA*AGELET LSNMTKQPCCSTPQCFLVNLQLNLYP YFP
8193	22094	A	8253	78	311	LTLYFHTRRKKGLK*YFYFI*SLSQD LKVGTPGAGATYNTNRTWGNKGLQAG KRIT*AQEFETSLDNTVKTCL
8194	22095	A	8254	303	81	TPCAENFKLRKRHHIISLQRMNVLIS FLYF*SHSLTILPRLVNSNWPQAILLP LPPKVGLOVSATLGL
8195	22096	A	8255	2	376	MGYNLVCHLLRPLERKSSIRVGV*FSG CPPSPFLPARKGYSILTPCASQVRQCLAL LWLTGLGLHPLSCPHCTSPSVMNPVQ LEWQKSPFVCVSHAGSCLLELFLGHGL TOSLSDFKKVI
8196	22097	A	8256	70	356	LITAYNLTYDLSNKMFPVYVLRKIYTLH WUECSIYTCW*EVSNWSNRIIDSPGK KKTNIYDQLIFNKGAKSTKLKNSLKN WQDKISTYKK
8197	22098	A	8257	403	85	PFCPWFFPVFIPFPLRKSQTPPGQPEF PGPGFSNGGNRPLKKSFKPSGWRGP LPPPSRGV*AGNPLGPRNRPWAKFVP LPSCGLGHKARFFPKKRRKIK
8198	22099	A	8258	249	2	YCEGLDGSYRPGVSKMEFSPRRDIRM PWPAGVCIAYNLSTLGGRCWIA*A*EF GTSLAYIVKPHLYTHHTHTHTMY
8199	22100	A	8259	2	189	IQCVCTKSHFCHPGWSAVAQSWLTAS TS*A*VDFSHLSLLNSWD*RRVTPRLVN LILFPS
8200	22101	A	8260	453	128	FFFFFLLIETVSHDVF*AGLELLSSSH LASAFQSAEITGVSHHAQPSVSNLHIS S
8201	22102	A	8261	420	79	KNPIPFPPFFFLIETVSHDVF*AGLELL

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						SSSHPLASAFQSAETIGVSHHAQPSVS WLHSS
8202	22103	A	8262	1	262	NSRTERLGSWQSHFCHKEAHFVVGSG VQWCDLGSRLRPLPGFK*FSCPILLSGW DYSOCRPCRTCSLIFMHSRSPSQSEKK WTC
8203	22104	A	8263	321	100	SATKNYLLSRQSFYK*NNGLGAVAHAY NSSTSRGLGGQIA*AEFTS*GNMMPR HCYRKQNLARHSTYSFR
8204	22105	A	8264	145	275	KPRDYSFFF*WKRDLANLPRLASNETH AILPMPKPVLRQG
8205	22106	A	8265	73	351	SLCYRSFARCDRPPKQGHFSKSLQDAQ WARTLLSTIAQNSAEHLKTTDW*GAV AHACNPSTPQGRGRIA*VQEITSQGN TGRPHLYKK
8206	22107	A	8266	382	232	LVETGFCHVQAGLKLTLTSGDPASASQ SAGITGVSHCAWL*TS*YDFQ
8207	22108	A	8267	397	130	IGQAGLKLTLTSGDLFTSAGTAGITGMS HRAWPTFSLIAR*NASFQGHFSPKYQV GTLAKSLKCHQVRSDTLEFILCCRIIYE TLKF
8208	22109	A	8268	309	97	DTWYTRRRKDHCTITETRIQSVRPLSPR *AITSRVTCYTSR*PEANEEPOKITER HCDLFLPTLTDQLTL
8209	22110	A	8269	2	224	DSSGIPGSPTRPPTPRPKQKLPDCPTVS LLGICIYDQQR*SVFQRDICHSMFITA LPTIVINWQT*HPLMDE
8210	22111	A	8270	374	2	TSWESARKPPPIHSHTLKQFFFFLFMEFF FF*NKICKDGLTMLPRVVLNSWAEGL LPSPFKVVGIOELATQRRASILLCNFTY ACGIPQHVVVNKLMLKQCPFCPAAPTK TONFFPRV
8211	22112	A	8271	1	379	PTSASOVAGTGTTHHHVLVFFFGIFFEK KGVFFPSGGF*TPKKPPPGFGPKRG KKGQGGPPPARGMGSGVFYPPQKPFV LIGGQILFKGRTLDFKKRAPPPPPSLF LPKHTPSFWIKNDP
8212	22113	A	8272	80	401	AWGMRFCLLLYSQCYLLSDIAHESKAF FWKREPPAPQVQKQGNLS*WNPWLQG *RGFSGLTTPKGGGNYGPPPPPLIFFFL RKNGFFPGWPGWSKTPDLRKPPC
8213	22114	A	8273	405	95	PPKRFWGSXGFPQREKLGSPFFPKKK KDFIYSYLSKSLKKE*INRPSAAATCN PSTLGGGGGRIT*QRFKISLSNIGRPH LYEKIKNVKLIKIKPNKL
8214	22115	A	8274	167	52	DREQRPGAMAHTCNFSTLGG*GGWITRF LANMVKLRLY
8215	22116	A	8275	276	23	KYVSSRPGTVAHSCKPSPLDGQGEWIA* VRKFKTILGNMMKPHLLFYKILTFKNVK CIFKKYCATESRYVTEKQDKRKGTKE
8216	22117	A	8276	1	114	FTMLARNVNIS*PRDPFASASQSGITG VSHHARPLS
8217	22118	A	8277	2	87	TMLLRLFLNS*AAQVILPWPFAVLGLQG
8218	22119	A	8278	357	347	SEGLALYQLEAFTVCDLREGRGCRRLS WPLITWAWRGVFLVQVQFVCCRLALG SLSPDFVLLPESGGPTSASQAGIIGVR DRAQPCNVFEIGSYSVTAQGV*HNHGS L*P*P

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8219	22120	A	8279	371	125	FFPKNEPFG*PPPK*KKPGKFLAPS PPFFGGGEFYKLKRGVLKQKPGPGVPK ILKTPRLKGNKPISPPPGQKKNQNF
8220	22121	A	8280	377	63	PPVFPFPPWGGQGGGF*ARGLRTFPWETR ENPVFF*NPKN*PGGGGF*IPPPWPG* ALKFPLPPRGGVPLTKNIPPPRFSHKR RVFFPKNLKKKNCLIESL
8221	22122	A	8281	2	284	LPK*VKNFVHAKICT*MFVAALFVITSS WKQPRYSSIEKWNKLMHISAMEYYSS LKR*ELSSHEKT*KNFKGSLSEKQSE KDTWCLIPVI
8222	22123	A	8282	318	40	APRLSLVFMVVFIRKRLDSSPGSRITWT NCFENHLCCVCDRFLLCQAREQWRVLG SQSPSPKFKRFSCLSLSPSSWDRCKTTP *PANFCGLC
8223	22124	A	8283	30	343	CYQKASHATEKSFMR*RVNPFCSLCCCY KILPOPOPSAVITLISQONKKKKKKKK KKKKKKKKKKKKDGGGALKKKKTFSPR GGRIFPPFWAKKNLGGGL
8224	22125	A	8284	163	392	FVVLYNFSVIYISIDECVYKEQLCKSVF SFLSS*SLDEPNPNSPANQAQLYQVE NKREYEKRVSAIVQSWNDS
8225	22126	A	8285	406	63	KKKLLAKPGVNDLSLRAPFPFFFF RHGVLCCPGWSKTPEK*SSCLSLWSS WYRREFCLAYSFVLNITHLSSPNVLL CRDSQESYDPIIMMMVIIITEGGMICGV IM
8226	22127	A	8286	1	322	TNTLLALLFIITF*LPQNGVYKSTF YECGLDPISPARVPSIKFFLGAITPLL FDLEIALLLPL*ALQTNLPLIGMSAL LLIIIALRLAYE*LLKGLD*AE
8227	22128	A	8287	395	181	HGSLHPGTPLGQFSLRLSPSSWYRHH PPCLANF*IFCRGGVSLCCLGSVEGLEC QARLPVLVRAELGLD
8228	22129	A	8288	3	246	SSTLSFPSG*DYRHVPCCANFFFWIL EKTFFCFVPQGGFNLA*TSPLNPFPA SKGAKITGGTGMGLINLANGRP
8229	22130	A	8289	138	421	LLSSVFFFERDFCFVQAGGQWNLG* WNFWRGLKNFPLTTPPRSNNGGGPP PLICFPLKKNRVSFRGRANFLLDGLT PPGPKEKE
8230	22131	A	8290	141	375	RTFFFFKTEGYFAAGKGGQGGHSSLQ POSFGLKSSLLRRWDGSMPPCSIFF F*IF*KNASLCPNNKSTGG
8231	22132	A	8291	407	209	IGGPFPGFSPFVFNKRNPLIFGPPKKK KNFPPPGKNWFF*KGPPPPPPPPPP FFFFFYTL
8232	22133	A	8292	86	433	PPXFNKLTXGGAF*KRHFFPPRGRVR FFFPQKQKTPAPGQNGGGGKPGSL FSPGKNXPPTHFXGGFVLGAPPFPGI VLI*KKTGLPLFVGRAGTNNLGGPPAP PPKG
8233	22134	A	8293	147	342	LVKFEYTVLPKNRYRLGVVAHYNSSSL GGQGRIT*A*EFKTSIGNILRSHLYK KRKEKLN
8234	22135	A	8294	6	152	CCGHAPHPANFYSL*RRSLAMLRLVS NSWTAQAILP*PLKVLALQV
8235	22136	A	8295	18	205	IPTRFPTRPIFGRNLNHTFTATRGVYV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						GQCSEI*GANHSFMPIVLELIPKIFEI GPVFTL
8236	22137	A	8296	1	199	YLYIYLSILLSTIYLSIYLSIYLSYLAT *LAI*KEIYYEYVLVMTAEIHFILPS PSWRPKVMV
8237	22138	A	8297	1	318	FTRPFRLLSRPIKIQIALHKKFSLCDEY LQ*ADYL*ELMIRDAUVPHACMLSIL GG*GRRIA*AOEFESLGNIVRPCLYCI IKNKIKKKKPLQI IAPFLCPKD
8238	22139	A	8298	416	304	GFLHVGQAGLKLITSGHPLA*ASQNVGI TGMSHHARL
8239	22140	A	8299	352	31	EMILKAAREKK*IPVNEPLICTVDPLV ETLQARREWDYIFKVLKKKNTKPIPYT KIEYLVKLSFKYEKVTKLLDP*Q*LRD FINTRHANRNTSNRRKRFIIHXK
8240	22141	A	8300	382	266	RWDFVMLFKLVNS*QAALLHVGLPKCW DYRREPPHIA
8241	22142	A	8301	2	273	PLTRGPFSSASDALSSGGPYHSECCFTY TTYKIPRQIMDYETNSQCSKPGIV*V VHTHTTGGRGSSQGLLEGSEWNGDP QRTSQV
8242	22143	A	8302	77	430	GMGLSMHRTHFOYLAHIHPCVHVHTH THHTHTHTHTLCM*HTEIHKSVRYGTE HAQDFPFSIYSPYTPMCACHTHTHTHTH THHTHTSVVYTHKVCETCLSFYFPESG TISHAQEILKRCLENKTHLGVNCFSTLL SVANIVFFSYKROVAARGLFFSLQA E
8243	22144	A	8303	137	396	SSVKTMNYLKFVVMHADRC*LFQCLPS KKKKKKKKKKKKKKGGPKKKKILTRGG GGIFFFFGAPKKISPRGV*KKKKKKKK KKKGGPLKKKNFNPGGGNFFFPWGP KKNIAGARLKKPGGKNRPS
8244	22145	A	8304	329	144	NGPFFFFFFF*DGVSLLCCPGWTAVARIS LTFVFFFTLNCSSVGIHSELQHWFDYL KLKTP
8245	22146	A	8305	404	157	RTYNS*TLGRSGGQIT*GQDFTSLGRD VGPLHRLKKNYSYSLVCEFYRIKKEYPE SHKKAMKMLFOLKDPDLHIPOHIAIN
8246	22147	A	8306	394	294	SLCLTFEPRDFNLGALYKNFYSPTEGW SCVLSKGGPFFFFFFFKDGVLLSCPH*S QNFVFVALEWSGTEPK*SSHPGLEPKAW DYTYEPHQAVQLLRY*RSFPVLLLDG ICIFHSFFSPRGSILP
8247	22148	A	8307	280	2	VVDSEVFTTFSVITVMLFSIQYVKOLEN IKSWFIVARACNPSALGGRDG*AOEFD SSPGNTAKPCLPQKNKTKQKTKNKVGGT LETRSWRL
8248	22149	A	8308	136	330	MSYQKRSVNKYKSNNAEEVITWARHSG SCLRLYNPSTLVGSGGKIP*TOEFETSL SNIARPLY
8249	22150	A	8309	3	118	IFVVLVQMGFHHVQGSLEL*PQVIHP QPPKVLGLPA
8250	22151	A	8310	2	366	TRVDPRVRVSTRNLNLCFSGSSHASTSA S*VAGTTSACHHARLIFSFFFFLFGSE KTGFNFQAQGGFEPLGEREDPPFGPGFG WGGGGGTFKRP RRWKFKQDIIPLVSN RGDQPEPFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8251	22152	A	8311	253	446	SKTFQARGGVTEMGRFHVQGTGLEILTS GDPASACQAAGITGVSHHARLRI*YFI RIFILMT C
8252	22153	A	8312	430	88	GVGRITQISWSFWLPKPKNSPGSPQ*VG APGGPPPPGYPFFFFFQKKGFLPSGRV *SGSKNFFVFPKNGWTSFPPPPPEGR GVFFFFFLSRDGASPCCPRPKVLGL QV
8253	22154	A	8313	400	323	HLNFWPHFDLFFLVETGSCYVAQAC ELLOGSNLPGSAS*NRITDVNHHAQ* KSSSGPGTQQC
8254	22155	A	8314	4	421	QGRRTAQEAKVAVSQOCTALQPGHRS KTPSQKTKKKKSPGGPPGPPGRFPPFF KT*KKGPFLKPPQGGDPRGKKRGGG LWKPGGKLGPTKTKTRGGGANPPFLW KGQGGPKGAPRAFPTTKKPPPSGRNQ
8255	22156	A	8315	213	32	RCFGTVGHGCHSPSLGGQGRIP*GEF ETSLANMVKPYFFLNSKKRTKNHPTKK NQAN
8256	22157	A	8316	422	153	AATLYTHKTHPCYFFLDRLNLLCCPWS QTPGLK*AFCLSLPSSDYRHKPPRPV SPIFRKSYDVIPPPYLE*NPMLYLP YCHHI
8257	22158	A	8317	1	284	ERODWESRLMEACAFHLEKSVNQSLLE LHOLAMEKGDQPCDLFLESHLNQVKA IKKLDYLSNLCKT*APEAGLAELYLFDK LTLGSEEDT
8258	22159	A	8318	187	37	TRDFFWPGVVAHA*NCSTLGGQGRRIA* AQKFESNLGNRVSHCLYKKFKN
8259	22160	A	8319	2	250	KYEQSLQEVWDCVKRPNLRIIGVPEEEE KSKSLENI FGGIIEENFPGLARDLDIQI REAQRTPEKSIARKSSSRHIVIRLSK*E WDCVKRPNLRIIGVPEEEEEKSLENI FGIIEENFPGLARDLDIQIREAQTPE KSIARKSSSRHIVIRLSK
8260	22161	A	8320	371	196	NNFSLFFFEFTRGH*VAQAGVLGLSSG NPPCASRVAGVGVGVHQYQDDFKNFR HN
8261	22162	A	8321	3	235	FISVSFKYSKHIPNNMHLPLVLFLNFF FRDGFMLRSG*SVVAILRCGHSLQPLT GLKQSSHLSFGQSWDYRRAPF
8262	22163	A	8322	1	395	LEVPLNLSLLASGVST*AHRLIES NRNQIQAALLITLLGLVFTLLQASEYF ESPFTISDGIYGSTFFVATGFHGLHGI GSTFLTICPIROLIFHTSKHFGFEAA A*YHWFVED*LFYVSIY
8263	22164	A	8323	322	83	MHQSFVLAKVKKKGHRNPFYSLMIKSA PVLVSHTNTLLCWPAVHACNPSLGG QGRWMA*AOEFETSLDNVCKPHF
8264	22165	A	8324	12	249	GFLLPFPGRGKRGPPPPPLFFWFFFK KGEFPLGGGNFLTLEPPRLAPPKGGK*G GDPPPPGFFFFLKKKPKLLKG
8265	22166	A	8325	139	335	ENILWAATVVLDCHPSTLGG*GGRIT*G QEPKTNLANIERPHLFFFLKRNFFFA PRVEGRPV
8266	22167	A	8326	1	246	FRROLVAPRVLLCYPGNRAVQS*LTA ASNSWAQAHLSLPKCWNYKHTPPYPTC *NSACWDESSFLLVSAMEVCGQPHS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /possible nucleotide deletion, ~possible nucleotide insertion)
8267	22168	A	8327	422	107	IYYVROQRKKRGLPFFFRFLPPGGGQ WGHFWFLQPPPRGV*RFFFPLNPRNRW DFKGLPPPPAFPAFLKKGVPPGGQDF *ILAPKGPPTSTSQRKNGPKD
8268	22169	A	8328	1	161	FRGIRWVCHLVFFYLSFFLRGLAVLR LILNSWAQATLLPOLPE*LGLOTTSS
8269	22170	A	8329	422	103	PYSPDPFGGPGGGVPKVRESGPPGPGOG NFFFPKPKNNPGGGGGLLPPSSGG*A KMGLSRPRPLPLS*NNPPPPPPGGQNK LPFPKKKKKKKKKFNFEHRG
8270	22171	A	8330	46	422	STFFPLASQAGITGVSHRRKSSSFQC TQIPLFPETLPLNLGFGSRGRGFSQVL PAQSSSFDLDLISVLGY*MLSHISLGN RALGFIPHLKSWENGSTLRSIVLSQIE GLSSTLSFPHVPS
8271	22172	A	8331	429	112	FSHLGSSFRQGTMLARLVVNS*ECDPP TSASQAGITGVSHHAQPHAVFYIRLPD SQVLCHQMPWPTAHYPHRWIFSLVLQK NLSVPPPLWPIQSQPKASILLN
8272	22173	A	8332	291	19	KTFPPPKI*KFPNPLKTFPGCGGPPPP FLKKFVSGNPPPKKIFFFFFPPPPPPF FFFFLRRGLSISIAQDGIQWHYHGLQ PQLPGLR
8273	22174	A	8333	307	123	KYFRGGGGGGR*FPPLGGVKKKRKNPG GGGSKPKLGPSPPTRGKKKNFSPKKK KKKK
8274	22175	A	8334	3	169	HASADWCHQAQALLLLLVETGLCHDGRA QPGS*SQEIHPPRPKVLGLOHFLY
8275	22176	A	8335	1	208	LCVCVCVCVCVCVFC*WRKGLALSP RGCSCTNMAHCSLNFSGSSNPSVSPSH VAETTVGRPILG
8276	22177	A	8336	1	352	ILFYFIYFVYFSCFEMGSRSVSQAGVQC PDLSSLQPLPPRFKRFCLTFPSSRDYR CVPPLHAKFCIRRR*AAIGQAGIELLT LSDPPASAS*SARNTGVSHSCGSPFINF LNQI
8277	22178	A	8337	420	272	KAPCFSGEKTVPKHCWNSWVPRKKO QQKONLCPCLVLYTSINSQ*TMGLNLKA RTVNIS*KYKEDP*TGKK*INKSCPWTG KKKFLARTQKTLAIWDTLINWTSPLK MSTKQRHLLKMN*PKWLLFPVS
8278	22179	A	8338	427	202	LIIYFCHQSQVQKGVLPFLQEREGWAEA SLKISNISLSHTHTHTACHTHTHTHT HTSS*NGIKTVITIKSFA
8279	22180	A	8339	2	164	TPGHGISLRCPGWSAVAPSLTATSASW VQTILLWPPE*LGQESRLRDHL
8280	22181	A	8340	422	1	PPGPPGGKTRAPPPSFFKGNPLLKKG GPAKPPKNGVFFPPPKVKQKQNF GTQISQPNKRG*KTFFFL*KKPQKKK GPPGGEKIFKGPKE*KKPSGPFPPFLK QGLTSLRPLERSGANTAHCSLKLSSSD
8281	22182	A	8341	1	456	RTRGAVSQGHAIALQPGQSETPSQKK KKNPAPGGKIGGTAKKGRNFDANI LGNPSRPGGAFGG*TAPEGKRGSGPG IRGGGSGGPKKLLSF*KAGGAKFFPS PUCITFFRGP*KGILLKKKFKKPGG NPNLSPTNEFF
8282	22183	A	8342	407	2	RQFILGAPGVPPPGF*KFPFKIIFWGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						KKKNFPPPPRGEKFFSPKGADPLFFFFF FFFFFSPFFGALPFFFFFTILFKTKFG VFSCKGIKPKFFKRSRPPNGAGRLPLL VGPLGVPGQGEAERKISQGSFQ
8283	22184	A	8343	441	1	PPPYILGGPRVFSPPPPFKTPPQIFLIG PQKKKNSPPPPGKIKIFF*RAPPPFFFF FFFFFPPPPFGALPFFFFFTILFKTKF VVISWKGIOPLKFRSRPPNGGRLPLL GGGPPPGVPRGGEAERKFSRGSFQRTGG SAEPFA
8284	22185	A	8344	466	323	FGVAGTGNPGRNRPVFSFRGGPPPGVPO GRNPPPPFPPLNPPKILTP*VTFPLE PFIEWVGGPP*PSYGVSSPVARK
8285	22186	A	8345	657	347	LFWFFFLRQSFTLVAQAGVQ*CDLGSLO PPPPGFK*FSRLNLPSSLDRCAPCPA NFVLLVETGFFHHVQAGLELLTSGDPFA SASQAGITGVISIAQPAQ
8286	22187	A	8346	3	212	DCSRGPPPHLANFGLLEKTSNHDVDAQ LKPLSLRDPASAS*SPGITGSHRAQF *PIFKRGMADKGF
8287	22188	A	8347	9	255	IPGPTHSPDFLLYETIDLPKN*KGPPFP PRGGGKNPPPPPPFFFS*PWKKITF QTPLTGVFGAPKNFNWGGFKKIGF
8288	22189	A	8348	79	312	NAAGFEVGISKA*ALETLGITREHGSN KPRYATVFSHEMGTVLHLVEQHTVGY ITASCALKC*IESGGFLNDYI
8289	22190	A	8349	1	369	PPFFLKRDVPSLSSRVYKWHYSSSLQ LQTPGLQ*SSCLRFLSSQDYRHIPPCPT NF*KCPVEMGSCCVTQGSOTPGAQAVL PPWASQRHMLGQVRPLCSLLLSNCPHS RLVWSWLFSGC
8290	22191	A	8350	434	324	LPILSPVWHRMPVPGTREA*EQ*SL EPGRRRLQ
8291	22192	A	8351	3	253	YMCSPFFLECSGAISAHCHLELFGSSD PPPPPT*NF*VIGTTGTCHHEWLLFELFG KMKPHYIAQVGFKLLERNFLTKTKVFP
8292	22193	A	8352	3	1431	SPRGGTISLKQVYSSLTNSRPSQHLF* EALQARAREBEKKRKEITSHFSQSTLTDI QQITQOQSERNNKLCQNTLAEKLSKI IDQVELREHDLTKFKREQLQQLVDAK LEQAQEWKKEAERHREKVELLNQAE WKLQAKVLKEQETVLDQQLTLYSGRFE FQSTLTKSNEVFATFKQEMDKTKMKKK LEKDTATWKARFENCNKALDIMEKAL RAKEYECPVMKIGRLNLCRALQERNE LHKKIRDAEISEKDDQSHNSDEEPEN VSVQDEIDAEVNSVQTAVENTLATAFMI IHHPSTPHQSKETQPEIGSSQESADRA LKEPEQPLIPSRDSESLPPLTPQAEA EGGSDAEPSPKASNPAGLGAETQCEGL PVGQAQDAQSWKPEASAGQAPAPTEA SLQKMEADVAPACAAEHVAMVPACE PSRQPPRAAAEELPVGASAGQPPRNVA
8293	22194	A	8353	376	65	IHCGDHVQEVPLKVCALHMSWACSGI PKAGDKLITDFTLTDLTGKCGTLLSG PHKGQEVYWHFSKALGTQHSHTKPCVHS RDQFKHIRG*WASQGYKN
8294	22195	A	8354	459	85	LEEVESLERVLKMKMIESEELSKQTRF

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						LEETIKQDKLNKSLKEBAMLQKQSCBEL KSDLVNKELLKQKTIETLRACQKQYEL E*ELAFYKIDAKTEPLMYTPEAEIDK APDESPIYIGKSRV
8295	22196	A	8355	231	158	PFIFYLYQSNDIARGLERGLEPEKVI G ATDSCGDLFMFMK*ESVAPMTVSGSRP LSKPRATSLWYK
8296	22197	A	8356	2	164	IHRGVENQMAEQGWDRVSYVWVGAVA HACNPTLGGQGRWIT*GQEFETNLP
8297	22198	A	8357	23	291	CTHTRACAAHANTHLFFYFLYIFNFEE TGSH*IVQACLELPASSDFPASFSQAG ITGMSHHAWPTSCILLKVKMALCSINCSA ACFLY
8298	22199	A	8358	1	307	FFFFIESCSFAQDGVQWCDLGLSLQPP PGKQFSCSLSLSSWDYRHVPRLANFC IFSRDGFHHVQAGLQLLTSDNPPT*AS QSAGITGVSPRAQPCPAF
8299	22200	A	8359	75	266	FVKTRNLTFLVLEAGKSNIKARAG*VSG EEHGLCLQDQALLPLEGRNAVSHPRGQ NMMAKAC
8300	22201	A	8360	1	295	NTWVFCFVLLFRDVRSLCCSVRSTVASS *LIVNMNLSFPSS*AYRHVSSHLDFFFG FKIORILILPRLSINFWPOEILLWLPGG LGLQPRPQVLVGN
8301	22202	A	8361	376	293	MGFHHVQAGLKLTLTGDLPASASQSGAR ITGAGHHAQPDF*HSGDSWQAPPEPRDQ G
8302	22203	A	8362	375	142	PQEEFLRFATDVGEYRAVTELERPVSES WNIOKDLL*QKGRVSTYCRHTYGVGES FSVQRGEHVGGRGLQPCLEI
8303	22204	A	8363	36	363	QLSFNPLIGKVKLRTVFIGKQFLFLLG GVREAGAGHGAQATVWHNLSHAKRF SCILSPSCDHHLPHRANFTIPTD*I PPCRSGHVOTPELQKPTILGLPKR
8304	22205	A	8364	455	235	GAQARAPPRTGIIFFFW*RGKFCMLPRP VSKPWG*VPLPWPFPKRVGLDSWAPPPR DFIFFSFVVKRVCIW
8305	22206	A	8365	432	175	STDQVSVAMGPS*PGAGYNLLVCRNLR LKKCSIRMVGS*FSRYCLSLPLDKKGN SLTPCARSVRCTVMLRLMLRGLHPLSD KP
8306	22207	A	8366	383	83	RRLIVFICVFSKK*GLPLLPRVSNFWP QVILVPPPPKVLGL*ALKKLWLDVTHA YNPSTLGGQGRIT
8307	22208	A	8367	27	304	FFGFILFLKSSN*CTLRFCFLSIGKVR IHTLGNILSRRGYGERCSLPHCLWESIC LPVQSN*ALHKKVQMHIFFDQAIPSRGI LPTDIGHK
8308	22209	A	8368	165	204	QNIPIAVSFFFFFLKRVSFCCPG*RAGG QSLFIGALTQV*GILIPYPPGNWELRG PPNLTNFF*FLNLRFLGGINLHYVHD KTSPLLYLFFFFF
8309	22210	A	8369	400	201	KERPLFRLIGSPFGQTNPRFSSKGVEK NSNFSKY*PPFFINAPRVCFEGIEVIT KFFQVRPFFP
8310	22211	A	8370	21	408	LIPLSTYVCVRVCEVCVCVCVNI*GYA CNTLLIACNILDVPTSPTKDKIPSGD FLTLVGKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
8311	22212	A	8371	1	94	NTLGHEN* LNSGFGGCGSEFRSCHCTPTWATE
8312	22213	A	8372	546	972	DIHSLYGR*DSFCLGLALFKTLQVMHFLKDSVRNLKSNLKVGLNFRSPQIQATISDPLQPKTKTYEEDPKSPKKEEKMEVNMKEWILRYAEQQNEEBENKENSLEEERKFDPNERYHLHLAKLLDAKEQAATFKLEKK
8313	22214	A	8373	502	178	QHFWRLRKOKSFALGG*KDPGKGGENPFFQKKAQNLG*WDQPVVPTTQKGGGGESL*PGRTKSPCTSGWGKQNPVLKKKKNPQKTCNIPLCIYHIFLNRKNTNTV
8314	22215	A	8374	362	112	YRMSVNPQVRKRVRSQRTNTPPNFFF*D RVLRLCRPG*STVQSQQLTVASISWAKAILLPQPPQAKYFLRLVKCSSEKGERIE
8315	22216	A	8375	411	21	VLGIYPTLVSPSPGLKMTRVKLPSGSKKVISSNRPPVEGVVAAGG*FDKPLKAGRASSKYAKRNCWPRVRGVMNPPVEHFGGGLORIGKPSAIRIYAPAGRKVLIAVRSRGLRGANTVQEKEN
8316	22217	A	8376	450	108	AEGGRGPRK*LRSCRPPVDGSAQSGPGLRTESLETGCGSPGVVQLEFPFRRPPGWWPFGPPGHRDRRQHRPPGARSQQGPESH*QRSGESRPPAVPRPPCPLPWKGGVL
8317	22218	A	8377	25	306	EQCPFPVAVHQSGPPGAPPEASPSHPGSGSEKPPVPEFRAPLVQPKP*LSPPHHPAQLLAHVALAGGPGTVQGRGLPGRAARAVSVRVPAAC
8318	22219	A	8378	376	149	PAHCSLLTGFGRSGSCLSLFNYYPGRA PPRVGNFFFF*EMESCYVAMLP SLVLT SWALAILPVLPPKLPGLQA
8319	22220	A	8379	98	374	SVPPFPVGTYEGDAATFGGGGLPALGR*GAAGGHVQOQHPGPHRGAAPKPSAQGGPGHSRECLPSGGAGGEREPFRAGGQGSWMRAPSMT
8320	22221	A	8380	2	807	RFQCCVRAPRAGAVSGVKLWSVP*SGRSAPHPTRS*VRWSRNLRTSQWTSRTRRRSESKVRVSYQAWTASPPPAASASARP A*RTSSRSYSSSSTCCSWLWPSWSGTGQSQTFRNSSLTCLCLTRKWIAMMPQVLPCTPVRPSCSAVSTITRSFLL*QALASRV T* IAPRGSITRTTPSIRL*NLP*LSRGP GK*KSQSWSSSSSA*TRVVRTSAPLITSSLLSRSSCKAQGT*ASCRPVVPVPIPAGSSLGASAPGSRCHW
8321	22222	A	8381	104	327	CIAPFEMLGIRYEVGKCPGSLKSLKILK NTHHTHTHTHTHTHTHTHTHALYLIREGRKK*CVCMRKRTDSTCVS
8322	22223	A	8382	400	270	KPKLEVRASGQVQVLSPIIPALEEAKAGC*LEPRLRHFMVCN
8323	22224	A	8383	178	588	ADLLSGAPGPGGSDQNNSSSEHSRACAPAAQF*WLPQWLC*WQSPLEARG*NPQVSHSSIRIGIPGAAGTSRPSGALPPQAGHGSSGELHVARGCACGRPLNSHRPGCGQLLRVTAADSHRCASRGAAHP
8324	22225	A	8384	423	78	OQOELAEITGVTVESPEEPORLLVSGGTVPLCLACSLHRTL*TVHGSSASSFLAQG

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						DMEPLGDRGLGGTEOLH*GGDRASLODI CFLLPVLSLLCPRSLDLHRHRVGVGTGFT ED
8325	22226	A	8385	434	176	FADDSRFDPLLLV*CAMLMIREQLLEG HFTVNNRLMQDYPITDVCCILQKAKELQ DSK*PGGKRPMPGREASRPCAVAPGTHR NL
8326	22227	A	8386	2	305	RLWEDPPGRNTPPGAR*PGFCGEGGHIY REEQACGWPRHSGPWHRPQAGPLQLGQ WRGKGAGGQARRSPQGSLESRPPTLSAA PPAIHICSVGGVRLICY
8327	22228	A	8387	331	91	EMRSHSVTQAGVQWRDYGSLQTRPFGLS FNVNWDWGL*GDPSSPMLLPSS*ARP GGWGGPGGEGHVSKEAAGRLQGP
8328	22229	A	8388	2	250	THVRLWSQLFRRLRWEDLLSTGGGSCSE P*SCHCTVTWAFPLESLCAHVYVYVTL LTALLGLSPCANPROTAVSLPQAGLV
8329	22230	A	8389	388	176	YWDQS*CMFSFAPVPSACICAIHNFS KSNVSIVACVCGSSHKYVFTHDGRCHHR EAPDVYRDI CDDDA
8330	22231	A	8390	445	330	EPFRTFSCSLRSSWDYR*PPPRPDNF LSLYSLVLET
8331	22232	A	8391	559	142	LRTLPVTLGKSLALSVSPFYVGGNWT NREPSAKRGSGPNRGHGAASCPARTH SLRHSFAGGVMLTQPRILILPETQHS ESAVARTDISKARWLHRSRPNPH*DET SAGAERPGIRCYIGHPAT
8332	22233	A	8392	104	400	YYEIFKKEMYSYHILHFFFFPSFFFFE TKFNSVNGPFGKGPLG*LKPWLLG*KH FCLTLPSGGNYRHVLPPFVNGFFFFF KKKKVFPFVAPRGV
8333	22234	A	8393	408	169	DQWIKDWNIGSLRPR*KGPTILITTP TAVKIEGIPAWIQHSQVQPAAPETWEVR PSLDNPKVTLKKMTSPAPVTLRS
8334	22235	A	8394	1	269	YCCPLFSKALQENSFYSSFRVLNPPG LSLHPEGEGGWINERGRELGPSAGPLL LFLHFAEAGRRQPPDWADSEADLQOVVRH KLGP
8335	22236	A	8395	2	204	KDCKVNKEVERVLRFHQAGKFIGCDAS TSLPAPAPWWSNNAALCCPGLSCVWCQ GESRTCVGEHQ
8336	22237	A	8396	3	285	KVTVKYDRKELRRLNLEEWILEQLTRL YDCQEEIPELEIDVDELLDMESDDARA ARVKELLVDCYKPTTAFISGLLDKIRGM QKLSPTQKK
8337	22238	A	8397	1	192	ETGPHHAGDGLLELLTSGDCPSLASQSA RITGVSHCTRAQLLTQEYFFGNQHLPS APFYKRAF
8338	22239	A	8398	8	241	LNPFYIAPLDPRFRQACTSMLLCCQSRS SGTSHSIRGEKASYSSSHSGSGPGPNMG KGGQMLEKSI PYSQETLVVD
8339	22240	A	8399	2	240	SLCNPFYIAPLEPFRRQACTSMLLCCQS RSAGTLLHSSRGEKASYSSSHSGSGPGPN MGKGGQMLEKSI PYSQETLVVD
8340	22241	A	8400	10	272	CNKQNAYLTVVKCAQDCEDYFAERLYRS MKGAGTDEETLIRIIVTRAEDVLLGIKP KFHQKYKSLSDMVRSDTCGDFRKLVLAA LLH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8341	22242	A	8401	47	248	TRGIFFFFLNTRSHSVAQAKGLGHDHSS LKPQPPRLKQSFNLSSLSTWNYGGLPH SALWKAESAAS
8342	22243	A	8403	497	303	TVEASVSYLLVYAMVQQLPWGKSPASGA ESHROGCGGSWPGGMEERGAEERGCGC LLFOALLY
8343	22244	A	8404	3	235	LTLLAHCRMMAAAHMGGPPMMMPMGENT PGMMPVGPAPGMRPPLGLHMPMIPGYPM MRSPARLMWVPSQPRMTRPRD
8344	22245	A	8405	3	246	LVFSVDVGLLAHTQRGLKRSQSGMSLL GKIGAKQKQMTLEKSKLDWESFKEEG IGEEALAHNRGKEWIKGAQPLQG
8345	22246	A	8406	1739	804	WEPDVSQSAWLAASAAFGMATFSGPA ILSLNPQEDVEFQKQVQVRRRTQKK QEQLTPGVVYVRLPNLLDETQIFSYFS QFGTVTRFRLSRKRTGNSKGAVFVEFE SEDAKIVAETMNNYLFGERLLECHFM PEKVHKLFDKWNIPFKQPSYPSVKRYN RNRTLQKLMEERFKKERLLRKLAK KGIDYDFPSLLQKTESISKTRQSTK GQVLRKKKKVSGTLDTPEKTVDOSQGT PVCTPTFLERRKSQVAELNDDDKDEIV FKQPISCVKEEIQETQPTTHSRKKRRS SNQ
8346	22247	A	8407	2	241	CLRFSSPAMGLLRSGTKLIFRRRPKQK EGLSQSHDDLSNATATPSVRMAGSFS RRLIKRFYFKSKPANGPSPQI
8347	22248	A	8408	285	186	KGLTSLPRLVSNWAQAFLLLPFKVL RLQA
8348	22249	A	8409	1	246	RHENREELQVIADICIKYDTLCSDEEF MNGVEYIWKGPCFCLTFTLYLKGDIFF RPPSGCLNLWIVLNPMPYVHILTSC
8349	22250	A	8410	1	102	AGSYTLHIKGGDGTGRVTRGTFTLHR IOTSEE
8350	22251	A	8411	877	647	FFFETESHSVTQAGVKGWDLGSLQSLAP GPKFKFSCNLPSRSDYRSPPPPLANFCT FSKNGVPCWPGRSSSTPDOR
8351	22252	A	8412	1	130	RMLNDKTLRTDIGNFPFNGWAAIATHS FEFAQDFNFLEATR
8352	22253	A	8413	97	401	CNPENGLTASALGRRCMLATCKAPRTLP DSGDTASCRFPVPRPPHSRRSSGSHL PGRPRCPALPGLWNSPPGPTSGYLEP TFSTPAASHQKTLGI
8353	22254	A	8414	348	516	VSAYGFTIGHERFSDHYDTSWKRLTF YINHDFKLEREVWKRLLHDEGIRLYQRL
8354	22255	A	8415	714	410	LGVFRSALHGSLLWLLRSFFQKSPNPLA LLFLQCNATAYQCLLIADQHCRTKYFL CLASGIPCVSHVWVHDSCHANQLQNYRN YLLPAGYSLEQRILDW
8355	22256	A	8416	2	102	GHPQDRLLAQDSHHNSDRNWRNRPW PKDSY
8356	22257	A	8417	1	309	FYFENALSKSNKPIHTIILNEHVHLVGD DAACIAYRLTQYMDGSGMPKTMQSEET RVWHRDGGKQNVHFRHSGSPVPIKPP CIPNGKENFSGGTSLWQNI
8357	22258	A	8418	3	242	ARALTNAASHVDMPNALSALNDLHAHK LRLOPVMKLLSHCLLVLDHLDPDEFT PVEHACLNVLASVSTVLTFKYR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8358	22259	A	8419	711	296	NVANS DGLTASLWKEYGKADARWVYDPDP TIVSVLELTVALDGLLFLIYAIIVKEK YYRHFLTTLGYCELYGCMWFLPEWLT RSPNLNTSNWLYCYWLYLFFFNQVWVLI P GLLMQSWLELKKMHQKETS SVKKFP
8359	22260	A	8420	3	97	FVVSLCNGLIATAQLFFYNNAKPPHRQK KAQ
8360	22261	A	8421	1	279	GCGIADLMSAIFNFQSLTIDILLICT CAYIPSLAPNLLDRNKTGLLGFHWKCAT IVERKSPYVAVCCILMAFSITLLIQKLVK MPQCI CHNI
8361	22262	A	8422	1	228	RHEVFIELNHIKKCNTVRGVFVLEEFVP EIKVEVSHKYKTPMAHEICYSVLCFSY VAAVSHSEEDLRTPPRPVSS
8362	22263	A	8423	3	182	SEDTGEEQVVTAEFINRGYEYIDTAGYR FOAKAKLYPVASLFTQKRKDDMELSDL HGK
8363	22264	A	8424	1	70	VQVFVDAVTDVITKNNLKDCCGLF
8364	22265	A	8425	2	151	ETTASSCTPASLESRRCCAPCRMPRTGF FGSSPLWRPSCGSRSLKPGFQQ
8365	22266	A	8426	1	187	RGRVPGGGERLVPGVPGAEAQQAGDGV RAGPLQARPPAPVGVSGRCQAAGAAAG PPRPDG
8366	22267	A	8427	520	423	GKYCLQSQENFEAFMKAI GECWTERQSC GSHQ
8367	22268	A	8428	1	627	GTSGTRGVGYFTFTTLYLETPKPSISS NLNPREAMETVILTCDDPETPDSYQWMM NGQSLPMTHRPQLSETNRTLFLFGVTKY TAGPYECEIRNSGSASRSDPVTLLNLHG PDLPRIHPSYTNYSRGDNLVLSCFANSN PPACYSHTINGKFOQSGQNLFIPIQITTK HSCLYVCSVRNATGEESSTSLTVKVS A STRIGLLPLLNPT
8368	22269	A	8429	3	390	ILGCNLTIRVYSLVTCVSPGSKFVILD PLVYIGSRSGLSRSTSSMASRTSSSW VDLNIPTTEAPPCYMDVTPEDHRLSP TTPLLDDMDGQSDSPIFYMYAPEFKMFP PTYTEVDVPCILNNVQ
8369	22270	A	8430	3	208	NGTHVITLLCLKTCGTVVNVANDMIVAS NLGCTGVPNQTPVSGDLLIRSNGLLIPG TCEITRLTYTISE
8370	22271	A	8431	3	563	LPTSRVDPFRVRLDRMKDQEEEDQGPF CPRLSRELPEVVEPEDLQSLDRWYSTP FSYPCLPDSQCPYGCFSYLEEHVGS LDVDEIKYQEGEEDQKPPCPRLNEVLM EAEPEVLQDSLDRCYSTTSTYFQLHAS FQQYRSAYSFEEQDVSLALVDNRRFT LTVIRHHLAFQMGVIFPH
8371	22272	A	8432	2	119	DGDNILVTTFTTYKSVTELNGDITTNAS WRCSERVAPSA
8372	22273	A	8433	192	1285	AGVLSIIEETDSEGLQTKVENQTYDER LEINDSEVASIYTPTRHQGLPRSAHL PNKAMADNSSDECEENKKEKKTSQLT PQKGFSENEDDDDDDSDSETDSDDDD DEEHGAPLEGAYDPADYELHLPVSAETKE LFDVNGLRVPTDVLHKLKLPIDPFI AVGDIDFLKVPDPGKPDNLGLLVLE PSTKQSDPTVLSLWLTENSKQHNITQHM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KVKSLEDAEKNFKAITWIESISELHRS KPPATVHYTRMPDIDTLMQEWSPEFE LLGKVSLEPTAEIDCSLAIEDIMCAILD IPVYKSIQSLHLFLSLYSEFKNSQHKF ALAEQKAPTSSNSTSQAGDMETLTF
8373	22274	A	8434	3	251	TLQADHFNRLSCGDAQTLWARTGYLG FVRRTeltaATGERHDALYVVGALDEL ELRGLRYHPIDIETSVSRHRSIAEW
8374	22275	A	8435	1	225	QTFNLEGGSIYEDSVLQSVFKSARQKI AIEESEDSENEDEDEYHEWKRYD RIGENMCLNCIWNNGGGYIV
8375	22276	A	8436	95	340	CCGCGIAGLAMSATFNFSLLTVILLIC TCAYRSLAPSLDDNKTCGLGIFWKC RIGRKSPIVAVCCIVMPSILTYQ
8376	22277	A	8437	1	317	GPKPLVTSREPGKDVITSGYSSVSTAC PTSSVDGGLGALPOPTSVLSLDSHTQ PCHQOARKSLQWPPSPPESTVSQQQV KRINLCIHSEEDMNLGLVRL
8377	22278	A	8438	80	213	PHLSFNAGITTKYTRNRANSLGQPHC WTCDDARRRGTLQSLD
8378	22279	A	8439	3	767	HEDNIKQKEMKFTYILNIYQDEINTIF NDYIPYVFKLKENCLNKHKNFEPION ELQASQELQIHOYIMAREEYDFPSI VGWTVKYVEEKIVSLIKNLLVALKDF HSEYIVSASNFTSOLSSQVEQLFHRNIO EYLSILTDPDGKNEKIAELSATAQEI KSQAIATKKIISDYHQPFYKQLQDFSDQ LSDYIEKPIAESKRLIDLSTQNYHTFLI YITELKKLQSTTVNMPYMKLAPGELTI IL
8379	22280	A	8440	103	354	NGCEDFLFLFLFYFPETESRSVAQGV QWHCLGSPQSSPRFKFSCSLTLGGRG GWIMMSGVQDQPGHGETTFLMQAGLKT
8380	22281	A	8441	3	160	KLYPLKIVFGMGRVWVKGTVQQTLL ANVLEACELMTLDQRIIMFLAES
8381	22282	A	8442	459	3	CGGLHPVRASWLLCLLPQKQAWAGAPPP AWLPFCSLISDCCASNQDSGVGPSP GAGYVLLVRRFLSEKRSIRVRVTRFS RCHLSPLSLTRKNSLTPTCTSRVRQCLA LLRLAHGALHPLSCAHLALPSEMTVP QWENAEITRLL
8382	22283	A	8443	2	318	RGQNMTAALQATLLNFPINTKSAVNR ARGIVLNVLSIFKANDIEKAVQSLDKNG VDLLMNYMYKGFSPSDNSNAMLQWHE KALAAEGVTSIRVSTALIPA
8383	22284	A	8444	2	109	VTFPFMSCDLQGCACRNPQAEHSRKD LRGYSHG
8384	22285	A	8445	1	69	LVLSNWPQVIRRPWPPRVGLQV
8385	22286	A	8446	1	163	PSEKHNIWVGVTQFSRCLSLPFLSTRKG NSLIPCASRVROCLTLRLVHGACTH
8386	22287	A	8447	1	147	GOAGLELLMSGDRPTSSASQAGITGVSH RARPSSISFILERGSRVKKF
8387	22288	A	8448	914	729	GLTMDTKDQVPPKQPMIYICGECHTE NEIKSRDPIRCRCGYRIMYKKRTKRLV VFDAR
8388	22289	A	8449	134	392	TCPPPFEPFSPLTCAVLVPQTRRWRLG SLFRACCVALLPQLLLLLFLLLFLLP ITREEDRSTLANNFARSFTLLMLRNPGPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
8389	22290	A	8450	37	248	AKITPLLOPGRQEQDSTSNKKILRCCLT MLPRLASDSSGFKRSSHFLPTSDWYRH SPDPLASVPFLLMC
8390	22291	A	8451	367	165	NFFVFLVETGFCHGAQQAQLQLASCDLP VLALQSAGITGVSHCARPISTLKDITKT SHFVPLKISCK
8391	22292	A	8452	2	282	GKRMAGGPEMMQLRLDGNRLYITTSNFS AWDKHLYPDLIREGSAMLHVDDVTALGG LKNLPYFLVDFWKEPLGSLAHELRYPG GDCSSDIWI
8392	22293	A	8453	4	163	HHDFHAQSLIANIERIAIYVFAACEAAA VLSLLVSIISNTYGLDYLNHLKLLQC
8393	22294	A	8454	374	197	TPFPKQSSHLGLSKCWYRHEPQHQARN STFDSNHSSLAEDAELLGYFGLSQWQPG YQP
8394	22295	A	8455	343	161	MGMGPSVPGTGYNLLVCRLLRPLEKCSI RVGVSQFSKYHLSRLPLPRKGNSTPCA FWVR
8395	22296	A	8456	1	193	MGFLHVQGAGLKLPTSGDPFPTSASQSG ITGMSHRVQPYVVLISICQTLHSVCILL ILLTTVL
8396	22297	A	8457	342	263	WLRPVVVALWEAEAGSGLELRSSRPA
8397	22298	A	8458	101	303	KAAYLFQRLHFQFNLNKKDNMLFNHR MENFKELFGPGTVAHTCNPSTLGGRGWG ITRSADRDHFG
8398	22299	A	8459	3	140	YLKHLCHYVCKYLRQGLMLPRLVLNSW AQRILLPWLPKVLGLQV
8399	22300	A	8460	327	248	FPRLVLNSWPKAILMPWLCKVLGLQA
8400	22301	A	8461	327	79	SIFPFLAFFIYLSFFFKETGSGSVTHAG VPGIIIAQCGLOLLGSGDPPDSASLVVG TTGTYPITPILSVFNNMPSFILLCLMP MGFQHVQGVGLRWQVLCFLWPKVLGL QA
8401	22302	A	8462	365	273	QAGLKLITSDDLPASASQSGAGITGVSHH AQPHHFFKIRFYIFSSPSVLS
8402	22303	A	8463	375	217	RKCFVQAFLYKCCSGGARWLTPTPIE LWEAEVGRWIT
8403	22304	A	8464	238	354	FGXRIHKNLTDHSPSEIKQITTSISIEP GVEVEVTIADI
8404	22305	A	8465	367	248	NMILGWAQVTVFVPAIGEAHWGGLLYP RSSKPNATQQNLLFTKKKNIIYYIYYI YIYERY
8405	22306	A	8466	341	153	VEMGFRHVQAGLELLTSSDPPASVSQS AGSSTSLPTADLLTPGWGVYVGLVDKNP VTLIAMQRLPAVLEKSKVARKNSENKIV LKRGO
8406	22307	A	8467	368	101	HVGQAGLALLASGDPPDPTSASQSAIAGV SHRARPEAPL
8407	22308	A	8468	362	248	SARLGLPKFWDYRDEPPCPADDMLILMV GILETFSLIFTATMESGRNYCVYFKMRNK HIIKSTS
8408	22309	A	8469	384	196	LAMLFRVLVPSNWSQVVLSPLPNMLGLQ V
8409	22310	A	8470	386	300	PKGNKFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF AIVYQTLACNNKFLQMERVTRKLQRC
8410	22311	A	8471	380	178	

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleo- tide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion
8433	22334	A	8494	327	70	KSGFSNVQAGLEKLTLSDDLPSVASQSA GITGMSHCITWPLYPYFGLGSRFSHSIE HCWYQLAPFFESCRRNPVVIVPFVHRFYL TF
8434	22335	A	8495	97	219	PQTVAHACNPGVLGGQGWMITSQGEFQT SLASAAKPRSTRP
8435	22336	A	8496	3	191	GIRGETILEVIEFTSNEEMLCRDPKGYK GYVPRTALLPLETEVYDDVDVCDPLENQ PLPILR
8436	22337	A	8497	144	304	SVFYEEILFSTVIKKNAIVSFATWTEL EAILSELSTOEOKTKYHMSLVSGS
8437	22338	A	8498	2	90	LTILVLAMWKGVFFKRNRFPLESDDDEG E
8438	22339	A	8499	1	156	PSSQDYMHAPPILANFLNKFVVKCLAM LPRLMNSNPQTILLSPPKALGLHV
8439	22340	A	8500	67	319	KMSFGPTLLSARCVSTQIGMNELNLN IDAMSVAATINNEIMSFARTWMKLKAIT LIIITLLEHTKYCMCSLIGSLRMTTQG
8440	22341	A	8501	3	299	ETGSGCVQGGVQWHTSAHCSDDLGGSS DPPASASRVVGITSAHHPLLWSLSSLP LIIAPHNMLNLLLLPSLSIVLNHIL PPLPLPRLLCSPC
8441	22342	A	8502	56	142	NNSAKKKKKKKKKKKKKKKKKKKKKKK AAF
8442	22343	A	8503	486	348	TGFHVAQAGLELHSSGNPPALASQNG ITGVSHHAQPAEYNFK
8443	22344	A	8504	158	403	RIFPFETVTGVAGDVGVRGALDLPRL FELFKRSCLSLPSSWDYKRAQPNPNDF KRQMAFDPKIORISLASKKKKHNP
8444	22345	A	8505	3	78	DWHIYAVVLVGPRRVIEEMESQ
8445	22346	A	8506	164	291	TRFCCWCVLVWVFCVLCVAVFPWCIL LFFIVLVLLLLL
8446	22347	A	8507	372	69	CAPLPLPKFFPPRGFIIRGGSGFIPFP PKKGVLPKNPKGFPPPPFLKPAQGA FNYPFPGGKIFFSPPRGKWAPGGFLKG APPPPPPPPPPPPLFF
8447	22348	A	8508	282	1	SQHVAAQAGKLGLGSRDPTLAAQSAGI TGVSHHARFVLVSSVLSMEFLTWSA VILPCICSFVSLAVPSSCILQQPLPPT CTYIKTETCI
8448	22349	A	8509	400	45	TPPVSLFFLELKEITFECPFPRLSLPP PPFFPPPLPFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFL SKEKNK
8449	22350	A	8510	241	419	TPLGWGEKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKGGGLKKPLGGANFIGA GNV
8450	22351	A	8511	317	28	QSLSPSQTVVVFYLIIVAVFTTLTI LISPSFSRMELKTLKRCVFAFPYAFALF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFSOPCAQTAGRAQV
8451	22352	A	8512	124	292	MCCYIMSLLVICTITKEPSTRKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KGVLPL
8452	22353	A	8513	1247	910	QAQGLDTSCTYKSGMILCRNDYIRLF GNSGAAGACGQSPASSELVNRQGNVYH LKCFSTCSCRNLVPGDRFHYINGSLFC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8453	22354	A	8514	99	262	EHDRPTALINGHLNLSQSNPLLPDQKVC
8454	22355	A	8515	85	2	MNKRFLNKKKKKKKKKKKKKKKKKKKKGG PFKKNPGGAQIFPGGKKIFFLKGGL
8455	22356	A	8516	244	423	GWGWAQWLTPVTPVLWEAEAGSGROE VFAVFNFLGWVMDMLINLAVVIIQCAC ISNHVHVHLEYIQFLFANYTSIKLGKKP SKSV
8456	22357	A	8517	3	114	KINGEDKQKILDKCNETINWLDKQKVCV FFFFFFFI
8457	22358	A	8518	413	91	GGVRGKISFRGGGFLKKKKKLLKKKKK WGGGPKKKKKRGGFFFFFFLNFPMWGGV KKKKKKKKKKKKKKKKKKKKKKKKRRK GRKBGREGORKEGEGORQENMTA
8458	22359	A	8519	1	163	SRLPGRSRRRSRRRRRRRRRRRRRRR SRVLIFFPDQGLDLNIVYIEEDVDA
8459	22360	A	8520	191	21	KFTTAVDAKATVTFVFLYESVFLHWGAC LELLPSDDLPAASANAVTVGSRAWL
8460	22361	A	8521	2	144	AAATQAAKWCWVVBATWEAEVGSALPK GRLOLPMTIALVHLVAT
8461	22362	A	8522	90	8	KTFPLPTLITARTLLTPTSLIITL
8462	22363	A	8523	305	146	VFRHSCGIRGSVDVKTITGSLLVIRETE NVPDGPNNKNKNFYAIQSSSIESQ
8463	22364	A	8524	176	2	LAWFLPLPKCDVYRHEPQLASLTTFV REWDKIGNAWMLTPVIALWEAEVGRSQ GQ
8464	22365	A	8525	2	200	CLIPSSWDYRHMPPRPANFCIFPPFFLGF HVSQVGLKLLTSKDLPAWTSORAGITGF SHMTKPGQFF
8465	22366	A	8526	2	217	SFSLFFPSPFSLLLPLASLLLPPLPSF SLLPSPFSLSPSPFSLLLPPSFSILL HPTFSHLYPPSPSFI
8466	22367	A	8527	2	186	IRGLRPLEKRGIRGVGSRSFRYHLRLS FARKGNSPTPCASVRRCPSLLHGLHPL SDKPQ
8467	22368	A	8528	3	153	CLGFLSGWDCRCIPPCLANLKKLFVEMG SLFWQWILPFPPLKVLGLQV
8468	22369	A	8529	2	388	RTAVHTFILVLQVCVCRHLSLAALTPA HLVCSHRLSYLSIRGSDHRCMTTTP GLVISIFFVEMKYRYAVHAGHILLGSSY PASAYQSAEITGVSHAWPTDSLWOPH MVICISCFLANVLIGTM
8469	22370	A	8530	293	64	YRISIKVSKWFGWVSSWIFFFFFFFFF SFFVFFCFMFFLKQYLKFIINIIL TQALYICTTSKICYSFLYFR
8470	22371	A	8531	2	250	SLGLPSSWDYRGTLPLCLANFCIFNRDG VSLCCQWSQTPGSGVIDEAVSYIYAY IALLIYVVAQWEVWLKHFCCILKYT
8471	22372	A	8532	2	201	FHHVGTGLLESSGDLPASASQAGIT GVSHCTWPSILYRNFKNLAVFIAMVI EGNYNTKTCI
8472	22373	A	8533	319	200	TFTFFLQRNGLTMLPRLVSNWAQAICL LQPPKVLLEWA
8473	22374	A	8534	160	297	KTETLALVAHCNPSLGGIRGVSSAH EFKTTILGNMTKPILYTKL
8474	22375	A	8535	333	228	PNRSHYIAIVKSHDFNLFLDDIVEVSS FLISYF
8475	22376	A	8536	3	325	PPSLLPFSWILDCASSNERDSVGVGFS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EPGAGVNLVCCFLSLEKRSIRUGVTR FSRCRLSPSLTRKGNLSLTPCASQVRR LALLRLAHSAHLPLSCSYCLALP
8476	22377	A	8537	216	5	KLGLVLNLVEFQVVFLEFFLEILLIE MRSHYVAQAGLELLGSDLPASASQSAE ITGMSHAALPNYSF
8477	22378	A	8538	136	22	RRRRRLVLNWPQAILLPWPVKVLGSQV WATCGRRPAS
8478	22379	A	8539	136	22	RRRRRLVLNWPQAILLPWPVKVLGSQV WATCGRRPAS
8479	22380	A	8540	8	319	YIYMSMYLIYVCIYVSIYICVCYIYNS ISPTNYMIYIYLVYVYVYVYVYVYVYV IYTNISIFNTHITPIKHSDVHTVSTTRC NLOGRGFCHTWPLDPLAGW
8480	22381	A	8541	331	156	SVNGLLSLPACLPVCLPACLSFLPSFL PSFLSFFLLLLLQKPVNSLIFSQSLS IS
8481	22382	A	8542	72	1	KIGQARWLAPVIPALWEAEAGGSP
8482	22383	A	8543	2	83	QAGVQWRDLGSLQALPGFMFPSYLVG
8483	22384	A	8544	293	2	KTWVHYLVNAPEVEIQIYISQETCKSMY QETCTRIFFIALLFIAPNWKQRQDTMNP GNKENGKVTALDSOGFLVRFQSLMRNCS PLYPFNKFPILLK
8484	22385	A	8545	314	122	LVETGFLHVGGRAGLELTPSDPPTASQ GAGIAAVSHRGQPVDFKNNISTQIQGRP IICNYKTF
8485	22386	A	8546	316	123	LVKTGFLNVRGRAGLEIPTSDPPTWASQ GAGIAAVSHRGQPVDFKNNISTQIQGRP IICNYKTF
8486	22387	A	8547	3	247	GIMATERLANYTGGIYAEYQDITTYINH VSVAGWGISDGTETWIRVNSWGEWVRC FHLGLVLPKRKSNVSRGLNWSVIV
8487	22388	A	8548	289	25	QRREKFFKNGPPIFFRGPGPFQIFUSF PFFFFKICVFFVFFFRSLVLKGDFFSN FLKINCFFFFFFFFFFFFFFFFFIKN RPCL
8488	22389	A	8549	289	2	KKKIGETLCKLCKKFLDVTPKAQETIK QKKEKLNWQPIKIKNFRSPKALLRRGK GKPGTRKRRNANHISDKGPLCRIQKQNS RGAQWLTLVV
8489	22390	A	8550	290	187	RQENPLNLGGGCGSEPRWCHCTAAWTE QDSINK
8490	22391	A	8551	293	183	RDEGRGISYMLPRVLNLSWQAILLPQ PKVLELQA
8491	22392	A	8552	364	87	MLPLDFLFGPSLDFCPFFCESGGGKIV PESTTPRASAFPLPPGAANIHHILQLVGA PRVPFGFHHVGQGLDLVDLVLRLPRPP KVLGLQGG
8492	22393	A	8553	57	225	KWKQKTPWAGGVAHANCLSLTGGRGGRK ACAEFKTILENIVRPLCSKNKWSISF
8493	22394	A	8554	326	2	KSKRGYSEPLVFSICARAPRSHSVSQS TVYGHAAHSTQFPFRLNRSSYLSLLSS GDYRHDPPLAYICISVIGNDVEHLFLC LLSTCISVNRSHVYSTLVPIFGP
8494	22395	A	8555	372	148	YICFLRSSVRQILFTPDSCDCSMMWPCN IRLPGSTHWCASAGGAGTGAARHARL IFFVVVFFCIFSIFSRNH
8495	22396	A	8556	422	269	AADQERLHTYQLNYYHFCRKRGLTTFPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8496	22397	A	8557	669	407	LVSSSWQAQLPTWPHKVLRLQA AGVWRNRLSTLQPPPRFRFSLHLSFES SDYRCPLPCPANYCIFLVEKEFRHVKG AGLELLTSGDPPANVSLIAGITGVSHRA HPD
8497	22398	A	8558	195	352	LGLQAGTTSAGSYSTVILGQMLKPRSWAN WPVVPATREAEVGGSLSPGRSKLQ
8498	22399	A	8559	345	219	MLARMYISLTFCDPPASASQASGITGMS HGWGLNLFKS IHL
8499	22400	A	8560	137	2	VKYCLFTRSLTKTRVPLSPSQATASPVIT CTYTPRNPVEVTEESQKN
8500	22401	A	8561	324	193	RSSGNLPASAAQSRITGVSHTRPKCI ISKKEYVAENNLHKSTS
8501	22402	A	8562	326	121	HNHTHTHTKNNKHQOPQHTHTYHTQTD IYVLAQASQKSLIILSSLAIV
8502	22403	A	8563	3	85	HEHTHTHTHGHHTHTHRTHTHTLCARM ARDRIIPCLTTFVSVFWRDGLLMLPRL VSKLWAQAVHPWLLKVLRLQA
8504	22405	A	8565	2	177	ARVGFHYVQAGLGRITSGDPPASASQ AGITGMSHRARFMSLTHILQDTWRAY AG
8505	22406	A	8566	353	212	AGFRHVGRAGLELVTDGPRTSACQSSG ITGMSHCAPHEKSTAIRLF
8506	22407	A	8567	76	191	ELIFCRDGGTLTVFPLISNTWPAVPL WPPKVLGLQV
8507	22408	A	8568	1	142	GTRGFLHVQAGLELPTSGDPPALASQ AQMTGVSHCASQKKEFLW
8508	22409	A	8569	250	95	SASRAPLPLFPFSLPLRAAGLSFLCPFR LVSSYRPHVILLPLPKVLGLQV
8509	22410	A	8570	3	226	HEHTHTHTHTHTHTHGHHTHTHTHTLV LVYSLCEHIWRFIVISRARVCCIYVVVF FECGYADRRVADKWLNIH
8510	22411	A	8571	1	216	GTRGLGVGVSHLVSKNTHHTHTHTHT HTHTHTATASQLSVFKIWAQFQSLDKGLT YISNSYCSKPYLNIH
8511	22412	A	8572	356	268	LTMLARLVNLFRQVITPQPWPFKMLGLQ A
8512	22413	A	8573	12	175	RWGFHVPVQAGLELLTSSDPLTLASQRA EITGMSHCARSPFFSFFFLSKWHL
8513	22414	A	8574	1	163	GTRTGPHHVQAGLELLTSGDPPVASQ SVGITGVSHRAPWVGLLIALISNEY
8514	22415	A	8575	344	176	EFLVETGPHRIGQFELLTLGDSQTS SQNTETZGVSHHAPAGLALFKSGNAQF
8515	22416	A	8576	2	179	ARGILCHSGTEKLLDSFMSVAHTCNBPT LGSQGGRIACQGEIDTSLKVARPRLYG QIF
8516	22417	A	8577	1	100	GTRGFTMLPRVSDSNAQVILLFWPPKV LELQM
8517	22418	A	8578	3	114	HERHEILSIYLTIIYLSIYLSIYLI YLPITJRI
8518	22419	A	8579	1	264	GTRFCRIELVYRVESLAKAQETSGBEIS KFYLPNCNKGFIYHSRQCETSMDEAGL CWRVYPWNGKRIFGSPETIDGPNCHIYF NVQN
8519	22420	A	8580	1	245	GTSGTSGILGFYLEREDRLQIRDTDTT LSHGYSTFSLNRCDSRHMMNRMFQMLYQ SPFLGYQLSHEVLAFGISIYIYNT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
8520	22421	A	8581	1531	1457	QARNETIARRLMDVSCDLGLPLTD
8521	22422	A	8582	191	2	TITSYFSPTAPGSHYATCFYKFDYSR YFIKVLNEAETGGSRQGEIETILANTV KPLRSRA
8522	22423	A	8584	2	212	ARAGIYPREYKSPFYKTCMRMFIAGLF T I P K T W T Q S K C P S W I D W I K M Y R Q G P I L S P M L E C S G E V S G F K
8523	22424	A	8585	2	192	ARGNSPASSSRVAGITGARHARLIFVF FLVFRFFFSFLKTGFKLVAHSNPQPLTL FAPLHFK
8524	22425	A	8586	277	66	PLDFRLGHKRRLLFPKKKKKSKFVCVC VCVVCVCVCFKRQCLVTLPLVSNWAQA ILLSWPKILALQV
8525	22426	A	8587	395	286	PHLGLFKCWDRREPPCLAEVVLKRYVW VTYSFRR
8526	22427	A	8588	307	177	RYPTSTINYSILNRDKIMPLDRMVKAR PRVMCLWPPKVLGL
8527	22428	A	8589	167	349	RNLRELGEFFFFFFFVFVGKFS VELLVGNLFLFFGGIGFLSRVMCFKEF RCFSS
8528	22429	A	8590	375	240	LLSRFSWFCFVRQGLTMLPRLVLNCWA RGILLPWSPKVLGQA
8529	22430	A	8591	347	215	ETGFPHVQAGLKLASSDPPASASQSA QITGMSRRAQPSAKRF
8530	22431	A	8592	340	114	HRTAHCSLYLSSGSDPATSSQVGTGTG KDQHTWLLFKYFCARVSKINKYKSINK FYELNQTPTSEYGNASPG
8531	22432	A	8593	86	253	LRCCCLSCSTAKKKKKKKKKKKKKI KKKNLHPKRGGEIEILFFPKGGKNLF
8532	22433	A	8594	3	135	GFCHVGQVGLLELTSGDPPALASQAEI TGVSRAWPPVLFPP
8533	22434	A	8595	2	274	PRVRTYLSLGLTVYRSHLISLLCLEGI ILSLFIATLITLNTSHSLANI VPIAIL VFRACEAAVGLALLVSI NTYGLDYVHN LNLLOC
8534	22435	A	8596	3	316	SIPYSWGEKEGIFCMAPPQIGTSTRIND FTALSLHLNTHHTHTHTHTHEIOHLP P QGITALILNSLLRHVCPSLAFPSLSPKQ NLTVRHICILSRDTNLATASK
8535	22436	A	8597	385	291	KAPLPLFFFFFFFVFVFVFVFVFVFVFV KKLGLV
8536	22437	A	8598	275	369	GVQVLKLLTSGDLPALASQAEITGVSH RAR
8537	22438	A	8599	98	344	VHYEEFMCVCVCVCVCVCVCNPRVRGVD MNPVEHPFGGGTHOIGKPCIRRNASA GRKVRMLAALNTVIRIGTKVTLRKT
8538	22439	A	8600	328	195	THVPPSLAKFVFLVMGFLHGGAGL DL STSGDPPALASHVFKR
8539	22440	A	8601	2	214	HVDVVMGTFAILSELHMDMLHVDPENLR LLDVNLNLANHFGDTFPPVQAAYQK VVADVANALAHMYH
8540	22441	A	8602	89	181	GLRHENRLNSGGGGCSEPKLCHCTPAWA TE
8541	22442	A	8603	340	57	KEGHQEMEQAEDGGHGRKAPGTPSWTLG ELPKSARGHTGLFVSYRGCRTPFRPKVP LFGGDRNRGLAMLPRILVLSNWPQEILLP QPSKVOGLQK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8542	22443	A	8604	330	132	TGFLHVGGSGSLKLLTSGDLPTSAFQNA ITGSGSHCTRPFSLFHSYLVLFYGCSSSQ VLSLTARM
8543	22444	A	8605	546	279	RPGPTVSPRLCEICIMAHCSLDFFGSG VSPTSASRVARTTSTHHAWLIFYSSVE TGSHHVAQAGLELLGSSNPPTISASQAG ITAL
8544	22445	A	8606	3	249	NRFNLGSGGSCSEPRSHCTPFWATEQET CTIYLEYCFPPVSHINLVYFKPLNVTIR SPYCLLGLHASSIGSSDILDCWD
8545	22446	A	8607	159	324	VIGYRTNLLHLHCEVLVFWLFLFLK KTYTGIGCMRWLTVPVLPALWEAAGS
8546	22447	A	8608	334	179	TGFPVHVGGSLKLLTSGDLPTSGSQAG ITGVSHCTLEVIYVFLNISITYPS
8547	22448	A	8609	278	202	QOPSTLRDPPAPKRLHLESGSDGH
8548	22449	A	8610	236	66	AASTFFLQKIKRHLSCVMAHGNPSTL GGRGIRISRGREFKTSLGMMVRPRVYK
8549	22450	A	8611	29	177	GKQVMALHCFIFFFHFRRLAMLPLV SNSWQELLPWPLKVLLEQA
8550	22451	A	8612	1	215	HTSRTLVHLRKNFNKYLTEWGLSNLP RLVLNSAQAVLPWPSPKVLGITGMSHC TWLYLHSLDILLKLC
8551	22452	A	8613	3	91	LREGNCLDPPGSGSCSEPRSHCTPAWVT E
8552	22453	A	8614	2	167	FTISLLGLVDRSLTHHINNIKPSPTRE NTLMFIHLSPIILSTRQALAIQHSRL
8553	22454	A	8615	2	281	FCILVETGFHCVAHAGLQLSSGNPFAS ASQSGVITGMSHCTSPNLSLLTQSKSFC LLIQHNHPYAFINSQLTSPILFLSYFI FYDSLFLFF
8554	22455	A	8616	282	182	GQAWLTPVLPALWEAEGGLLEPRSSR PAWST
8555	22456	A	8617	379	207	SNOTTKKYINFFVEMRSHYVAQGLKF LGSSNPPTASQASASITGISHYVWPISP S
8556	22457	A	8618	705	483	DKSFALVARAGVQNHHLGSLQPLPPGFK QFSYLSLSPSSWDYRHAPPRANFCILSR DGVSPCPGWSRTPDLR
8557	22458	A	8619	359	220	RQSLTMLPRLVSNWSAQALFPWLRL GLQALAPIPGKSYNEKTP
8558	22459	A	8620	3	186	HEVSWVKRKQDEWIEFDODTTSIVAPED ILRLSAGGDCHIAVLLYGRPRVQILEE ESEQ
8559	22460	A	8621	1	116	GTSFCRDGGLTVLAQLGSSFWPQILFP WPKVVELA
8560	22461	A	8622	369	188	MYSLEMFGTGNHAGLELLASGLSALA SESAGITCMSLRYRTFRSPKRTAGLDL SLQS
8561	22462	A	8623	202	22	YILGFYFMPVICYQERKKDKRWVETTI MSFVIGIMELGAILSKLMQEKTKYHI FSQV
8562	22463	A	8624	387	315	SNLGGGCGSELRLCHCTPAWATE
8563	22464	A	8625	2	135	TRDLCSLVYLLTFPPLSHDPAKSPSVR NTQELSIKKKKKGRPF
8564	22465	A	8626	3	232	HASAFEEPVIYKSRQRKRNPNPKLVSS QPHGLKSKKKKKKKKKRGRGLKKKKK KHNKKFKGQKKYNGRGAF

SEQ ID NO.: of nucleotide sequence	SEQ ID NO.: of peptide sequence	M eth od	SEQ ID NO.: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, =possible nucleotide insertion
8565	22466	A	8627	97	373	QHGLFKKKKKKKKKKKGGPLKKPLG GNPFTGDGKKKFFPKGGIKKPPGEFLK KNLFLGGKKNKNPFPKKNLPGKKNFK GKKGNPP
8566	22467	A	8628	2	188	RYGCPFPYHTFEFPYVIKSRQKRKEWNP PKLVSSQPHGLHDFKKKKKGAALVKD PSGGPS
8567	22468	A	8629	287	68	GEGRTKQGERNGGSGSERKEGESEHAR RTGRGEGGGGAEKGRPRSARRGRGSRG SKSQTPSRHLPAHII TN
8568	22469	A	8630	364	136	VSLLLGLEYSGTITAHYSLNPLLFTVET GSHYVAQTGLKLLGSSNPPTSQDQTFEI TVGSHGAQPKVQFWSKNLDT
8569	22470	A	8631	355	70	LEPDRFPFFPSLPSLKKFFSPKGFNF REFFPFI SPSPKKRVLSKNSPGGYPKPL RGKIPTFFPPPVKGGPRGLFKGPPPPFF FLFFFFFFLVI
8570	22471	A	8632	2	266	APTISLLGILVYRSHLISSLLCLEGITL SLVIATVITLNTSHSLANTVPATIALVF AACCAAVGLALGSI SNTYGLDYAGHLN LLOQ
8571	22472	A	8633	1	186	LTHNNIKPSTRENTLMFTHLSFILL LKKKKKKKKKKKKKKKKGGALKKK PGGGN
8572	22473	A	8634	2	80	VLEIAIAQAVVPTLLVSLVLRDNT
8573	22474	A	8635	713	333	EGPFPFPRSKKKGTOGGGRKPPSPFEKTF GNPQGRKTGPPPGRPRTYRPPGSGP TRGGGSSSSSNTNAPGEKIFFSKNPGR KTFPPRAILVFFSFFPLKNFFSLRLLI FLGGCAFPFFPPK
8574	22475	A	8636	389	1	FFSFLEFLITFIINNNFFFYFSSLSF FFFLFNLLKHTPPIILFFPFSLSPIFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF LLRARGCKQYKNQKLIYLTIF
8575	22476	A	8637	2	192	VRTLGLRTDAIPGRVLQTTFTATRPGVY YQQNYEICGANHSFMPIVLELLALTIFE IGPEFTL
8576	22477	A	8638	1	87	PTRPLEIAVALIQAVYVFLVLVSYYLHDN T
8577	22478	A	8639	2	132	INGLASTLIITPILILITLLEIAVALIQA YGVTLVLVSYYLHDNT
8578	22479	A	8640	2	113	LFPIAEYNTIITINTLTITTTIFLGTYYDA SPLELYTTY
8579	22480	A	8641	375	22	FIPIISPLAYLFFLPFPFFFIPLPCFFFF IFLFPFLSFLSFLIFLFFLSLILIPPS LFFTFPFFPFFPFFPFFPFFPFFPFF PFFPFFPFFPFFPFFPFFPFFPFF PFFCWLPHRVMIAKVGVISVSKKI
8580	22481	A	8642	180	34	WEISDSLWLGVAHTCNPSLTVGQGGWI TCGRSPSPVKRPTSTOCABA
8581	22482	A	8643	338	133	NLPILGLFYSLQKKKKPLFRPFTGLGAPK GNQGAAPLFGKAPLFPFFFFPFFPFF FFYGFFFFLFK
8582	22483	A	8644	156	287	LTYPYKPPLLCSQKKKKKKKKKKKKKK KKKKGGAGPKKNVCSQAQI
8583	22484	A	8645	1	325	LHCHTNTFVNKVCFTIRKKKKGKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKREKKKKKKKKKKGGGLPKKPPGGPK FSGCGKKKIFPORGYYKPPGGFLGKTL FLGGEKMSNPKKIKPLGEKKIF
8584	22485	A	8646	370	3	PVRASRLCLPKQAWAMAGAPBPASLPP CSLISDCCASNORDSVGAGPSEPGAGYN LVMHCFLSPSEKHSIMVGVTRFSRCCPS PLSLTRKGSNLTPCASQVRQCLALLRLV QGAGTHRTRG
8585	22486	A	8647	341	88	KKKKIFSPPIKRGPPSVYFICPPPPFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFGMGCGRWHGELYNKI PIWHKLCGL
8586	22487	A	8648	1	108	PTRPTRGVASVLYFTTILILIPITISLI ENKILKWA
8587	22488	A	8649	3	96	EICGANHSFPIVLELILPKLFEIGPVF TL
8588	22489	A	8650	457	297	SPSFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFLEYFALF FIYLIIDKNYMFQC
8589	22490	A	8651	84	352	YEKTVDKIIISILPNTDYMLEYNLHLG QIKMLLISKCKKKKKKKKKKKKKKINK FFWGGILITLLGIVLSPLEALKISPSF GFLEK
8590	22491	A	8652	2	111	NNIKPSFTRENTLMFTHLSPIILLSLNP DIITGFSS
8591	22492	A	8653	1	305	RQQQQQQQLRNLDRFLVYNRMTELCFO RCVPSLHHRALDAEEECALHSCAGLTH SNHRLMAATVQLPALVQRRIADYEAAS AVPGVAEAPGVSPSGS
8592	22493	A	8654	129	268	LSEVLYLFPFKKRLILCLFFRNPGSS NLOKITKEPIIDYDPVOD
8593	22494	A	8655	281	117	CITITLSEINTLQAYITWLVSFSEVCLV SLSIYLSIYLSIYVFEYRIKISPHL
8594	22495	A	8656	3	177	DLHAHLGVDPGNLNLSHCLLETLAGH LPGEPTPAGHAFDLKFLDPVSTVITYKY R
8595	22496	A	8657	3	270	RRRGRAHCSLDLLGSKNPPASASRVAT TGTRHLANLIVVGGFLFPVLRLVLRFH ATDKDIPKTGQFTKERGMMDLQFHMAGK ASQS
8596	22497	A	8658	107	11	QFEHTKPTFPLPTLIALTLLLPISPFI LIIL
8597	22498	A	8659	21	136	VPIEHVDVPVNSRAELLKMFIDRDLA QAVRGLITKA
8598	22499	A	8660	1	395	LVTALYSLYIFTTITQWGLTHHISNLEK KKKGKGGKKRGGALFKGIFGGSHFGV WELLFFFLKGGIKKTLGLFKTLFFGG GLLAGPLPKIKGLREKKNFKGELGVKN RVFFFGNFSSGLGVLYKKY
8599	22500	A	8661	1	255	RTGRTRGTRGLTRGKKKKKKKKKKKK KKKKKKKKGGAFLLKPPNGGPIFWGLPKF YFLPNKGSFPNLIGDFLKRFPFWGAYF G
8600	22501	A	8662	136	358	PHIVKGVSIIFKFCVLKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK NKIFPFWGFPFKRWGV
8601	22502	A	8663	198	368	LINLVQFTCILGTLGLIFLYFLRRAT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8622	22523	A	8684	1	406	LYYFLTKSTTTTTLAVQPFFPTPTPSR AKKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKRGGGPKKKTRGGGGGOKKKKK GPEKNRGGCETTPGEKKKKKKGGGGKK KKKKSGGGKNGGKPRGGGGGR
8623	22524	A	8685	391	265	GRFFFFFLDGVSLLLPRLECSGVILANC NLCLPGSPDSSSA
8624	22525	A	8686	2	177	DHALYSLYIFTTQWGLTHHINNKKPS FTRENTLMCIHLSPILLLSLNPDIITGFS SS
8625	22526	A	8687	479	366	GLPKCWDYRREPPIAANFCISRDGVS PCWPGWSCL
8626	22527	A	8688	35	161	SNPFSFAFQVAGTTGRVHHDLQTFPFFF FLGGTGQILCRGGD
8627	22528	A	8689	1	122	THHINNKKPSFTRENTLMFIHLSPILL SLNPDIITGFSS
8628	22529	A	8690	2	152	NIILAFITSLGLIVYRSHLISLLCLC GIILSLFIATLIYPTPSFSCY
8629	22530	A	8691	541	85	IFLROFLSPRLEYSGVIKACHCSNLNLS SDPPASAFKVAAGTTGIRHHANLIFVFFF AETGPHYVAQGGLELNLNLPATAPQS AGIIGISHDDLGIQITWTLLQKLSYLG KKICKDQETGLLHAFHLHPYVPMPSSP QLLQGPDIITNG
8630	22531	A	8692	122	38	GRVDHSFMPVILELIPKIFEIGPVFTL
8631	22532	A	8693	276	77	GVSPCEPVFFFLGRGNPPANGVPRGRD FFVLSPFFVVVYILLFFFFFVFYFLF SPYCFNGSNK
8632	22533	A	8694	3	70	FMPVILELIPKIFEIGPVFTL
8633	22534	A	8695	230	3	GGGIFSPHGHPSLPYHLEREWLAKTGIR DTSNSVHLLLECLRSQRGRARWLTPVI PALWAEAGSGSRQGETPI
8634	22535	A	8696	401	240	PPFPFPGGSEFPFPHPSPSPGSRMFP VLALSQESOMTFFFOAKKLHLVYL
8635	22536	A	8697	103	313	EKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKGGGOKKKKEAFPSKTP GGVSGGGGPPPLNFFLNPDPFPF
8636	22537	A	8698	354	110	KKGTLEFVSESYFTTGVSAKINIRISIT VSVNKVARCIGETPTDAVQSAFOKEVGG VSDSMVHKVEYAGCVDVKVCCHGL
8637	22538	A	8699	2	164	FLVETGFLHDGQAGLKLITSGDPPASAS QSAEITGMSPHACNSSTLCGRGGRIIT
8638	22539	A	8700	191	371	PPDSRWAIQGHLELFTTTRODLAQAPR RKILALLEGSGGQAGWLTPVIALNWEAE ASGS
8639	22540	A	8701	2	170	ARAGLYHVQAGLKLITSGDPLASASQ VRITGVSHRTPKIIKLIFFLFFFF
8640	22541	A	8702	31	229	MEKYNVHPHSGILKRSHEKQALPTIAK RWRQPSYPSIDEWINMWSHTVEYYTA MKRNKQLYSQ
8641	22542	A	8703	3	126	LOELRDPITLTFRLGSPRPVVETRPVD DPTAPSNLYIQE
8642	22543	A	8704	438	31	SEFCAGYNLLVCRFLSPLEKHNRVGV RFSRCHLSPSLTRKGNLSLTPCTSRVRQ CLALLWLARSALHPLSCMCLALPSENN PVPQOMEQKSPICIAHAGSCTEPLFLF GHLGSTPLTHLLSLRINVFRTSE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, /o=possible nucleotide insertion)
8643	22544	A	8705	429	319	PGATIAHRLSLNLPFGSSDPFTSASQVAGN TGVSYCARP
8644	22545	A	8706	426	245	RAATPSPIKLTKKKKKKKKKKKKKKKKKK KKKKKKKKKKRGAPLKKTLGGPQINRGK KKIFFFF
8645	22546	A	8707	1	108	KHFRGGSGVGCALANVAFPLALVSGIY VIHLRKRE
8646	22547	A	8708	3	146	QIEGHTTISALGDGAANVVOGLIRHFRPE LEERMORFAQOHRQAAS
8647	22548	A	8709	2	83	LVLEIAVALTOAYVFTLLVSLVLDHNT
8648	22549	A	8710	1	81	RPLSKTVRFNVILKVTKAGTKKQKQK
8649	22550	A	8711	156	4	RPLSFHPGGKKLFLKKKKKKLCAVAHA CNPS TLGGRCGRIMRSQDRDHGP
8650	22551	A	8712	440	233	TPSYFVLLVERGSMFLRLVSLTSGDFP ASAFRSAGITGMSHQAQPTRGSKAYLP FLEEPDLKHIFPF
8651	22552	A	8713	92	302	AMHPTMGPDQGHGTGLLYAHTPLHPSH THANTLIHSHIYAHASHITPATCPKGP TQPYLCLSPHIEL
8652	22553	A	8714	2	166	KKINSFFSQGLTOAKVHGGRPSSLGPOT PVLKRSSCLSPSSWDYRHEPLYPAN
8653	22554	A	8715	1	129	GFRHVGQADLELLSGDLFASASQTVRI TGVSPCAQHEFFKSN
8654	22555	A	8716	381	105	RRSLHSLVNLGAQAGVQWRDLGSLQFPF PSSLPPPPKVPRLQPLPGRHVPVVEVRV SARPP IVDVRSFSANLPSLESEERLCL AAIPSGK
8655	22556	A	8717	385	125	FFFFLPPAPLLSGXFWFFFFYIFSSFFF FFFFLGSPPPIIFFFFFFLNKIIFFFFF FFFFFNLLFFFFFFFFFFFFFFFFFFFFF FFF
8656	22557	A	8718	409	264	KTDQRWSTSSSKIMSSQSVSKGVDFES SEDDDDPPFMNPPSLRRNR
8657	22558	A	8719	3	269	KKHKRVLSHLKASCPEELLHFSSWPQL LELQLMGSGSHTHMDQHTHMHPIHYT HAHTHTVAKLNLPNVEMNLLSLGAFQ QRLP
8658	22559	A	8720	430	141	LFFFLSFFFDGVLCHFGQSWVAOSOLT ATSTSSKKKKKKATPGIPEKILGKSGK PPRVLLIGHWAPFKFFFNPRILAFF
8659	22560	A	8721	386	290	RNGLTMLRLVLNWLQATILLWFPKVS GLQA
8660	22561	A	8722	3	157	HEVFLVETVFLHVGQAGLEPTSGDLPT SALNBAEWGGLLEDRTSSGPAWET
8661	22562	A	8723	493	186	FSPOGGEKRAILGLRLNCFPGVDFESAR PKPEVGNREGRVPTKLFFVFLKKKGFLP IGRGGFKSRPWESP RPAPQKGVQRLNP PPGPPFFFDLIWPNRNGS
8662	22563	A	8724	3	186	GGGTTPFPFGVWGKNGGGTPEAKTLPPF PSPLFFFS CPSPGEGGREPLLSPLA CICI
8663	22564	A	8725	370	67	FAPPKNFYKGAPPIFFIFLFFILFIYFF FFFFIFFKFLVFLLETGFHHVSDLDL VIHLPPQPKVVGQAQWATTGGFFVFLI ETGLHPVNGDGHNLTL
8664	22565	A	8726	966	652	LGSLLKPPPTGFRKFSCLSPSSWNYRHA PPCPANFVLEETGMLHVGQVSELELTS GDPTLASQSGAGITGMSHRDLGQHLTV

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8665	22566	A	8727	85	425	NHCYLFYQGHKTRSLPPF HMHSFAHELHTFLHTHTNSHINSONQSP TYTSKSHTHSYNRITDSHDSQMOTTHRH SLLHMTQLYTCCTHTHTTRTVIPLHLHS VKGWLNKVALGGRTSHGRESHAGRL A
8666	22567	A	8728	393	124	LGSGEPLQFQSPFSGGPPGPKSHWNSW NANPVPYPIIESAPPPPHFPFQAQSKY SGQQAALCPCPFFFKKKKKKAPGSGT GTFSQ
8667	22568	A	8729	25	217	AVOPTRVQWRSLQSPQCIILAFSLAK VDMEMTQLTQENADPATRDYHSSLVN REQLMPHY
8668	22569	A	8730	1	611	PGIFYSALLSLDTILNQLCFIMHRYRK NLTAARKNELVQKXSEFNFSKTYQEF NHYLTSMVGLWCTSKPFKGKIYDPEIL EKTGVAEYKNSLVNHHPSFLSYAVSFL LQTSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSPSPEERTVMVSSIRGKKMSWYLD YLFSSQGLQGLKLFIRSSVHSSIPRAEG INCNNQY
8669	22570	A	8731	120	378	VEKTAQSLGCKCSTPRAALGFRETRFL LRRCPCCGPPEAQWELKRALGSQAQWL MPVFPALWAEVGSLEARSFETSLGNI A
8670	22571	A	8732	2	68	VYVVCVCVCVCVCVCRAKVG
8671	22572	A	8733	382	258	NYHSSSLHLETPGLKQSSCLSLPKSWDYR HESPCALIFNSL
8672	22573	A	8734	479	326	PPLYGFFFFFFFFFFWGOGFFFFFFFFFFF FFFFFFFFFFFPPQTTF
8673	22574	A	8735	422	2	GRRPFPGLYFFFFPPGKKNFGGRGGFLFF FPKGFPPPPPIGFFPSSSELGKDWP PKGVFSQRFFPPPPPLFLFLFFFFF FFFFFFFFFFFSSFFPPPPPPPPPP FFFFFNNKQVFIERLLCARCFRPPAS
8674	22575	A	8736	7	75	IAVALGAYVETLLSVLHDNT
8675	22576	A	8737	2	176	NFGLLAETGFLYVGHAGLEVRSSSGDLPA SASQRAGITGVSTAGFNRIFYKQITYY YC
8676	22577	A	8738	408	111	GSSPPPRAGGENFLKKNAGKKNFGGEG GGGFPPLYPKFFFSFKGFTFWGGGGGK WPPPKGGFSKKPKVFTTTPPKKKKF WPPGGNWPKNF
8677	22578	A	8739	5	249	YEGKLKLHWQASPFGRGHVPNHKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK EGALGKFLAQTSGKEKQKVFYKY
8678	22579	A	8740	1	226	PFLRQSLVTOAGVQWCDLSLQLLAFQ GSSNSPTSASQVAGITGVHHHQLIFIS LVETGFHHVAAGLELNLQ
8679	22580	A	8741	4	96	DGLIMLPRLVNSWFPQGLPFPFPMGLG LQV
8680	22581	A	8742	19	112	PGRILLVREKKKKKKKKKKKKKKKKKK GGGPL
8681	22582	A	8743	362	234	KMDQKCLSEVLQWRWFCCCCCCCCCCC CCFSLPFIPEPSS
8682	22583	A	8744	3	419	LTLRRFLNLTLTKKKKKKKKKLKKKK KKKKKKKKKKKGGPLFKNSLGGPIFG GGKIFIFFFWGGLPFGDFLKKTFPLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8683	22584	A	8745	444	1	GETSPPPPKNLTFLGKKIKFGVGGKN DPLFLRRKKFGSGGFKKIPSPGLQF KKFSKILYPNSRFFSPFLKFFFSF KGFNSWGGGGLPCPPKRRFSSKNPPGG FFSPPLKEKIFFFPVPVNLQPPRDLEKFG APPPFFFFFIFLWMEFYWLSSLSSGSGR LPQQVPTVPSSELGGMGAYFVSKRSTYL QGRWQPER
8684	22585	A	8746	104	222	NKTFCLLKKKKKKKKKKKKKKKKKKKK KKKKKKWGGAL
8685	22586	A	8747	403	201	MEKYNVQPHSGILYSHEKEQAALFFIA KRWQPSCLSIDENIMMSSLTVEYTT AMRKNQLYSQ
8686	22587	A	8748	1	90	RTRGAVYAALERMGLDGCVELRSRLQR GP
8687	22588	A	8749	444	85	SPPPFGLFFFFFFFKKTSPPPTKGGFF SPPPPKQKFFFLKPPFFLGGGPNFPFP KKNFFSKNPPRFFFPFKKKNFTFPFP FFPAPPKFFLTPPPLFFFFFFFPPFP FFFFFFFL
8688	22589	A	8750	2	309	EFFPPYWEFLKINACMFSEPKKKKKKK KKKKKKKKRGPPLKKTGGGQPIPRGGK KKIPLPKGGQKPPRGFLEINPLEGGGP FGPPPPKINPPEKKKNF
8689	22590	A	8751	3	76	TASVSEGGGLQGITMKDSEDEEEG
8690	22591	A	8752	433	145	SEFFFFFFFFFFFPGKKSFFFTL
8691	22592	A	8753	2	124	GHLMLHIGSATLAISTINPLSTLIIFT ILIKKKKKGRPF
8692	22593	A	8754	80	201	FINANSKKKKKKKKKKKKKKKKKKKK KKKGGGLLKKTPGGAQF
8693	22594	A	8755	415	1	IYFPTPEKFGPPKRETLKKGAPFFFFFFKQ KFPFFFGGKGQKGGFSLQTLPPGKKKI SRNFPRKRGFADPPPPGKVFLLKKKG VFGGQGGFKTTPRDLAPLAPLNGAL FFFFLROSLSLSLRLCESGTILAHAF
8694	22595	A	8756	3	136	FTATRGVYVGGCSEICGANHSFMPVL ELIPLKFIETGVPVTL
8695	22596	A	8757	80	326	KKFSGLSGGGRGVFRPPLGLKLOTTAL NSGAKGTTPPFLPFPKRRGGPPAPGWE GIFCPHFPPMGGKGGGLWHTGEGPH
8696	22597	A	8758	1	164	SLISSTGGHKQCRFPQGLPRKTRDFCS HVYLLTFPPLSYDPAKSPSLRNTQE
8697	22598	A	8759	431	79	FFFFFFIFLKKVSTQSPPPQVFVFFFLKT FFLQPLLLKEGSSWGRGDKPPPLAPFK KWGVFFFFSFCCFVFFFLPLFFFLFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFPRCVLRL
8698	22599	A	8760	60	194	ARPTCPATAVTQKKKKKKKKKKKKKK KKKKKKGGVLLKKKGGRKY
8699	22600	A	8761	383	38	CASMTFFPKKKKKKKKKKKKKKKKKKK KKKK
8700	22601	A	8762	399	164	HITVKSLLVPMDDPPKKKKKKKKKKKK KKKKGGGFKKNLWGGQKLTGEKKKIFFF LKGKKKPLGIF
8701	22602	A	8763	353	48	NFFFKVFFFLKDFSHKGAPPKGGPPPK TPPRKKFFFLKIKPLFFIAFFFWSLFG FFLIFSLFFFFFFFPPPPPPPPPPPP FFIVFTITLHMFKILYH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USNN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion
8702	22603	A	8764	2	93	FAMLPGLVSNWPEAICLPWPVKLLGLQ MM
8703	22604	A	8765	398	63	PPPPVFFVFFSGGPFVFWGGGQKSPFRER CFFFKMHPGFFYIPFPVGGKVFVLEGV VCLPFGFLSGGAFFFFVFFVFFVFFVFF FFVFFGCPFFVFFVFFVFFGFFSVSHL
8704	22605	A	8766	3	83	ILEAGALICAVFTLLVSLYLHONT
8705	22606	A	8767	450	306	QKKKKRNRNKEGLGTVAACNPSLTGG RGWITOPQQQEGNFSKY
8706	22607	A	8768	1	111	WSLALVAGAGAGFGKQFSCGLPKPSWDY RHEDPCPL
8707	22608	A	8769	385	261	FLAEMGFCRVQKQKPKLLNSGDPASAS QSAGITCVIAPVL
8708	22609	A	8770	3	293	SLGSKPLGLLSLSPVKFRIFGKERNKV WGDKGDTDRNQSSAFKHLQRGSDPKQ NKIKACSSKFYLRRCKVRSFLLIKKKKK KKKKKKKKKKKKKK
8709	22610	A	8771	2	281	CVCVVCARVYIYIVVYIYIYVYVYVY MYCIYIYHVYIYVYIYVYIYVYIYVYIY ICVCIYTCIYIYIYTHYKHSVYVYVYVY YINPKLLQS
8710	22611	A	8772	295	161	THTHTHTHTHTHTHTHTHTHTHTHTH LAQLLGNCCIKAAISILYIL
8711	22612	A	8773	1	318	FFFFVRSFTLVQARVQRDLGSLQPL PPGFKQFSCLSLSSWDFRHTPPCLANF VFLVETGFLVGVQAGLELPTSGDLPALA SRGAGITGVSHHPQPLCLPL
8712	22613	A	8774	3	70	FMPIVLELILFKIFEIGVFTL
8713	22614	A	8775	369	191	TYINKIGAWWCAPLVPAAKAEVEGL LEPGLRPASVIQDDPHLKKGTYSRVLT THL
8714	22615	A	8776	2	124	GFRHVGRAGLEFLTSGDPLASAFQSAGI TGMNHVQPIVE
8715	22616	A	8777	1	162	LKYITADENGKTSRLLPQRPSDECGAGV FMASHFDRHYGKCCLYTCYFIKPEDQ
8716	22617	A	8778	346	138	YNSPPYKERTPLQARVNGPPRDSLSKR PPFFVFFPKQSLTMLPRLVLNSWAHGI LLPWPVKVQLQA
8717	22618	A	8779	2	117	LNLDITAVQVRNYPRIRESYKVSFLSAL EYTKLNTQ
8718	22619	A	8780	2	97	WDLTMLPRLVSNWAQVILPSWPPKVLG LLA
8719	22620	A	8781	403	276	ITSTVFQGRSCFIPSRKEVCSEPRRLQ KDLTGFPHTVYKH
8720	22621	A	8782	2	119	OAGLELTSDDLPSATOSAGITGMSQR ARPHFQCKNVP
8721	22622	A	8783	245	101	ELQFKMRSGWRSSQPSWGLTLVPLRLIS NSWAQVILLTWPVKVLQQA
8722	22623	A	8784	2	124	AKLEKKKKTKGRKKRMQYNNRFVNVVP TFGKKKGPNANS
8723	22624	A	8785	3	355	VGPSEPGAGYNLVCRLLEKLEKHGIRV GVTFGRCHLSWPLARLKGNSPTPCASW VRHLALLRLTVCGLHPLSCTHCLTSPS EMNPVPQLEMQKSVFVCVAHAGSCLREL FLFGH
8724	22625	A	8786	238	9	PVKLGAGPPOAPFVLRKWAPLIKPFKKG PIGSLQILPFFFLRQSLTLPPRECSAT

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						WLTESSTSWHAI L LQ P P E
8725	22626	A	8787	336	10	CLSLPSSWDEHRLPPHPASFCS
8726	22627	A	8788	1	147	IFYLLETGFHYVGQAGLELLTSGDSPAS ASQAGITGVNHHALPEIHVF
8727	22628	A	8789	3	130	DLEEGTQILMGRLEDGSRRTGGIQLKLDH SSPFSKTRELYVPF
8728	22629	A	8790	206	3	VPPSPGPIKKGDKKNLYLFLIKNVPNK KLKRGVSLAI P P F F F F V F L L E T G F H H VQAGLELLTS
8729	22630	A	8791	124	390	RAGAQNLMWPPPSGVKALIFFNFPPKKW GNGT PPPAPLI FGLKKKGVSPCGPGGS EPAPGPGSP LAPPKGNGRDLRPPPP DKFLN
8730	22631	A	8793	2	301	HEERERERERERERERERERERERERER ERERERDALFAFFPPRGARPPPEIRGV FVGAGSVREIYPTLSIFFSPPAHARGRE LRSRCVSHSLHLISRA
8731	22632	A	8794	1	285	ARGERERERERERERERERERERERERE RERERERERERERERERERGAPPP PLFLLGRGGALRAHAISPPPLGAPPYI YIFHMRARPPIHRYLCAQRETRPAL
8732	22633	A	8795	1	321	ARGERERERERERERERERERERERVS RIPRGDLRQFPHPLASRDSFCGSADH FGRGVFNKSVVTPDPPIHRTVSSSLGGV ERDLTLTSGGGTYAPWQMCATGEDQ
8733	22634	A	8796	2	140	HEERERERERERERERERERERERERER ERERERERERESLPPAGCAKAGWG E
8734	22635	A	8797	2	223	SARERERERERERERERERERERERVS RNLNRGGGVPPPLQNVRIHSGGPARGT LHHKKKTSLTVDGLAQ
8735	22636	A	8798	1	176	ARGERERERERERERERERERERERKISF LGGRGTFQFAIERGVIOFCGRRITTRGV RN
8736	22637	A	8799	335	27	FPFKFFFFFPLVEMGFCCLAGGLELLS SSSLPASAYQSAKIIGVSHAWVF
8737	22638	A	8800	342	191	STSLSLPKCWDYRREPFCCANLSYFFKD PFSKCNPRLYWGLQLQHRNGF
8738	22639	A	8801	104	332	AVFLTMVKIQPWLKRVWRPHNKKLEPL CDPAISLLSMYPKEMKSLCQDVCTPRL STGPTLTAGMWNPPKRSMD
8739	22640	A	8802	563	258	FFLNLETRSWYVAGARVQWLETGTVTVH YSLDLASHPPIASGVAGITDACCAG LTLPLFLKGLGLGSGGVGYPSYFGLG FHNDCSRVRVLQMSYQ
8740	22641	A	8803	2	199	ARGLLVRRFLSPSEKRSIRVGVTRFSRC RPSPLSLTRKGNLSLTPCASQVRQCLALL RLAHGACTH
8741	22642	A	8804	266	108	KLVSCKVCLPFSFSSSSSHIGCACFF FTFHYDCKFPQASQAMLEQAVEP
8742	22643	A	8805	1	140	KVVVFKRPGVYVGGCSETCGANHSFMPI VLELPLIKIFEIGPVFTL
8743	22644	A	8806	2	90	SSAAAEENNDKEKEAEKTEDMEFGLF D
8744	22645	A	8807	229	34	KKKIFFFFPGFFWPPQKFFKAPPPFFFF FFFFFFFFFFFLLDLYLIILSYTK LISIRAAPI
8745	22646	A	8808	43	173	NADSGHAQWLTPGPMALNEAAGGSQDQ

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8746	22647	A	8809	259	134	ETETILAGAGKPRLY IYIMIFKNKFFNRDRGLPMLHRLVLNWAQ VILLSWPPKVLGL
8747	22648	A	8810	391	193	VLPKIPGIQFPFPPCKFRKPRPRFKKPP PKKKISFSNPKIWPQQYFKRGPPRL FYFFFFVUIL
8748	22649	A	8811	304	3	TPPPNIFPFCFLFFIFILWYFIFIPFF FFFFFFFFFFFPPPPPPPPPPPPPPPP QCFIGDDQRMVHTHTQTSSHLQGGG NPQGGQSGPWLMCA
8749	22650	A	8812	395	268	FLVETGFHHVGAQLELPASSDLPALTS QSAGITGVSHHGW
8750	22651	A	8813	782	1174	LSRLFFFCVLFCLYMTTOLPYFRGLVC LPVLRLGLTSLSRLECSGMIAACSLNV PGSTDSPTSASRVVTTGVRHTQLIFV CFVEMWFHYVAQGLEPLGSSSPALSS QGAGITDVSHTTLELCF
8751	22652	A	8814	95	236	ATMPGLKNYIFKKKKDKGLTMLPSVLK SWARVILLPWPVKVLGLQT
8752	22653	A	8815	381	58	SCLLFPFFFGARGGGPPRAGGSNPPGPP GLTPFPFKPKKNYARGGGPFI PPREG WAGGFLLPRRGVPLAPGSNNLELGP/LP SPPGYQKTPFSKKKKKKKKRKR
8753	22654	A	8817	441	158	FFFFLRTDGYLTMLPRLVNSWQAILL PQPKMLGL
8754	22655	A	8818	415	342	RLVLDSWAQETLLPWPVKVLGLQV
8755	22656	A	8819	400	171	NFFFPFGVKFLGGGGPQFPFQKRGFPQ KTPGGFFKPPPKKKKKFPFPKIGPPO GIFKKAPPPPPPPPPPPPPPP
8756	22657	A	8820	2	268	INITLAFPTISLLGILVYRSHLMSLLCL EGILSLFIATLITLNTSLANIVPI AILVFACEKKKGGAVLKDPWGGQSLR VLAR
8757	22658	A	8821	2	258	LCLPNQAWAMAGSPPASLLPCLSLISDC CASNORDSVGVGPSEPGVYSLVRRFL SPSEKRSIRVGTRFSSWVRLTVIPA T
8758	22659	A	8822	250	456	GGGDKFGLIETFPFGLKFFLLNLSGW ELOPLAPPPKFCFPKGRGFFLPFRVF VANLLLTCCCKRD
8759	22660	A	8823	492	376	QENCLNPGGRICSELRSCLCTPAWATER ACLKQNKTNQ
8760	22661	A	8824	1	116	LTLPFPSPAPSVDDNLRKTPPEWVCSLPF HPORMILSN
8761	22662	A	8825	2	191	FLVETGFHHFGRAGLKLNSGGAITSFAF QRAGITGVITGVSHCFEVENRVWTGTQYF LCYILKS
8762	22663	A	8826	393	75	PRFFPPPPPKIFFPPPPPPPPPPPPPP PPPKKNFFPKPPPGFFPPPLKKKIFF PPPPFPSPNNFFPPPPPPPPPPPPPP FFFFFFFFFFFFFFFFFFFFSI
8763	22664	A	8827	81	380	KIITHNIARTNPTFCIMNYLKKKKKK KKKKKKKKKKKKKKKKKKKKGGGFLK NPGGGQNNPGGKKNFFFPFGGKKNPPG FFKKKPPFGGKFGAPPPPKN
8764	22665	A	8828	354	13	TKPKTPPLTKGPRRGFLAPRVGGGGPI TPPPQNFLEKGTLLARKKVPFPGRPAPK RPPRKNNGFMRLKKNPGPWKFLGFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LANPFGFGPKKKPENQTHKKCORRKP RF
8765	22666	A	8829	1	215	KISTTHSHCPRTIKLKKKKKKKKKKKK KKKKKKKKKKKKKKGGPPFKTLGGPPF SPGGKKKFFFLGGL
8766	22667	A	8830	1	127	ILFFWQRRLALLHLVSNSWAQVILPP RDRVLGLQVIYFK
8767	22668	A	8831	264	55	FFFXFFXFFFFFFFFFLEVFVFFVFFVFF FFFFFFFFFFFFFFFFFFFFFVFWCS VVLFIQPFIKSFH
8768	22669	A	8832	399	85	PPQKNFFPQAPKISGGGGPQIAPPQKK GSFQKTPGGFFIPPOKKKKNYPPPGKM GPPQGFVKRPPPLFFFFFFFFFFFFFH NRHLFKVKHLQNSPHLVQLRL
8769	22670	A	8833	47	288	NCLYRTKKKKKKKKKKPPYKKKTLRGEN FPPAGPPAPLPISGGGKKPSRGLLRPP TLGGAAGPPPPPKLTLPLRKKKIF
8770	22671	A	8834	1	146	INITLAFTISLLGLVVRSHLISLLECL EGIILSLFIATLITPSTLC
8771	22672	A	8835	2	79	EDPKTSPKPKITQTRRGLPPSVSN
8772	22673	A	8836	1	156	PTRTTITPILTLFLITQLKILNTNYH LPSPKPIKKKKKKKKKKKKGGP
8773	22674	A	8837	152	292	AKTFNFYKVEFINVFNGCLLLIKNTL PKKKKKKKKKKKKKKKKKK
8774	22675	A	8838	1	122	VASNSIHPKAKENTAPHTHTHTHTMT HTHTHTLPMATFK
8775	22676	A	8839	2	106	HVGQAGLELTLGDLPTSASQSGVITGV SHRAWP
8776	22677	A	8840	364	224	APLCGRQICDCDCTYSPFHTYIHTHT HTHTHTHTHS
8777	22678	A	8841	266	1	NSLSVEFLILFPPPNYSFKQCICSHQNC LNFWIKCVNTPHPNINLRMPPLAKRG AHACDPNTFGGGGRNITRSVDRDHGQH NETP
8778	22679	A	8842	343	52	KTGFRHVQGPQELLASDLPASASQAG ITGVSHRVRDGLHILDNSSFLDTSFADI FSVLYLKAGIASLHIIYHFLPLRLDLL LVSSLTVSFPPTAV
8779	22680	A	8843	256	35	LFIFSLSLQYIFCVGCVGVMSLCLFLV CAWGHVQLHVCSVCMVCENDVCVCGV VQMCFCIKNFOKEVYQI
8780	22681	A	8844	333	11	PPIKKKAPPKGRAPFFFLKKKKGGPP PPQKKTGGGGPKRGRGVKKPPGFFPGF FGPLFWGPPFLPPFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFISTKNLF
8781	22682	A	8845	15	288	RCGLFVPLMLVSDCAQVILLAPPRVL GLQAGASASTPITVNSQGAIVPEVGT TGSTIIAAASSGGGFDSVLQNDICMFL TQQPHF
8782	22683	A	8846	1	397	ECAHHTQLIFLFLIESLHVHVGAGLKL PISSDPPTSASQSGTAVSHHA
8783	22684	A	8847	1	179	ARERERERERERERERERERERERER ERERERERERERERERERERERERER GGGPQFPIGGGLTQGGGG
8784	22685	A	8848	2	233	HEERERERDRERERERERERERERER ERETFFSSGGGPKETTLFFETGAPKEG YQNMHARLIPSAVPFKIRGRG
8785	22686	A	8849	2	180	HEERERERERERERERERERERERER

SEQ ID NO.: of nucleotide sequence	SEQ ID NO.: of peptide sequence	Meth- od	SEQ ID NO.: in USSN 09/515, 1 26	Predicted beginning nucleotide location correspond- ing to first amino acid residue of peptide sequence	Predicted end nucle- otide location cor- responding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Prolin, Q= Glutamine, R=Arginine, S=Serine, T=Threonine, V=Value, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /-possible nucleotide deletion, V=possible nucleotide insertion)
						EREREREREREREREDFVFYRWGEHIDRQVCSPFCPWCHCPMPEEREREREREREREREREREREREREERERE
8786	22687	A	8850	2	79	
8787	22688	A	8851	1	178	ARGERERERERERERERERERERERERERERERERERARLFPARGEKKHTGGGPPLFYLYITRRERERERERERERERERERESPFA
8788	22689	A	8852	3	76	
8789	22690	A	8853	5	227	ERERERERERERERERERERERERERERERDFFFFFLEKKYLFSPIGLKGROGSLSLTLLTGKNWPCPPPH
8790	22691	A	8854	1	189	ARGERSRLRSLPRESVCVARAGGAASSPRGHEEREREREKEREKREKEREREREREREREREREERPGRKEYICRVPPPQLISPADSLLVTNLCSHSSTPGRERYVALNSRTBRC
8791	22692	A	8855	2	271	
8792	22693	A	8856	2	309	HQCQQOQOLNRDLDFLVYNRMTELCFRVPSSLHHRALDAEEACLHSCAGKLHNHMRMAAYVOLMPALVORRIANYEAASAVPRVAEQGVPSFGSSGYSTCVGMHARTIHOTUTHATRYTHIQCLIOIGLCTFACTCSOVNKSMTELIFTFVLVERGLHYVGQAQGFELKASDDLPALASOGASTSGSVHCSSSKMSGLTFPRLSCHATTATHYSLNLGSSGNPTSAQSQVAGTTBSRPCETQTOTALORGPHD
8793	22694	A	8857	44	203	
8794	22695	A	8858	329	182	
8795	22696	A	8859	1	175	
8796	22697	A	8860	3	350	HEATGLRSNIKNGLDHFLFLTFTPTFLIPILAMITEILLVOPIALAVRLTANITAGHLMLRNLSATLAISTSLPSTLIIFTLILTILETAGALIQAIVFTLLVGLYLRDNA
8797	22698	A	8861	139	3	TKEADIKGGGPLHALSFACFIGRDVSFCWDGWSRTPDLKRSTR
8798	22699	A	8862	3	134	SPTFPSSKPSSIIRKSVDNLNVMSLSPAALS PASSQRHES
8799	22700	A	8863	346	219	RLVPFCDLNFNLFCRYSCLTNLPGLVNSWAQVIPLPOPPKD
8800	22701	A	8864	1	147	GTRFFEFGIDHWQGAGIQLLTLDGPPTPASRGAEITGVSHHTWPWFIF
8801	22702	A	8865	267	132	KRKFWFFFFFLRDGWSLLLRLVNSCAQEALLPWPKLLSQV
8802	22703	A	8866	343	215	LAAQLKTPIPKRPVPTHQKKFKCESERTRICDRS CWGPSLS
8803	22704	A	8867	1	242	TSCKTKDKLEYIELKCFTAKETTISRVRPVWEKI PANSSPEKGLIRSINKKAENSSAI AAHNCNPSTLGGOVRTIT
8804	22705	A	8868	1	219	GTRFTWTATWNPASTKKKKNSFFPETESTRTYPAQGGQGNLSQLSPCLKRFSLCMSPGAPKQSGSGSLMG
8805	22706	A	8869	1	181	ATGGILLDLLDVSLAYSKHLEGAKSESAEELKKRAQELBGKLFNTLKIHEMLOPDGDQ
8806	22707	A	8870	1	253	AAAPPNAPGGPFGPOPAPS AAPPPHPH ALGGMDAELIDEALTSLSELGLHRVR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						ELFELFLQGSEFDCFSDLGSPAPPAGSVS C
8807	22708	A	8871	383	233	ATTFFPNPGFLFVRLVFLVQWDHEPPPGF KQSSHFLSPSSMDYRHPHPPPG
8808	22709	A	8872	211	294	AXKKKKKKKKKKKKKKKKKKKKNIWGG
8809	22710	A	8873	398	100	QKERPPGPPFPFKPGPPQKRGKGAPPKD GEHYFPFWLEKSTGFPFKTKRVYVPSFV YPHPPAPQKGGFPGSGPPRPIASPPGG KKKKKSYIEKENLF
8810	22711	A	8874	3	214	DAWVLGILVYRSHLISLLCLEGIILSL FIATLITLINTSHSLLEKKKKKKKKKK KGGAFKKNPGGAQI
8811	22712	A	8875	2	254	PRVRPEGRNTPQSWFOANPHACMTFSK KKKKKKKKKKKKKKKKKKKRGGF IKM GGGKNPREKEKNFLLRGKI KKTGGDF
8812	22713	A	8876	2	135	TINLPSTLIIFTILILLTILEIAVALIQ AYVFTLLVSLYLHDNT
8813	22714	A	8877	2	296	LARGAEVLGYGSHSRGRVFGALVGQAG RLTFTEHPGSSPATLAIYPTPEGTSVAVS ISAPPKARSRPYPPSRCHNLISLAGSSV LVPPGCVHRWVGR
8814	22715	A	8878	164	29	RKIGFARNLTVPVIALWETEAGSGRGQE IEIILANTVKPGACEVL
8815	22716	A	8879	381	219	GEKMTTEEVEHMLVAGHEDSNGCINYEGR R
8816	22717	A	8880	2	156	ANGNSFATRLSNIFVIGNKNKPWISLPR GKGIRLTVAEERDKRLATKQSSG
8817	22718	A	8881	3	402	SGFNIEYAAGPFLFFIAEYNTIIINT LTTTIFLGTYYDALSPELYTTYFKKKKK KGRPPFFFFFELKKKKI PPPKKKNFGKK GETLKGCGGAPFPQPKILSPKKKKKK RCGAFKKS LGCAKTNCGGRN
8818	22719	A	8882	1	406	RYSTFSEGEVGERYSTPFGETLERYSTP PGETLERYSTPGETLERYSTPGETLE RYSTPGETLERYSTPPEALERYSIPT GGPNTGTFTKYTPSKKKGGGRFKEPLG GPRPTGVRVVKVFSVLNGVLNAR
8819	22720	A	8883	484	307	KKILNRNRVRLTVPVITLWETEAGSGRG QEMETILGNTVKPPASASQSAEIKGMRI IIF
8820	22721	A	8884	1	131	GSLTHHNNIKPSFTRENTLMVHLSPI VLLSLNPIITGFS
8821	22722	A	8885	406	106	KGGAGPKIAPPKKAFSPIPPPFFWPPF VFLKPPPPSPNFPFPPVFFRGFLFF FFFFFFFCETVLPFPFNNLVFTLPHVF AWLIPIDQYLFISHC
8822	22723	A	8886	425	325	SSTHTHTHTHTHTHTERSHLLAFEPSAG ELWMM
8823	22724	A	8887	394	278	VCVVCVNCVYICYPCWNLPCWHMCLELY KVFKGIMKGV
8824	22725	A	8888	2	86	YSRTRAALIQAIVFTLLVSLYLHDSAY
8825	22726	A	8889	400	62	FLYLKSPFPFPERGVFSPLFPKQFFFSF KALNFLGGGCKPFPFKRFFKYPFPRV FLYPHKKKNYIPPPDDFGPPRVFFKA PPPHFFFFFFFPPPPPPPPFTRLEWVO
8826	22727	A	8890	3	100	SLEPGTSLGKGFSLTLFSSSEDYRHEFP CPAN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in UNSS 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion
8827	22728	A	8891	32	142	VRTRFGQVAVLYPTTILLIPIPTSLI ENKILKWA
8828	22729	A	8892	3	382	TPHNLSRPSYEPKDPASTSPRAKKKKK KNPKKKKKKKKKKKKKKKGGALLKKIT LGGPKLPGGKKKNFFPFGGKKKPGD LKKTLFLGGGNLAPPKKKNPWGKKKT FWGEGGKKNNFFPFG
8829	22730	A	8893	368	199	KKRRTSPSRKKRQDGLRPTPTPKNL YYLLPFFFLILYIFFFFTFFFTFFFTF
8830	22731	A	8894	3	136	TINLPTSLITFTLITLTITLITAGALIQ AVTFTLLVSLYLHNT
8831	22732	A	8895	1	144	IATINLPSTLIITFTLITLLTLEIAGAL IQAYGFTLLVSLYLHDYPYN
8832	22733	A	8896	153	375	PKRKKKKKKKKKKKKKKKKKKWGGGF LKNSSGGAIPFGGGKFFFFFLGGGFKTP RGFGKNPFFWGGKKKN
8833	22734	A	8897	332	400	WLTVPVIXLWDAEAGSGSEVRSS
8834	22735	A	8898	215	359	TELVPNVAFCLPCLSCSHHLLCAIHA RVTIMPKDIQLARRIRGERA
8835	22736	A	8899	414	73	PRLLCFKAWAMAGALPALLPPYSLI SDCCASNORDSVGVGPSEPGVGNLVVR RFLSLSEKRSIRVGVRTFRSCPSPLSL TRKGNLSLTCTSRRLRQCLPILLWAHGA RTH
8836	22737	A	8900	374	88	VSPSPSLKIFFSPKAFNFWGGVGPHEFF PQKRVLPKPPGGFSPPLKKKKFSPFP PVKLGPFGKSGFGPPPPPPPPPPPPFGL DFMYTGSSNVW
8837	22738	A	8901	433	56	PBGPPPPGGFYPGKRGFFPTPLVVFPG KRDPPPRGKKNPSRSGGQKTPRFPD LLKAGFFPGGPQRLKGAQGPFWFFPGP KKKTOTGPFFPKLGDGPWGKKKPPPG GAPRLGPKCKEL
8838	22739	A	8902	3	73	IAYVLIQAVVETLLVSLYLHNT
8839	22740	A	8903	3	149	PNLSYIIGKTWHEWNPDECDDEQEN KOCODLQAPTESMWVPGCPN
8840	22741	A	8904	351	137	FPEEDFAKKSGLIFPSKTWMEVEVLF LSQLMLQOQTOYCMPSLINGRLIIKAP SLKGDHHPPLGLLEG
8841	22742	A	8905	142	5	KIFLQKKKKKGLGTVAHACNPSYTLGG GKWIMRSRDQHPGQW
8842	22743	A	8906	367	244	HVDAQAKFFCFYSRDGVSPYWPWSRT PDLMICLLFIVEL
8843	22744	A	8907	146	248	SOIQLRLROENCLNLNGGCCSEPRNCHF LAWAKE
8844	22745	A	8908	2	197	AAASTHARHLFCLVCLFAYLLVEMEFH VAQAGTELLDSSNPPLASQNAIGMS HHTPOYIC
8845	22746	A	8909	1	127	KKTLRLERACMLTPVIAFWNAEAGTLL ARSLRLPWFNVL
8846	22747	A	8910	368	280	LTMLLRLVLNSWACAILLTWPPKRVLSQ A
8847	22748	A	8911	355	211	QQNLHLFWPGTVAHTRNSTLGGQGM ITGAYEFETTLGNTARPHLY
8848	22749	A	8912	325	190	KKKKKGGGGGPKKKKKNNPPPTSKKKK KKKKKKKKKKKKKKKKKK
8849	22750	A	8913	1	411	VNVFAPRGGAYRGQASPSGGHLHPVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						YRFLCLPNOTTNSAMAGAPPLASLPFCS LISDCASNKRDMGVGPSETGTGYNLL VCHFLSPLKCSIRVGVTRFSRCRLSPL SLTKKGNLSPTCTSRVRCCLALLRL
8850	22751	A	8914	258	9	GAIFCLHCETNPSTSTSTQLQTEPQL PGVPLELPPPGCSFCKRKSQGHWAECPO PGIPKPCPCICAGPHWKLDCTGPRL
8851	22752	A	8915	326	42	EKIHRRKYFCYSFFVFLVEMGPYFVGGA LKLASSDLPASPSQSARVKAMSHCVRP VLVIFKNKILONTENSTKIYVYPPPNQ ILTFCHFCFK
8852	22753	A	8917	3	106	GLELPTSGDLFASASQAGITGISHHAR PIMTYS
8853	22754	A	8918	320	171	AASTTGGSYKCLCLPGYVPSDKPNYCTP LNTALNLEKCPFLPHLSGSS
8854	22755	A	8919	1	201	VKPSDRYHLMPIFTAAYPHQNSTYNVVP STRMVMAEEFKQGRKLSLCSLDYRKDLR TIVDPVVS CAT
8855	22756	A	8920	3	182	LLRPLEKRGIRVGVSRFSRYHLSRLPFA RKGNSTPCASRVKRCPSLLHGLHPLSD KPO
8856	22757	A	8921	142	1	SCHPGWSAVVRPQLRLRLRYENCLISGG SGCELSGCHCTPAWTTG
8857	22758	A	8922	1	117	LFNFYAWGWSTTLRLSLNSWVHVILT PWPPEKLGLOA
8858	22759	A	8923	357	121	LGAFSDDLHLNLDNKGTFATLSBLCHDK LHVDLENFRLLGNVLVCLAHIFGKEPT FPVQAAQYKVVAGVANALAHKYH
8859	22760	A	8924	343	133	LFNFNFLETRLREWLIFVFSVETGFPPI KRAGLKLQASDPPARGSQSAEISGMFSH YAWPCKSNRAFKCS
8860	22761	A	8925	321	44	PDGSGSPASASQVAGTTGACHDAWLMFI FNMNININIPFSAKRDKLSMDKINEIIF SLLIHRISSFQIMYFLCSSRIESRKRRL KQTGRKKE
8861	22762	A	8926	335	106	HFVFLIETGFHRVGHAGLELLTSTDPPA LAYKSSGITGVSYRSPTKLHLCAVCCLC IYTYGLVLVLSPTPGSWEKKT
8862	22763	A	8927	2	160	LSRVPPRSANLISVFAEKRCCHTMLPR PISNSNAQGLLPSQAPKVLGLOA
8863	22764	A	8928	3	140	RVITEEKNFKFASLRMARANARLFGI RAKRAKEAAEQDVEKK
8864	22765	A	8929	126	59	NSGGGGCNELRSCHTPAWATE
8865	22766	A	8930	3	104	KNWACYCRIPACIAGERRYGTCTYQGR LWAFCC
8866	22767	A	8931	311	112	MENYLSKMOOLEKNITRELKEAAAELE SGSIA SPLGSTDESNLQDLVWKASREY VQVLKKNYMI
8867	22768	A	8932	345	134	GGSSSPWFPFPRRRADSLRVGLNPP GPGGGAPFLKXPLIGWGGGARLWFLKI LLRVRPENSFDGPR
8868	22769	A	8933	262	39	RPRRPHPGNFFFFNSGSHYVAQAGLEL LDSSDPTLPSQSAGTGMYSQANPLDHT FENRDCVLLHCSPPVSTNT
8869	22770	A	8934	84	22	TPAWVWLTPVLPALWEAKAG
8870	22771	A	8935	277	111	ERINHAAGSHGVSGTFMKYDLSSLMVT VIEBHPMFQWFFVRLCGIVGGIPSSGT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8871	22772	A	8936	2	106	DSATPRRLECKEDVQQRQEREKELQHR YAEVFP
8872	22773	A	8937	1	193	LMWDFSPSGLDGAFQGRGYWYNYKINV KSGSISGFTMVLGAGMLFIYCLSYKELK HERLCKYH
8873	22774	A	8938	240	69	DGNGQLKRSFSGRARWLTPVLPALWAE VGESLEVRNIYYILGNMNSIGNIHLIIK
8874	22775	A	8939	329	177	RKNLMLPRFLVLSWAGATCPSWPLKML GLEAPSPSCPARTNFKVTSPLRH
8875	22776	A	8940	358	120	HFSNFFVFLVMGHHVGGQGLELFPAR YVPTLAFRSOGITGISHCAWPKWALPR KASPGLSGRGSGPKATCSKAW
8876	22777	A	8941	333	104	PHVYENGHICLSILTBEDWSPALVSQVSC LSIHMLSSCKEKRPDMSFYVRTCNK NPKTKNWHYHGQEFVITF
8877	22778	A	8942	1	241	APLVAFTQVNLDEKGLSKLVEATRINF NDRYDEICHHWGNNVLPKPSGTIRAKLK KAKAKELATNWKCTLLSFLYIKR
8878	22779	A	8943	1	240	APLVAFTQVNLDEKGLSKLVEATRINF NDRYDEICHHWGNNVLPKPSVTRAKLK KAKAKELATNWKCTLLSFLYIKR
8879	22780	A	8944	306	150	AASTLCPRLECSGATMAHCSLNLGSGD PPASASQVGARGSLPGRWRLQ
8880	22781	A	8945	284	2	GKSRSPDLCTSGFTGTSTHTFLITICWV PRYVATCPPIGLNLFVIKTWNSHYIVQA DLKLMVSSNPPVASQSGAGTGMSSHWT LENRLLTTKK
8881	22782	A	8946	1	226	WSFALFAQAGLEFLTSGDPPASASLSAG ITGMSHHAQPAVSLNSIFSASTFCATSS YCAKMKELKELFMLIVDA
8882	22783	A	8947	363	96	NTAFGYMPLLSIFPLVLSKAVFLFLGM FTAALLIIAQRWEPKCASTDEWINKMW HMHTMEHYSTCCGVHAAVNSIQISEWN CWEN
8883	22784	A	8948	1	208	GRVGQFGLRLLTSGDLPASASQAGVAG VSHRAQPTPALNVCVLTWVLQHYIKHNR GKRSEYFTIFNDM
8884	22785	A	8949	69	298	SRGHQVADAALLSFPDVCIGLMLWGS SSIVCILHRHKRRVQHIHRTSVPTSSP ESGATKTILLEQERTSRPRS
8885	22786	A	8951	2	201	LYDLNMRISLPLPSLVCHSHSTHEHT YTHIHTAHTYTHTHSHMWVLSLKQKMW KHRPELSVWI
8886	22787	A	8952	1	285	GASPPASLPFPCSLSDCCASNQRDSVGV GPSEPGAGYNLVRRVLPSPSEKRSIRVG VTRFSRCRSPSLSTRKGNLSLTPCASRV RQCLTLWLWVH
8887	22788	A	8953	341	256	LGLGGGCGCEPRMHRHTPAWVTERDFIS L
8888	22789	A	8954	227	43	ILFFIQTGHTHTHTHTHTHTHTRAKCLFP PARFPTSPNSTNCTFPTEPAANPGLV RAGLG
8889	22790	A	8955	310	79	RPRRPGLMERVNVNIFPSILRESYPIKRI TNQAQCCMPVPTVQTEAGRSLEPKSL RLAWAIQONSISKNNNNNFF
8890	22791	A	8956	374	198	FFFFLPNRHGLAMPRLMVLHWQAVLPQ PPKVLGLOG
8891	22792	A	8957	138	10	RPRRPRLCQAQWLNPTIIPALWESVAGGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^possible nucleotide insertion)
						LEARSLEAFWFFNT
8892	22793	A	8958	354	216	AGPRVFPFGGGGFRPPPGGSPQGGPPK GSGGCKPPPAHWVF
8893	22794	A	8959	364	223	LQARSKKKKKKKKKKKKKKKKRGGCK
8894	22795	A	8960	259	11	FEALKDPNNLQSLFSTVTLTVAHVY EKLSTLTSLAARRGLAMLPRLANSRTQ TILLPWPSKVLRLQARATEPGLGLL
8895	22796	A	8961	334	213	AASTNFERMENGTLTLPMLVNSWPOV ILLPNPESMRL
8896	22797	A	8962	260	3	KGGFFFPFPIGKPGFFSPALIPKVF IFSONFVFLKKIFFFFVETVGSHVVK AGLELASSNPAPTSSQAGMTGMSHIA W
8897	22798	A	8963	425	248	ADEWIHKMRHTEIYYLAIRNEMLIH ATAGMHLENILSEKDHMYDSIYMKLAW ANL
8898	22799	A	8964	1	118	GKLMELHGGSSSGKATGDETGAVERA DGYEPPVQESV
8899	22800	A	8965	2	130	GRVGPRMALNSWAQVIHLWPWPVLGLQ VAMKRRKIMILSTSY
8900	22801	A	8966	119	364	IGWYLTEKTIQCCPSGLADPFQOMISP LRDGSILTVPKLVNSWQVLPQPTRK VLGLQAEVTAPGHIIFMIIMINTFK
8901	22802	A	8967	238	333	TRCLRLPLVNSWQVALLPSPPKVL GLQV
8902	22803	A	8968	297	169	NPPPHIYKFFIFINIFPFFFFFFF FFFFFFFMSKILIF
8903	22804	A	8969	2	212	RVRPRDRPLVRVGRNKGDAETTPSP LLPAHLTFPLDYHLNQPFIFGLRDTDTG ALLFIGKNMDPRGP
8904	22805	A	8970	242	357	TLDTIESFKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK
8905	22806	A	8971	191	265	ILMPXKKKKKKKKKKKKKKKKKKKK
8906	22807	A	8972	398	97	MFLYNRLWFFSPHPPLRFPFSPRATIF LGGAHPFPKPGFSGKPPGVFLSPF QEKIFSPFPLFLAAPPKDFKSPPPFF FFFFFFFVSTGSVS
8907	22808	A	8973	370	265	YNSSLFSSWDYRHVPCPDNCFISRGW SQTDLR
8908	22809	A	8974	3	119	GLKILTSDDPASASKTACITGVSHHTQ TIFVFSHKS
8909	22810	A	8975	1	110	VQAQGFVLVSSANPLTASQSRVTVGS HRARSMQ
8910	22811	A	8976	3	152	WNQPKYPSTGEWEMKNYITKLQVPM HGPHVAQDGFEGSPQTQIHLS
8911	22812	A	8977	375	193	FQDLPLGSTSNISFFKRRNSPAMVRLIS NSWPOEILLPQTPKVLGITGMSHCTWPG GHISI
8912	22813	A	8978	2	395	RAALPTQASAMAGAPPASLPSCSSSD CCASNERESVGVGSPGAGYNLLVCYL LRLLKRSIRVGVTRFSRCHLSPSLSTR KGNLTPCASRVQCLALLNLTSALYP LSCTHCQTLPSSEMLVPOL
8913	22814	A	8979	120	19	ARVQWHDGSTATLNSWFOVILLWPPK VLGLQA
8914	22815	A	8980	204	48	LNRDKGLTMLAREVRNSWFOATPLWPP KVLGLQALATAPQMSFLRAPLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
8915	22816	A	8981	335	221	FFFLFLFCMTSHSCSVNVLGASDSTPS VSHIAGTIGT
8916	22817	A	8982	360	150	LSHMPLLFVSLYPDRHFMQVIFVFFFT ESPSVTRLECSGAILAHNCVCLPGSSDS PASASYAGYSFYLL
8917	22818	A	8983	346	116	GQGRGVETESCSVTQAGVQWCDHHSLLS LELLGSSDPSTASPVGTGGHYHTSS HFLFSVSSSYFFTPVCLAYR
8918	22819	A	8984	350	263	LFMLPRLVSNAPQAIFFLLWPPKVLLEQ A
8919	22820	A	8985	3	159	EEYNLLVLCRLSPLEKSGTVKRVQFSR CHVSPLSLTRKNSLTPTCASWVR
8920	22821	A	8986	2	253	KHVUGELKDLSTIGTTHSVDRYLNKL TNLSVIDSEKYPHMLSVKNCFIQSVTR YMLQPADEVHKQLQDARKEPLQCKQ
8921	22822	A	8987	2	115	GARTVGHLLHALKQGEYGLASTCNGGG ASAMLIQKL
8922	22823	A	8988	3	159	GFYHIGQAGLKLMSGLPASASQAGI TGLSHCAQAGIFFLPYDIFTVF
8923	22824	A	8989	1	123	SHYVAQAGPKLIGSSNPPASASRSAGIT GVSHHAWPPLSLFL
8924	22825	A	8990	462	303	LARTPSRPTRPPTRPPTRPPTSPPTRP FMLSVDCLLLY
8925	22826	A	8991	382	178	PPFFFFFFFFFFFQKQKGFQKGF PQKPPFFFGGKPKVNFQKFLRAKGGK GEKPKPQNKVVF
8926	22827	A	8992	532	432	RDAGLTMLPRLVSNNSWAQVLLPGPFKV LTLOV
8927	22828	A	8993	418	172	KRGKKKKNIPLIFFNYFFLIFFIFF FFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFGGAWSLFRGGDSGEVKOTDSMS RQCQGF
8928	22829	A	8994	2	722	AVRLNISYPPQNLMTVFGDGTASTTL RNGSALSVLEGQSIHLVCAVDSNPPARL SWTWSLTLSPSQSNLGVLELPRVHV DEGEFTCRAQNLPGSQHTLSLSLQNEY TGKMRPISGVMLGAFGGAGATALVFLSF CIIFVVRSCRKKSARPAVGVDGTGMD ANAVRGSASQGPLIESPADDSPPHHAPP ALATPSPEEGEIIQASLSFHKARPQYPO EGBAIGYESEINPK
8929	22830	A	8995	498	323	EFKAELENGDIARVHLKREEGWFKGTLQ RNAKTGLLPGSFVENT
8930	22831	A	8996	21	511	LITDGVEAYALNASGVNLIIVDPKGWA LFRSFKAIVKEKLDTRRGNSSELETAVKD LGKAVSYKMGYDVAIVVYSGQVYBNGV KKNFLPDNTMVLGNTQARGLRTYGCIQD ADAQREGINASARYPKNVVTTGDPAREF TMIQSAFLMLLADPEFVSOLA
8931	22832	A	8997	178	306	GAINAINWFFPNVGMGKTLGFPNLMAL KQIPFSPVGEKTKRR
8932	22833	A	8998	351	211	STQSLRMQFVPCYISGRHHYHSHHHIH HHHYSSFLKXPOEYLRPL
8933	22834	A	8999	1	381	FLFKPALMELCSIEGIDQPLFFVFGF FFFGKEASFGPGQGGREGGKFLMEPLAK GVKGISCPKPPHPCLNPPKPKRGGESSP PEGPKKTGAPGAKKGLFLTKGNKNPW GPGKTRKKAFFPKNF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8953	22854	A	9019	3	209	GNLTLIQVQSEGA CPFLSPGCTNSARAEPSSHVALPDALNNLRTHESGDGPGSSSVDMNRPEDEVYPQGIYVIGASPIYAREA
8954	22855	A	9020	504	20	NYAQMSYSTARASANESMAYFMGRKKFV ASRQASQWFLCNLEATVRVVVTLPSKA RFSQFARSANWCNDWIGSGRMAIDGLK EVQEAUNLIEAGLSTYEKCAKRGDDYQ EIFAQVRETMRRAAGLKPPAWAAAAF ESGLRSTBEEKSDSRPAAGS
8955	22856	A	9021	3	168	LPRLAAARIRHEERERERERERERERER RERERERERERERERAPPPTLCET
8956	22857	A	9022	2	89	LCSVLVLLTFPPLLSCDPAKSPARNTQ E
8957	22858	A	9023	508	371	FFCRDKVLATLPRLLANAWPQVIFLPQ PKVLRLOPCTTSLKDL
8958	22859	A	9024	2	170	RTHSAGRPVQCQCEKAFHSSSLTVHK RTHVGRETRNGSLPLSMSPHYCGPLAN
8959	22860	A	9025	3	185	PPAAATPQGPSPINSPTTKKAKNNRTR KTKKKKKPPPSKKKGPKTKTKTMMGGL KITT
8960	22861	A	9026	104	319	LVFLSKYTPPLVSLVHIGLSLLSFLPS LPSFLPSLLTYLLPSFLPSFLTSVINPL PSLFFLVFKLSQFMT
8961	22862	A	9027	476	364	SLKRLTSGDLPASASQSAVITGVSHRAR PIIYFKYVQ
8962	22863	A	9028	36	154	FLVGQAGLKLTTSGDLPASGQSARITA VSHRTWRTHYF
8963	22864	A	9029	2043	1237	WLNRTRVAPALPERLGACTQLGFLVPCSQ PYVVCROCPYRQAAQPPHCPAPEGEP GAPQALGDAPSTSVSLTTAVQDYVCPLQ GSHALCTCCQFPMNDRARERQDPRVAP QCCAVCLQPFCHLYWCCTRTGCGYCLAP FCELNLDGKCLDGLMNNYSYSDILKND LATRGLTWKMLTESLMALORGVFLLSD YRVTGDTVLICYCCGLRSFRELTYQVRQ IPASELPVAVTSRDPDCYWRNCRTQVKA HHAMKFNHICECTHFN
8964	22865	A	9030	15	389	IVDHYPCGGIPTSGSVTQAGNQWHLGP LQPRPLGLEGSSCLSLICSMGRHAPPH LARGHFSSEVQLRSRLQGAUVFVKRK GTPEDPRQGLRTLISLCLHLVALALWF SLPFHGPRIHMQ
8965	22866	A	9031	3	243	RHSLAFNRFSCLSLPSNWDCHRFPSCPA KFCTPVMEFPHVQAGLELLTSGDLPT LASQSAGITGVSHWANTRCCCF
8966	22867	A	9032	1	245	PTRPAGIATICMCMKNHRATRVGILRT THINTVSSYPGPPYPGHDEMYCADLP PPYSPTPOGPAQRSPPPPYPGNARK
8967	22868	A	9033	46	124	QELMTHGAKSPDGTVRVHNAFLPVTTV
8968	22869	A	9034	235	435	KKKKKKKKKKKKKKRFRFLKGFKPP LKPOGLFEAPPFGPPPPGPPFAGGGA PPRGFFKKKGK
8969	22870	A	9035	333	70	CPYIQIPILKDOVNLSSSPFSHLYKD LWKTLFISYITELFVCFVEMMFHHVAQ AGLELLGSSNPPTSTFQSAKITGISHHA CLNI
8970	22871	A	9036	297	411	NKTMSPAAWMOLEVLISKLMEQKTRY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
8971	22872	A	9037	461	167	CMSSLYSGS KNKYPLLGGPPFGSPSPENLANGGFPITP GGGGPINPNSPPPPGGRRPPFLKKKK KKKKEKENTYILQDTCDCSAVLPTMQ VKIVMICLIHMLRF
8972	22873	A	9038	466	292	NGCLLEPASWNSLANIFCFREEGLTML PRPQVILPPLPKVLRLLPPLSS
8973	22874	A	9039	34	124	GIRNIKFSLSSTFAHKKYCSHAABH VK
8974	22875	A	9040	54	239	RRRRLLRRWGLAMFLPRLVNSWHQAILW PPKVLRLQACATTGTLRRWLHGQINSP GAGSV
8975	22876	A	9041	469	223	PWAVCVVCVSVVCACVRCARASES QTCMAVPSLGPAGAGRFPALGCCAVCEDE VGSCPHARPLPRAAVDKAAGRRLCF
8976	22877	A	9042	491	380	SPGVVAHSYNFSTLDGRGSHTRVRKFM TCLATEGAV
8977	22878	A	9043	144	360	IYSHGWYLDVSLTAAHLAINPDCFMVY YIPSQCTDKLTEKEFIEGTLANKEILRL IQFEPQVREKMKNA
8978	22879	A	9044	23	263	RWNSDGKSLRPAWATWDPVSINKNTON THTHPTPHSPHTPHGQQPFLSPTPFPP PVSSPSPPPPFSHTCLSLPPGA
8979	22880	A	9045	461	287	PPSLANIYLFYILFIRGDVSLFPRVLVS NCWAQAILLFWLPKVLGLGQEPNLAALK SL
8980	22881	A	9046	485	6	NNKNSWAWMRVPLPATREAGAGESLES GRRRLR
8981	22882	A	9047	475	307	LELRDGLSLTVLPRVLSNSWFOAILLPWL LKGLCLQARATHWACSCINSTQNILO
8982	22883	A	9048	483	338	LRGEFQREGEREREERERENDRERAH TTAFTQLLPQYVAIILLPCY
8983	22884	A	9049	680	303	NDLLFGSLVVKFOAASGTGRVTLPEPSE EQVVCRLCFQDLFGDDHNKNGPKMFDSS NVHGGDLFLPKDATVRAVPVGEKTYVRGW LGLDYVAALGMSQQCSGAGRTGPPCR LPWCYSDFPTEP
8984	22885	A	9050	26	165	AFGYHRVGGAGLELLTSGDFFASASQSA GITGVSHHARSQYFFVYV
8985	22886	A	9051	461	83	HKINLPSHKKKKKKKKKKKKKKKKKKK K
8986	22887	A	9052	475	209	MAAPPKKKKKKKKKKKKKKKKKKKKI
8987	22888	A	9053	531	404	SVTQAMQWQHNSLQGSTLEFFQSSLL SLPTIWDYKHADLS
8988	22889	A	9054	66	416	KKKTNTKIMGGGGLPKFISPPFLKKTLS WKKGAPKTPPLEMAPFFFPQGGKNSPF KGGKIFFFFPKKTFTKGGPPGGHTPPL GGGPQIFSLPFPKGVQKNPPLLRGGL FFT
8989	22890	A	9055	1	104	ILAVNGETLEGVTHEDAVAILKHQRGT TLTVLS
8990	22891	A	9056	3	106	LKRRGIAMTLGLVLNSWAQVILPSWPPE VLGLQV
8991	22892	A	9057	1	299	PTRPINILAFSTISLIGILVYRSHLISS LLCLGELISLFIATRIYPIAPPLPLP EPEKKKKKKKKKKKKKKKKKKKKK RKIKAKRKNLGGGGGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8992	22893	A	9058	482	146	LTSSKKKKKKKKKKKKKKKKKKKK
8993	22894	A	9059	2	290	YFLFAYTILRSVPNKGVLALLSLK KKKRGPPKRTLGGPKFNRRGGQNIFFL MGGGLKPNLGLGRNLSLGGGKNWNL PKIKGFRENKFN
8994	22895	A	9060	413	48	PQKGGFFQKNPKGFLKPPPKKKKKRFP PGKIWPPQKIKKKPPPPPPPPPPPPPP PKFFFFFFFFFFFSSIRNPSSSYTKW LRSLDVCHLLPPIPPQVGPPTVLFEST LPDCHNSLL
8995	22896	A	9061	2	274	FTISLLGILVYRSHLISSLLCGLGTL LFIIATLITLNTHSLANIVPIALVFA ACAAVGLALLVKKKKKGRFPKRIILG POINFG
8996	22897	A	9062	42	235	QEFFTRERERERERERERESSGVVR AKFRSNFSAAGIAHTIRVMLPPSGIYS EKSINKCGFALLFF
8997	22898	A	9063	20	413	YALRNSARAGDPHQGLRRDGAUVGRGW LMFREALHPWWANVAQWAGSGPLFLGAP WPQGGVNLWLVCMVSASSSSINGLPPQ KKKKKKKKKKKKKKKFWGGGPGPQSPF WGGLKKFGRFLKRRGGGN
8998	22899	A	9064	6	306	ECESHTTYSHPAGGGGFMVVGGDADARS KALLGVCVSGTEAYVLVLDPHWGTGPK SPSELQAAGWVGWQEVSAADPNFSYNL CLTSLSSQQQOORTLD
8999	22900	A	9065	463	126	AHYQLVYTKVCGTRSSKRISKLAYHQG VVIVTCPGCQNHIIADNLGWFSDLNGK RNIEEILTARGEQVHRVAGEGALELVLE AAGAPTSTAPEAGEDGPPSPGKTEPS
9000	22901	A	9066	23	244	SCHAGIRHEERERERERERERERERE REREREIYFLALFSQKGRVHGFFTPRG GOKRELLSNRVNTLCTE
9001	22902	A	9068	396	143	KDIONFGQAWNLTPVIPALWEAEGGSR GQETITLVNMVKPHLSVLLAKNSSHC PMCLAELOQWYDLCSFKIIFFGIILPG
9002	22903	A	9069	828	99	VDREFVDREFVUVCHPDLEERLQAWPAEL PDEFFELTVDVRRRLAQLKSERKRLEE APLVTFHAFRAQIKELKERYFKVALRVL FPDPRVLQGFERSPEFTVGLRDFVRSIL GNPELSYFLFTPEKTVLDDHTQTLFG EPLGRSGCNLGAEEPAAGVYLEGLLEH AISPAAADVLVARYMSRAAGSPSPAPP DPAPKSEPAEEGALVPEPIPGTAQPV KRLGLKVPKWLKLPASKR
9003	22904	A	9070	20	427	DGTRERERERERERERERERLYLTET LHSLSELEGASGASVCVQSVYPTGASAP HSIINGHKKRVLVLCVETETHFLAEKOR APLGDTSVFVGAAPVGGANTGASAGGAP PSRGEKESGESHEMDMGFLFV
9004	22905	A	9071	297	126	CSIYDKRIPTFGLGEGVSEQRQLTLLP CLPPALTETPTSSDQSTDATPTLTNS
9005	22906	A	9072	117	286	VVLRGSEKMFQVQEQNEQYLQCLIKGI FLVKKKKKKKKKKKKKKKKKPRPEYIK
9006	22907	A	9073	3	302	PPMETLRQWTTIVHSQEEEEHFFVTKD EVKVVARKHGQPGTEVAIALQLPRTSA APPAQQQLPQPLAPTTVLVSADWNALL ORPNKYIWLQVLEM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
9007	22908	A	9074	437	79	NQREEEERKKRRRRKKRRRRKKKK KILRQKKKKRRKAGSREKKILRHLEK NKRKKHVELINALRLQDRLTYQKH FYILAKNNWKIKLKIYHQLALENKVPR HKWETYA
9008	22909	A	9075	51	185	CRADFMMFHDKITVYLCSLVLLTFPPL LSYDPAKSPSARNTQE
9009	22910	A	9076	452	310	QFSRCHLSSSLSLDRKNSLTPTCTSWVR CLALLRLTLGALHLLSDNQ
9010	22911	A	9077	438	326	LLHCWWDCKLVOPWKSVMRFLRDLELE IPFDPTLHF
9011	22912	A	9078	37	169	GTPGFRHAGQRRLQLLTGDLPTSASHS AGITGSDRARPPSTF
9012	22913	A	9079	1	408	RKGRLSKEETERMVOEAEKYAEDVQR ERVSAKNALESYAFNMKSAVEDEGLKKG ISEADKKKVLDCQCEIYISWLDANTLAEK DEFEHKKRLEQVCNPIISGLYQAGGPP GPGGFGAQPGKGGSGSGPTIEVD
9013	22914	A	9080	31	168	VRRNFRLEHTVTITVAYCSLELLGSSNLP ASASQVARTIGLQLLNLO
9014	22915	A	9081	460	319	YFFVEMGSHYIAWAVLELLGSSNPPFASA QSQAETDAHKPTDCRPLR
9015	22916	A	9082	465	326	PCVAEFTCTHTHTHTHTHTFKCVGSHL HTINND
9016	22917	A	9083	33	269	PGNSRPISSVRGIIHPCLANFCFLNVF EMGSHYVVLAGLIGSSDLALAVQSGR VTGMSHCWAPETIFFLENNIIL
9017	22918	A	9084	47	300	DLITSLFLKQSSLATMNIQTFFKNIYF DLIKTLFLRFFIFCFIYFYFLFFSYGG FSSFFFLFKGSSFLPPRLNGCAKIWN
9018	22919	A	9085	437	220	NRAIKSLSLSLSLVCMCVCSACVC MCLSLSLFSPSLSHSLFFSTPNMDIS HLPIILSTOENMLLLQ
9019	22920	A	9086	227	23	DCPKANILGLTFRVLSNSWQVGLTFWP PKGQSLRCQGGEDRWTHWPNWLLHPP PQAREPPRTHFH
9020	22921	A	9087	206	326	PHWAQWPTVPVPAWAEAGKSGQGEFE TSLANTVKPRLV
9021	22922	A	9088	364	123	SRVVLPLKAPGEDTSLPLPASGGSCSL ANGSIPTISASITPWSVLCPCEIFPLL FLLYGDCNLGPTLIPDDLIMRSLP
9022	22923	A	9089	373	205	MPPRLANFCYFSRSDWSYWSGWSQTPC WDYRRPPFPFCVTSYSVQYCACVAGL
9023	22924	A	9090	283	2	REFFSFAVLAFKTFWKLFSPFFWVRP EDWFIPIGGCGNPNFPCCPGVGKKG PRFKKKKKKNFISSQAQMLMPVIPAFWE AKAGGSLEP
9024	22925	A	9091	16	261	CPEDLLVGNVVKVEDSDMGDPDRPFMCM FACFYLLVYRRCCLAMLPRLVNSWAQVI LLPQPASLELLQAHAHTHPALCLSF
9025	22926	A	9092	17	109	RQGLAMLPRLISNSWTQANLLPWPFKEL GL
9026	22927	A	9093	282	114	KKGGKALLVFLRTGRKPPFFFLRQGLA MLRLVLNSWAQAILPWPVKVGLQA
9027	22928	A	9094	205	337	NANLHGRMQLRTPLCLPETWEATGGSGG QEIETILANMVKPCLY
9028	22929	A	9095	62	287	EHSCAKLFCFAFESGPYSVAQAGVQWHD HSLQSQSTFGLKQSSCLFFPASAGFYKE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9029	22930	A	9096	170	9	SFSFFKDKSCHHLGKHSGA AASFTYICGRFCTKLKIQSGGQVRWLSP VFKREAEVGGCLLEARSSRFIATW
9030	22931	A	9097	2	104	RRPGRRAEPRARVGRDRDPFVLLRRHYH IFECC
9031	22932	A	9098	350	142	LCLSCPKGGCYRAMAPFRNGFCSPGKNG GFPMLGRVVLKWPQMGPLPQPPKRVGFQ GLSPPPGPPPLV
9032	22933	A	9099	494	342	YFFVFFVFWSHHTVQAQLELASSNPF ALISQHAVITSSGSHHTCPKLYF
9033	22934	A	9100	30	232	GGIMLCHGRACCFPAFCHDCFKFPKVFQ PCFLYSQNCFSLYKIPSLRSCRLOLAE LLSIYIENPL
9034	22935	A	9101	26	171	RNSRLRHKNRLSLGGGGCSEPRSCQCT PAWQTARLSLKNKKQKKP
9035	22936	A	9102	486	239	HHTCPHQVCVCVCVCVYRVCVCVCVY IYMYCIIYIYIYIYICICYCREKERE REMWPHVQAQGLELLGSRDLAPAS
9036	22937	A	9103	487	344	TGFPHVQAGIETLLTSSDLPASASQAR ITGVSHHAQPLFMI FCAK
9037	22938	A	9104	470	221	TPGLKRYTCLSLPKNDYRCEPHARQGA FLCAFSPLSOQPMGRPHFHSYETNK VERGKRLPLRSPSTEQGDFRCVLFTQ
9038	22939	A	9105	468	259	YVFFCRDGLTISRVLNLSQCPQSPCL SLPKCNDYRHEPPCSCCSNLLMFHT NVFLIDSECSHFT
9039	22940	A	9106	466	329	RVAGTTGTHHAWLINIPSVETGFHVHG PQVIQPPRPFKALGLQA
9040	22941	A	9107	409	306	AGFELLASSDLPASASQSAEITGVSHHA RPSLIF
9041	22942	A	9108	417	269	MVVAQADMESSKEPGLFNVIINDSLVQ AYPELKEALYEEIKKAQRGA
9042	22943	A	9109	533	399	RGSLRHETRLNAEARCSELNSRQCTPA WATERDAVSKTKQA
9043	22944	A	9110	16	239	LHVFEVRWNSHEVSLTADSRKSHLIFQ PNYADTLINQSEYEKSEPLLITQDLLET KGEPRQLQVSFFPPKREE
9044	22945	A	9111	68	219	EPFHLANFLQRLVFTMLTLILNSWPGV ILFPGPPTVLGLQDKLPVLLPS
9045	22946	A	9112	192	57	DRVPLCPDWSAVARSWLTAASVSQVKG ILSPQTECAPQNSP
9046	22947	A	9113	21	201	TVSVVFEFNLGGGTCQBPWRCHCTPDW GTERDSVSGEKEDKDVARRHWVGSFYN GQ
9047	22948	A	9114	2	144	TFTIDRCADLFVAKQVGTKLSVNEFLS FSVESILKRPSSAITRVSQ
9048	22949	A	9115	156	316	MILNKKKKKKKKKKKKKKKKKKKKKK KGGGPFKKTLEGAKITPGWNYFFFMG GV
9049	22950	A	9116	1	84	TKPTPFLPTLITLTLLDLPISPFLLIIL HLNLGGGVCSEPRSCHCTFPWATELSQ KKKKKNGFKWFEPFRPKQEGGGRKKPDG VP
9050	22951	A	9117	1	176	AAAGYPGQQQNFHSVREMFESEGRGLNN SPVNGNSSQCMAPSSQSLYRTSGAFVY DCSKF
9051	22952	A	9118	1	184	AAAGYPGQQQNFHSVREMFESEGRGLNN SPVNGNSSQCMAPSSQSLYRTSGAFVY DCSKF
9052	22953	A	9119	69	374	IYFSKKKKKKKKKKKKKKKKGGPFKKCP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WGSPIFVLRRVLSFFIRGEKKNTFGDF LKKTFFWGGKLGKPPPKKTPWGKKKI FKGERGKKPPFLGGKKK
9053	22954	A	9120	405	53	EFSPLLLTINQKRGFFPSPFKIFFFPK RIYFLGGGPHFPFPKRGFPKQKQGF FFSPKKEKKYNLPPGKFCPPGFFFP PPLFFSFFPFFFRQCIK
9054	22955	A	9121	2	380	WDYRCPFPPTNFCTPSGGVSPHWFGW SWPQVICLPQPKVLTPWVRDRDLE GGDLWYGACLGACLHGPQAASFGHIL GPASLLCCIPKHVHMDTSPGVKLQSCD TGVALRVGKREGS
9055	22956	A	9122	2	534	DMIREQYIYHYLAQREEEKAEKEFD RILEEDAKKLAEDKELRLEKEARRQL VDEVMTCKRLQVQKLEAKAEQERAM EQKHINESKELNCEKENFARRQLRAQ EYKQLQMQIAYQQSQSEARKEKREF EAGVAARKMCLDKQGVLSHVOILAQNI HMFQCOHPO
9056	22957	A	9123	389	46	GFNLFPPPIGFFSPSPSLKFFSPKTL IFLGDFPPIFPKKKSPFKNSGVGFC PPFKKNLFLPSPINPAPRVFFKPPPP FFPFFFFFPFFNFYRLYFIWVNLAKV VW
9057	22958	A	9124	422	59	AQQKKKKKKKKKKKKKKKKKKKKKK K
9058	22959	A	9125	333	168	KGPPCIVVCMVSPFKLEAGSHSVAQAGA QNCNDNLQTLTGLKRSPPHPSLPSR
9059	22960	A	9126	175	89	KPPHFFFFFFFFFFFFFFFFFFFFIFC
9060	22961	A	9127	368	250	CFNYSLRDRGLPLPLGLVLKSNFOATLL POPKMVGVOG
9061	22962	A	9128	392	157	FFSPKRLNFGGGGPKMPPPKKXVSPQK PHPGFFSPQKKKKKFFPPPVKMGPPKS FLKSPPPFFFFLLSSIRGLFL
9062	22963	A	9129	396	13	FPFPPPIFFSPRRFFRGGGSVALSP PKKVFLLNPPVPVFFSPPEKTSFFP PPFFCPPQILFLAPPPYFFFFFLLF VFLLFFPFLPLFLGKTSFLLLLFLF IYLETGSCSVAWARVQ
9063	22964	A	9130	55	180	LLYNKLIPTLRKKKKKKKKKKKKKKK KKKKKYEKTAY
9064	22965	A	9131	2	95	SFVHMEHEKAVLLKSFQNTVDLGIQRE LTV
9065	22966	A	9132	172	404	KKKKKKKKKKKKKKKKKKKKKNGGGF PKNSWGGPKKRGKKIFFFSLGKKKT LGVLEKPLFLGGKRMAPP
9066	22967	A	9133	1	125	QVVSYPPTIGQVAYELVFTTILILIPT MSLIENKILWAY
9067	22968	A	9134	1	120	QVVSYPPTIGQVASVLVFTTILILIPT ISLIENKILWA
9068	22969	A	9135	7	269	IATGQPRQLKLTLDPTLLKRLFLTKKK KKKKKKKKKKKKKKKKKKKGGGHHK KKPPGPNTPVKKKIFFFKGKIKKPP WGI
9069	22970	A	9136	1	64	LVYSINTYGLDYVHNLNLQ
9070	22971	A	9137	400	259	SQPLRLRLKNTLNFGGHHYSELGSCHC TPAWDTQDSIHSWLLSV
9071	22972	A	9138	3	310	ECFNSPNMNGHCNLLVQSTSPSISTMP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CPKYVALEKVFLLNLVWFFYLKYRDNRP GSAHTCNPSTLGGRGWITGAQEPETS LGNIAIRPSLIKRKKYKLF
9072	22973	A	9139	34	142	NCKKLNTHTHTLTHSTHMLTHSDTFTHTHTTKYK
9073	22974	A	9140	146	2	PPPPPPPEGVSLCGPGWSAVARFRLTASS ASRVHAILPPOPQQLPTRP
9074	22975	A	9141	3	102	PPASASQASGVGTGSHHQAQPIEPLRCS HRTT
9075	22976	A	9142	245	51	NREGDLLCCPRWSQTFLGKQSCGLGPFKC WEYRRGPPHLAYIMSPKKNLILQIMIFY NNPCLLYS
9076	22977	A	9143	2	108	GAKCVSDRIKHAFLIKEQKIVKVLKQA AGSQAK
9077	22978	A	9144	3	200	MGFLHVCGAGLKLPTSCDLPASASQSRG ITGVSHRAWNPVSFFCEAKCEFWBEQL INLDKNSQK
9078	22979	A	9145	405	227	WFFFLGFLKGLKGPDKMFPRAPRVYSFP FPPFFFWPPPRRIIPPGPFKFVFLAG PIW
9079	22980	A	9146	387	220	PLFFVUGCFFFFFFFFFYFFFFFFFF FFFFFFFLGCGCERNFIRKNINN
9080	22981	A	9147	539	220	VINFKHILIKTIVGSLFFFERGSCLP LECNMIMAHCSLNLGSSHPASASQV AGTTGAYQHTQLIFIEFAETGSCYVAQA GLQLGSSNPPWPPEVLGLQV
9081	22982	A	9148	3	141	GGGGCCSPRWSHYTPAWATSALCLKKK KKKRFLKSCSLTPLLKA
9082	22983	A	9149	413	240	FIFCRDGGLTMLPGLTSNTWSQVILPPO PPKVLGLQAYHADELPHLATWGVLGLT V
9083	22984	A	9150	395	193	LLFGFCLLNLITQVSCCHLLDIKLQMTL SEGYPPLNIQESPFYRAPLDDPSVRHAR GEILPISLPGG
9084	22985	A	9151	1	77	LVAATVLGGTGWGPKNIRRGSGGA
9085	22986	A	9152	365	181	IVDRDPDCRDADQREVTLSARYPKIW VPPGDPAEFFFPQSAPVMLAAPDELV SAQLA
9086	22987	A	9153	373	251	FKKIFFCRDRALNMSPRVLSNRTQAIL PPQPLKVLRLQA
9087	22988	A	9154	204	95	DYHWSQPGMVAHACNPSTLGRGRWITR SGDRDHFG
9088	22989	A	9155	44	280	AELFGTLMREDGLSLGGGGCKEPEKSC NEAWATEPDCLRKRRKESPYLLVVTTPD SSYSPFFFLLPADPNNDYFLS
9089	22990	A	9156	2	117	ERLRHENCNLKGRGCSFPGWCHCTPAW ETKQDSISKK
9090	22991	A	9157	3	207	HASAHASADANDYRVFPCPANFCLIV SHVGKAGLNLSTSDLPISASQAGITV VSHIARTPTTV
9091	22992	A	9158	117	267	NRVLLCCPDWQTFGLGSSLSLLSSWD YRHIPPLAARSSYLCPGFYH
9092	22993	A	9159	415	167	LEFFPKKXNFFFPPLFFFFFPFPPX XXFFFPFFFPFFFPFFFPFFFPFF FFFPFFFPFFFPFFFPFFFPFFFPFF FFFPFFFPFFFPFFFPFFFPFFFPFF
9093	22994	A	9160	217	41	SSQIHRDRNRNVROGAVAHACNPSTFGG KGEQITRAQEFKTSLANMVKPRLYKPC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LY
9094	22995	A	9161	341	164	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFVCF VSVLKKKQWNSYFDVRIILRVPEP
9095	22996	A	9162	190	402	INTGKHPCYRNSYSVLFLASKKKKKKK KKKKKKKKGGGFKKKKNNLRGGGELIFFF WGPKKI FGGGGLKKG
9096	22997	A	9163	108	209	LSVKRCAKNPKGKVAPGKKEIRTRSHQ DSEDI
9097	22998	A	9164	2	145	KHCGRRPQPGPLPRKTRDLCSLVYLLTF PPLLSDPAKSPSARNTQE
9098	22999	A	9165	170	402	YSCHFPSSLISYVKITKTIKAPKSKSK KKKKKKKKKKKKKKKKGGGPPKKKNF LGGGGGELIFFFLGAPKKKRG
9099	23000	A	9166	399	113	WRLRWEDCLSGGRGCSPEGSCYCTPMW VTEQDQSGYGEFGFPPSSLSKARIPSA AERSMCPACVCNLSVEHLSLSCLLAQ QGKALYKLLNK
9100	23001	A	9167	3	138	SWITGVCHYAWLIFAFVLVETGFHRVQQA DLELVTSGDATTLRSH
9101	23002	A	9168	134	301	EKLTSQHSVTQAGVQRLNVHSLRPPPPR FKRFRCSLSPSSWDYRNLVLEQETH
9102	23003	A	9169	201	1	GATILRFKTKKNNVFPKKKKKKKKKK GKGWSGTSERWNLSGGSSGLRRRLQA PAGPQEFKLA
9103	23004	A	9170	2	191	FVFPQLPLGFKRFRCSLSSLDOWDYRCP PHLANFCGFFFLKFFFFFKKNFFSPR GRGGALI
9104	23005	A	9171	2	191	GGTESCFVAQAAGVQGDGLSLQSPPTGF SETASQTVDPDPKVKDGPGLRTMVAELP KTIIVTDS
9105	23006	A	9172	3	143	SWFLYVQAGLELLTSGDFPALASHSAG ITGVSHRARLQIGIFRAV
9106	23007	A	9173	361	174	VLGIILSMSETEIFNFKCLDQSGTVAHT YNPSTLGGQGRVIRAQEFETSLGNTR PHLFIKI
9107	23008	A	9174	493	351	LVETGFNHVQAGLELLTSSDPPASASQ SAGITGVSHLALVLISRKSC
9108	23009	A	9175	1	115	FRKIWIYITMEYCIYAVKKKEMLSFTITW MNLEDFMLVR
9109	23010	A	9176	286	96	PLFFFNWRGLAICLGMSAVAIHERDHSA LQSQTPGLKRSSCLSLSSSDYRRVPC LANESHY
9110	23011	A	9177	399	237	RNTKWLFLRRSLTLSTGLECSGATSAH CNLRLPGSSDSLNGIFKDLALLDM
9111	23012	A	9178	427	101	GRTRGRGGRGAPHISHDGRFGDAPRFPD VMAAGKRSSRLPRWDGGRATLLTFQTG QPGRGAPHIPDDGRPGGDAPHFDPGVVA GQRLQSQHFGRPRQAAGRRL
9112	23013	A	9179	193	41	IVFLFIYLFCEFFVGTGFCYVAQAGLKL VSSGPLASAPQHVIGTMSHHT
9113	23014	A	9180	292	119	KITTKINKQLNLSTYLDQMDLTDICRIF HPTATEYRFFSRAHGTFFRSGTGNSAWH I
9114	23015	A	9181	3	279	ALSPPYSSCECKLGSFNRELSSSPSGGQ KSEIKVSGAPRPLPRVQGDSPPLPASG GPRCSWACGQITAVSASGVTHPSPLLIH VCCVCLI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, / = possible nucleotide insertion)
9115	23016	A	9182	402	238	QMOWHNLWPLQSLPPEVTPFLCLNLPNNWGYRWPPPPPTNFFFLKGVSLGRPGSV
9116	23017	A	9183	3	207	EFHHVQDQGLELLTSGDPPASASESAGITGVSHRAQQACRFLHFFEGTCTFLSQELS YLKLGRDTIIIC
9117	23018	A	9184	3	106	YPHYVKSVASTFIISLFPTTIFMCLDQ EVIISN
9118	23019	A	9185	110	248	GVLVGSPLRTRFHSQQAQGAESIGVVT VMKGDLVLPVVCVLEVDV
9119	23020	A	9186	925	1132	KCPSAWAAPHTSEIRTSQGGQAQVVLV LPLLKPGDVIIPALWEAAGSGGQQGF ETSLANMAKPRLY
9120	23021	A	9187	399	292	ASQVAGTGTGAHHARLIPFVLVETGFH HVSQDENF
9121	23022	A	9188	7	82	PCDPPASVSQASGATGVSHHAQYF
9122	23023	A	9189	1	117	LPLSLPFSFLPSFLPSLPSFLPSSFLPF FPDSSVTPVLK
9123	23024	A	9190	238	46	NKAFRIKAPVSPSNKKFSSFFFLNEMK SHYVDQAGLELLSSGNPSILASQNAKIT GVSHHVRP
9124	23025	A	9191	2	282	LIFPYVDNMLVRAGLELLSSSDLPALAP KVLRFITGVSHHTRPELYFORLLADPTLL INSQAAGTNFPIGLSRIKPTQSGHMLQ EVWGTSGLR
9125	23026	A	9192	44	136	CLCVCVCVCVCVCVCSCQTLMCCFLNF DV
9126	23027	A	9193	469	347	PCPANFVFLVETGFLVHVGAGLKLLISG DLPNSDQKFYVN
9127	23028	A	9194	427	238	PFARPTAFPIYIEFFVEMVFRYFGKAGLK VLISGDLCASASPGVGTGVSHHAQPK
9128	23029	A	9195	34	178	SLVHVVEFERGRAEWLTPVLPALWEAEA GGSRGQEMETILANTDFWTG
9129	23030	A	9196	22	338	CGPYSMWNWSIKRERKEGKKRKKRKRK EQKERERKERKERREGGREGKERGRREG KKRKINKRKKVGLIGSPCIVFTNQAAYC EESGGVWPGGETHTQGLQV
9130	23031	A	9197	3	91	QGLSLGGGCGSEFGSCCHCTPAWATERDS I
9131	23032	A	9198	1	203	RTRGNKSIDDTSNFDDFPESDIQPVN TTEPDYKSKDWFLNYYTKRFEGLTQRG SIPTYMKAGKL
9132	23033	A	9199	2	144	PTRMPCCCCCCCCCCCCCRCFLMTGVL FFCCHNOFENHSGCLPROI
9133	23034	A	9200	1	99	YAAKELVHDRIYPTIEMERRRGLNWLVP RLSLG
9134	23035	A	9201	3	149	LNAGVRNEWQLKVGLDPACHKSLCVNE VPSFYVPMVDVNDPFLVLLA
9135	23036	A	9202	284	21	KGPLPLFFFFFLRQGLVLMHRLYESGMT TAHNCNLELVSSDPPTLSSQNAETTVGS HCAQPASLILSKPYIGFLHQIQKSLPV TFL
9136	23037	A	9203	1	77	LRLVLNSWRQAILLNPPKVLGLQA
9137	23038	A	9204	529	340	GVLLWRQAAGELSLGGGGCSLKVRRH TPAAWTRAETPSQKINELIKSMVELTD DFIT
9138	23039	A	9205	413	241	HPFPPELKLFSICISLISRWCHRRPCCP YVFLLAETGFHVQAGHKHTYCCVSLF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						T
9139	23040	A	9206	33	152	QLQGLSEWGMERCALPGYPVVFVTLNCKY RSWIETMRDK
9140	23041	A	9207	70	402	HVDWEALGNDFPLVNLGICCKLKASGIHE WVHTRTCAHTMHMTHTTCTHCSPRVV VLNLGCTFELPGALKNARAYPHPNATKP MTSESVGIRPTRQVFKAPRAEOHCSTA
9141	23042	A	9208	46	262	GGTFPAVRGGRSLWRDLVLSRLAAGRR RRGTRRGGRGAGGGRDRVRGSRREPA AARTAAEGERAVRGKC
9142	23043	A	9209	15	206	PIEPLSERTNSAGAPPPASLPPCSLISD CCASNQDSVGVGSPGDSIMQTSLWA KVPVSKD
9143	23044	A	9210	475	110	NLLAPHLVLSLEKHSIRMGVAOFSRCHL SQLPLARKENSLTPCASGVRRCLALLRL MLGGLHPLSCTHCTPTGPSEMNLVSLQEM QKSPVFCVAHAGSCRLLELFLGHLPL
9144	23045	A	9211	420	132	PPPPNYFGGAGFFFFPPFFLRPPPPFF LPKKKKKIFPPRPGKKIFLKPAPPSFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF LVRSHFILTIM
9145	23046	A	9212	353	87	FFFXKQXFFPPSLFFSPXPXSPYFF* YLKYPLPPSPFFLFFTPPPXFFFFFF FFFLPPPPPPPPPPPPPPPPPPPPFF FFFFD
9146	23047	A	9213	2	276	FIQLLKRRLCELGYEVLPHPSYSHDLLP TNYHFFKHLNDFLRKPFHNGQDAESAF QEFABESMFEYATGINTLISPWQKCV CSVSYFD
9147	23048	A	9214	402	276	LSCLSLPSSWDVRCPPPKGYFFFFFL LVKTCGPPLAQAQ
9148	23049	A	9215	386	37	GFKKRVCSPPPPPPPPPPPPPPPPPP FFLQKKVTCNNPSSNKKLLGLQKKKE IQPALMKJNISOS
9149	23050	A	9216	1	142	KDFRVQVWNHSSQPPPKGQSSRLS LPKYWDYRHEYLHCIOQAP
9150	23051	A	9217	402	181	FFFFRXXXXXFFXXXXXFFXXXXX XXXXXXXXXXFFXXXXXFFXXXXX FOEKLFIYFVNIIVTF
9151	23052	A	9218	2	87	SGSLYFGLIYICMVCVCVCVCVCVCVC
9152	23053	A	9219	420	271	YYCIFRETGFHVGQAGLELITSGEPPA SASQSAGITATAPSPFLTFLLV
9153	23054	A	9220	139	413	SGYHSKTLFQKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK IFFRGGGNNFFFLGPQKNIIGGGGKKR GGGKPPPPQIFFFVG
9154	23055	A	9221	134	236	LHRWGAPMLPRIILNTWPOVILLPRPPK VLELQA
9155	23056	A	9222	364	280	STHLSLPKYWDYRHEPPCLAKKDAQSFS
9156	23057	A	9223	1	147	TLLPMLESSGTIMAHCSLNVLGSSDPST SASQSARITSVSHCTOPPLPF
9157	23058	A	9224	1	208	AGAPPPASLPFCSLISDCASNQRDSVG VGPSEPGAGYHLVVRRLSQSEKRSIRVG VTRFSSLLSSHA
9158	23059	A	9225	1	145	FOHVGQAGPKLLTSGDLPASASQSAGIT VSNRVRPKTKNFYTGNTRN
9159	23060	A	9226	396	210	KCWDRHEPPYPALTNLLFIEMSGYGA RAGLKLGSNNPPISASQSAGVPLGSHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9160	23061	A	9227	2	154	AQPIF FHHFQAGLELLTSSDLPTSASQSABIT GMSHHTQPRMVFFSNFSSTAQC
9161	23062	A	9228	1	238	PFLALGTFILHATYLYSLYSLTHPPSMH PFLSLYLYSLYSLYSLYSLSLSLSLS LYSLYLYSLYSLYSLYSLFLSSAR
9162	23063	A	9229	3	65	RGDLITPEFLPKLLTKVGS
9163	23064	A	9230	25	188	YERTAWNQAWWVETVATWEAEAGGLL EPTSSRLRCVAVAPVNSYCTTAVWS
9164	23065	A	9231	44	232	YDLKFNHNVVFFLFTETEFHSLSKVECN GAISAHNHLCLCDGARLHRRGGKTKK QKTLPS
9165	23066	A	9232	3	195	FFVGLGSPYVQGTGLELLCSGNPPAS LNARI TGM SHQVQPN TGR LS PYLGSS IY GSIHAMI
9166	23067	A	9233	380	244	SVPLAEMGFHHVQGSPELLPPVTHSSQ PPKAIGLQARATAPSLH
9167	23068	A	9234	11	101	LLLINTLNFILHLSPIILLSLNPDIITGFE G
9168	23069	A	9235	411	226	FFFFFATNSQGGPTSPFWGPRNNAQVAGP LRNKITFPVGPSPKKIFPSWETPVF
9169	23070	A	9236	404	262	QGLAMLPRLVNSWTOALLPWPNPQSA GCGSVSHHTQPIFISENIH
9170	23071	A	9237	369	152	HAFVSVTWSRSHVNSYMTVTVMYHNL SIPLPDPHFFFRGGGLAMLPRLVSNPWP QAILPPQPPKVLGLQA
9171	23072	A	9238	389	190	RPKKKKKFFPPPGGKGVFFKGAPFFYFL NFIFFFFFFFFFFFFLIYTHNFIIL FLNCDRLYIT
9172	23073	A	9239	330	3	CGMEPPFFPPTGAQWQVFGSLQNSPPEF KQFLCLRLPNVLEYKSIIPCPNTFCSFY KNGIFPCWPGWPFKQKKKKISWVWCA LAEAGGSEPRWRRLQSAKMAPL
9173	23074	A	9240	122	248	KKKKRGGTLPTVIPPLWEAKGGGSRGOK IQTILAGGGKAPLY
9174	23075	A	9241	2	286	FFVQTEFHHVAQAALQVLSSRDPTPTSAS QSVDITGVSHCAQPVIVSCDDQVTLVOR RGVTVTSLTAFQCQVAYPKGAKSQWPGSF FFSEPFLLSL
9175	23076	A	9242	2	95	HMKKCSSSLAIREMLIKTTMRFFFFKLI TCY
9176	23077	A	9243	377	293	PLSRPLVLSSSAQMTLLLPPLKVLGSOA
9177	23078	A	9244	422	147	KKGTGGSPPBVRKGRNFFFGPPKK KKNPBPPRGKIFFLKGPBPSFFFFFPF YFFFFFPPFFTHKYFLGDLILLIYHLS KKNSYFF
9178	23079	A	9245	402	208	TIGRCHTQLNLKFEVEMGSHVVOAGL KLDLSTNPSSAFQSGAISGVNPYANTE IMFLYSIPI
9179	23080	A	9246	314	168	EPYHLHFLPPHHYYCRNGIIVLPMVLS NSWAQVILLPWPVKVQLQV
9180	23081	A	9247	3	320	VVOAGLKLSSDQCPASASQSAVITGVN HHARPLIFLYEMDYGSRVLIIRKWDEN EQSNRTIFLKKDEL TGNRSACLKYPMD INVNSGLGWRYRFGMHHCQRW
9181	23082	A	9248	22	303	KGSYFSTYEAQTESCTARLECRGATYS AHCNRLRLDSSNSPASASVAETDNHKT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LUPERSCFTEKERNVIQKGQEESEMSNHLFTWLPILH
9182	23083	A	9249	13	174	LGLKVRHRLWLIPLVLSVTEPHHLGQAGLELLTSGNSPAGITGVSHCARPTSHS
9183	23084	A	9250	3	141	HVGQTVLRLTSGDEPTSSASESAGITGVSHRPQIFISLFTICIR
9184	23085	A	9251	56	262	LRILPTFGGVVKGEEEDRAVMHLRLCGDDSPMSLSLHFIKLPRTVLVDEDARPEKKKKKKKKKKKKKK
9185	23086	A	9252	401	275	PADLFIETWEDGGTMSPLRVMSWSQA TLQPTWTKVGLGV
9186	23087	A	9253	411	258	PRVFKYRCDDPRLAWLFFVQSLPLRLGLNSWAQAFLLPWPFRVLGLQA
9187	23088	A	9255	391	167	GLKILTSGDLPASASQAGNTGMSHCHARPLMSFKIRYFLFTIKMKLLLVVPVMSAGVHPHPFSCPIVITNKPRI
9188	23089	A	9256	9	255	FFCRYGGLAVLPRVLSNSWTQAILSPWPKVLGLQACTHFFPLMVNSNAARIKTIELLSEVDNFFVALLCPSFTISHFHL
9189	23090	A	9257	487	42	RYVIFLFFVFIKTBTSYGYVAQARLRLGSSNPPALAFQASARITAVSHRAOLTCIKYTFLFTHIP
9190	23091	A	9258	1	243	ILSSGGSFISLTAVILITFMIGEAFASKRKVLIVIEEPSINLEWLYGCPPPYHTFEEPOPKKSEIYSKCFEFSVVFHGGWG
9191	23092	A	9259	411	2	FFFFSPVLSLVCLESSPPPPFFFSPPPKKGGFSPPPFFFSPPRVPPPPVFFFPFPFFFPPLKKNFSPPPPGKIFFFFPFPFFFPFFFLFFFPFRFFFSFFFLRWEVLYFTMCHHISDAYPPNVDMNKE
9192	23093	A	9260	417	219	SVEMGFLHVGGASIKLPTSGDPSASGQSAGITGLSHCARPHSQLSVCCYSVPVQCLNLSLARY
9193	23094	A	9261	408	172	CNHHFRKQSHRGCCPPPRVTEFFVRDGVYVAQAGLELLDLSNSPASQSNCTGTGMSHLGQQLFILNDVIAVPLQGSF
9194	23095	A	9262	401	132	GHQDNKPAFPFFFFFSPPPKGFFSKPYPVSPRRFPFPFLNPAFLFYFAGPKKIKFFFPDPAIKFFFKRAPLEFFFPFFFP
9195	23096	A	9263	393	220	LFLLNKIPFFPPGGSKGDEGPHNTNFFPGVKPIFRPHPEEGGPKGPPRPREFPLGF
9196	23097	A	9264	206	438	FFILKTHFRILGTVAHTYNPTTLGGPGBGNCTSKFTSLGTWGPFFHKSNCILGWGVPCGCPFWGAQQAQSAWSEGL
9197	23098	A	9265	333	48	ALLAGPTFFFLGKKKTRFGNRLHFFFFFLNLEVLNCPGWIMVVAIHRCDHGLTPPPTPLGRSSCLSLSSSNWYKLPPLHAGVRLDFDVS
9198	23099	A	9266	3	275	TGPHITGQAGLKLTLTGDFPLSASHSAGITGVSHHAWPMHLESYWRVQVYFPMQVLYFWAPSGAQHCAQIENAIPTLLSRPOE EPASEA
9199	23100	A	9267	49	226	HGPEFCMDADAQREGINVSARYPKNWESTVDPAREFTMISAPLMLADPDEFASVQLA
9200	23101	A	9268	159	236	PRVLVISNFOAILPPWPPIKRVGLQA
9201	23102	A	9269	1	208	IFNYCVFSSGVALAGYVQKQDPLAKEK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PRGVVFDVMGHSAYQVSACAFNRGQLKV SIYFFSRRLVVW
9202	23103	A	9270	1	209	IFNFCVFSVVVALAYGIYKQDLGALEEK PRNVVFDVMGHSAYQVSACAFNRGQLKV SIYFFSRRLVVW
9203	23104	A	9271	379	263	ESCSVGRLECSGAVPAHCNCLCLDPDSS GSPASSRLC
9204	23105	A	9272	312	3	FRREGLAALQPPWPNKVSXKKRKKERE RKRRKKRKKRKKEDGATADGISEAE VIRVHPYVPGFVLSEGIWEDMRAGR RPHAGESGDTVMLPQAGE
9205	23106	A	9273	405	246	PTKKNKYLHAPPLPHEFFFIYTPNPNFFFF FFFFFNFPPFFFKTGCEFLYFSY
9206	23107	A	9274	2	227	LVETGFRHIAQAGLQLSSSYPPTSASQ SVGITGVSHQPGPSHFPERKSLGLKTL LCVKVGRACALPFGSS
9207	23108	A	9275	70	304	NLEFLKASTYSESHLYLHPPTIYVYTRKR LDAMAHACNCTLDGRGGMARTPDLC SAYRGLSKCWDYRHDPRPLV
9208	23109	A	9276	2	260	TVFYHVQAALELLTSGGFALASASAG ITGVSHHAQFLLILVISLFPNCQSFHI SPYRFSPTQLNHGNTVLYPLVINISEI FF
9209	23110	A	9277	406	330	PRLVLNSWTOTLLPWPPLGLDV
9210	23111	A	9278	2	160	ELLTSSDPPASASQSRITGMSHHTRLK YIVYRVSRKSKNIPCLKHIGIQSFP
9211	23112	A	9279	1	91	GLTVFPLVWNSWAQMLPWPCKMLGL QV
9212	23113	A	9280	3	107	LGETGFHHVGRAGLELLNKMVPPNAPR VLGLQA
9213	23114	A	9281	336	234	AHYKLLKIKLFGQAQMLTVPITLWEA EAGRS
9214	23115	A	9282	3	241	DRPEFCWDADAQREGINASARYPKNWVT TGDPAEFTMTHTAPMLLADPDEIESV QLAQSWPFGATASLGRSPCKRN
9215	23116	A	9283	404	277	IFFVETRSHTAQAGLELLGSSDPFYFF QVFTMSLSQALF
9216	23117	A	9284	399	231	HYVQAASLKLLYSGDPASAFQSAEITAG VSHCTWPTGSLNKIQNNHRSISM
9217	23118	A	9286	394	231	APFFFFFGGERGFHIVARTVLLKLDSSN PPAVVSQASGITDVSHDFLISLYRIY
9218	23119	A	9287	420	311	LNFCRDGLAMLPRVLNSWAQAVLSQCF PKVMGLHA
9219	23120	A	9288	398	173	LLSFFLYFFYFFFIPLFFLFFFIFFFIFF LMFKALLFSCHYFPAMVTFKFSLSISGV VRTSGYIMLFYSYLCLLKTMT
9220	23121	A	9289	270	23	TEQCGRGKLFITYSLILYVRDGVLLCCS GWPVVAIHKDCHSTLQHQIPSLKQASCL SLSSWEYRYAPMLHLASANFLKVTV
9221	23122	A	9290	273	46	HLNMLFLFIWIERFLFYLCFVFLV ETGFFYITQAGLKLTSDDPAYASQSA EIIGTSHCTRCICYNNVTNI
9222	23123	A	9291	424	230	CLPFTHSLSLSLSLSLHSHTHTHTHTH TTYMKN
9223	23124	A	9292	2	146	NFLVIVETRSHHVARASFKLLSSSNPPTS ASQSEITGASHRTWPEVFF
9224	23125	A	9293	393	202	GRERERKRERERERERERERERERERER

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PSGSLTYCVREGITAAANLGRKRHKASRT LISHKNKN
9225	23126	A	9294	252	193	GFCCCCCCCCVCCSSDKRHF
9226	23127	A	9295	409	269	SQYFGRLRRVDCLSGGVQDPGQGGQETP SLLKYKIYIHISWAGWHV
9227	23128	A	9296	2	213	FCGGILHLIYCKTEYSSQSTVAIHRCN HSVLOPQTLCAFGKQFSLHLLSSWDYRS PLCPAYIFNLSTGY
9228	23129	A	9297	169	408	RFAHMHNSPHEERLPPAGIRVRFPPOP AASLGPPMAPSISRRTMTYYKHNDP AGQAQWLMFVVPALWEAENGSSSE
9229	23130	A	9298	199	51	LHPFFPFLSLSLSTHTHTHTHTHTHT TLWLGRGPAPQDVVLVWGNLT
9230	23131	A	9299	1	176	MGSHSLAQARMQWNCQSSSLQPPFGLKQ PSFPLSPSSWDYRHRVPPCLASIFFLKLN YH
9231	23132	A	9300	412	209	MGFHHVQSGSLELLTSGDPPTSAQSAG ITGVSHRNWPHCGFNVLVFLMPDDVKHLF MCILAI CVSSL
9232	23133	A	9301	195	347	KIKGPRPGATARAGNPSALGHQGGRTAI AWFTISMSNMGRPCLYRKYN
9233	23134	A	9302	386	190	GFLFFFFPKKVEVFPFHLFGPFGFPF PPFFKRAPEFFFWGPKKKNSPPRALN FFFFKGAPP
9234	23135	A	9303	27	173	SFQLWGLKVPRIKPRADHLRSGVDQDQ PDQHKTLTLLKKYKISRAN
9235	23136	A	9304	374	121	QWCDHGSLOPQTPLGLKQSSCFSLPKRWD YRREPPTSLSPYIVAMPCTLCPPPLS ALWKHLHQKCDGVMVLQVPGRTHNVT T
9236	23137	A	9305	70	196	PQVHPGQAGLELLTSGDLFASASKSAG ITGVSHHAQPISHF
9237	23138	A	9306	378	256	QKNVSICCPGWSQTFGLQESSCLGLPKS WDYRRQPQPCLT
9238	23139	A	9307	206	3	PCHLGSVAVQSWLTAASNSWPHAILPP QPPKVLGLQASLFLKAGITQVTFSDYN KILANKEIKRGR
9239	23140	A	9308	338	161	HFKKKIYIYIVYIHTYIYIYTHIHTYI HYTYIYRYIHIIYIYIMVYIYIYS LFF
9240	23141	A	9309	503	288	FFIANDKSQBWMLMPVITPLREAEAGGS LEVRSSRPASSDPPTSAQSAGIGMRH HARPVVLENGRION
9241	23142	A	9310	418	309	FFCKNGISICCLPKLVSNNSWQAILQPO PKVQGT
9242	23143	A	9311	442	275	VSPPPIGGGFLSPPPKPPPPFNLKGGP PPPTIFLLIKGKKFCPPPPFPFPGLP
9243	23144	A	9312	2	95	HENRLSLGGGCGSELRLCHCTPAWATER DFI
9244	23145	A	9313	318	154	FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFI FILFIYSLLYVVCVGLGS
9245	23146	A	9314	388	199	EQPKCVHRIKQIWHICALLEYAFAKKKK VLPYAVIQIKLEDTMSLEINQSWGKCYM IFLIGGI
9246	23147	A	9315	2	97	STPGLKRSSHISLEKYNDYRRGPGFPAS ILF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9247	23148	A	9316	3	235	TMVNAEGTPIRTLDNSTTVQYACLLH HLTMAKSTVRDIDPDNDLTLRIRSKK HEIMVADPKKEYLLIVIONPCE
9248	23149	A	9317	253	71	LEFFFLFFVDTKFHHLAQDGFQLSSSN SPTASASQSGGTGRSHQAWPYVHLLTLQ KLNy
9249	23150	A	9318	425	95	CLLFCPKKKKKKKKKKKKKKKKKKKK KKKGGPKKKKKQ
9250	23151	A	9319	25	214	VRIDDRPEPCMDADAQREGINSARYPK NWVTTGDPARECGMHSAPLMLLADPDE FVSVOLA
9251	23152	A	9320	50	231	GHRPEPGRDADAQREGIASARYPKNWV TTGDPARECTRIQAPLMLLADPDEFVS VOLA
9252	23153	A	9321	401	226	QWLFTNMIIGHCSLELLGPSNPPISASR LAATTGTRHQAQPSKFRNLKGWLCakra RT
9253	23154	A	9322	410	159	LGSLQLPPFGSKFRSLPSLSSWDYRGC SELRLRHCTPAWVTQDQSVPPKKKKQIF RPFPPSYGESLGVLGRLHLCFSKPSRRF
9254	23155	A	9323	310	25	KWGGGLFFSPKKRGFFQVFFCVPPVF FFPFPFKTGPDIFLQPLKKKIFPPPG GKKFFFKRGPPPPPPPPPPPPPPPPPP FSEVECVCLCR
9255	23156	A	9324	406	289	PGFYHAQAGLKLTLTSGNPSASASQAR ITSISQRTPH
9256	23157	A	9325	1	116	LHSVLLFFYFCVVCVVCVVCVCKHK YVRAGGAPGR
9257	23158	A	9326	2	158	FIFLFTVGGLTGIVLANSLLDIVLHDY YVAHFHYVLISGAVFALIGGFH
9258	23159	A	9327	3	107	RGCEPRLRHCTPAWVTGDCVSRKKKK VPEAWG
9259	23160	A	9328	257	2	GFFSNISASVIIPPPISRKNLFFPPRVY FGPPFKTKGPPPPPPPPFLSPRLCSG VIMAQCSLTGSSDLPLSASCVMATVS I
9260	23161	A	9329	66	384	GNLCGWKMSAWDNFVVRKADWQIRRES LECPNTGMLKKKKKKKKKKKKKKKKK KRGGPFLKISWGGPILGGRKKIFPPFFG GGILTTPRGVFNKSPFFWGGKKK
9261	23162	A	9330	1	98	ITIGQVASVLYFTTILILPTISLIENKI LKWA
9262	23163	A	9331	33	412	NLFVYMAELHTHTQLCCQVKLHLSVPR PSLPLCCNWNFSVLVHEHSQPAEKKKK KKKKNNKKKKKKKKRGGVFKKPGGAP FCGGGENFFFFFGGGLKKRPFVFGKNT FFWGGEKRRPPPPY
9263	23164	A	9332	401	311	PTRPVDLLVDDSVKESLIGYGPTEDSKE FS
9264	23165	A	9333	5730	452	TRSAPRAASWLEDPREVRSVCLSATFFFT LSLQKPELLLSPSVVHLGVPLSVGVQL QDVPRGQVVKGSVFLRNPSRNNVPCSPK VDFTLSERDFALLSLQVPLKDAKSCGL HQLLRGPEVOLVAHSPLWKDSLRTTNI QGILNLFSSRRGHFLQTDQPIYNGQR VRYRVFALDQKMRPSTDTITVMVENS LVRKKEVYMPSIFQDDFVDPDISEPG TWKISARFSDGLENSSTQFEVKYVLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
9265	23166	A	9334	46	324	<p>NFEVKITPGKPYLITVFGHLEMDQLDIQ ARYIYGKPVQGVAYVRFGLLEDGKKTF FRGLSEQTKLVNGQSHISLSKAEPQDAL EKLNMGITDLQGLRLYVAAAIIEYPGGE MEEAELTSWYFVSSPFSLDLSKTRHLV PGAPFLQLALVREMSGSPASGIPVKVSA TVSSPGSVPEVQDIQONTDGGQVSIPI IIPQITISELQLSVSAGSPHAIARLTVA APPSGGPGFLSIERPDSRPVRVGDTLNL NLRAVGSAGTFSHYIYMLSRGQIVFMN REPKRTLTSVSVFVDHHLAPSFYFVAFY YGHDPVANSRLVDVQAGACEGKLELSV DGAKQYRNGESVKLHLETDLSLALVALGA LDTALYAAGSKSHKPLNMKGKFEAMNSY DLGCGPGGDSALQVFAAGLAFSDGDQ WTLRSKKLSCPREKTRKRNINFPQAI NEKLGQASPTAKKCCQGVLPMMRS CEQAAVQQLDCREFLSCCQAFASLRL KKSRDKXQAGLQALBELQEDDILED IPVRSFFPENWLRVETVDRFQILTLWL PDSLTTWEIHGLSLSKTKGLCVATPVOL RVFRFPHHLRLPMSVRRFQELRLRPVL YNYLIDKNLTVSVHVSFVPEGLCLAGGGOL AQOVLVPAGSARPVAFSVVPTAAAVSL KVVARGSFEPFVGDAVSKVLQIEKEGAI HREELVYELPLDHRGRTLEIPGNSDPN MIPDGFNSYVRVTASDPLDTLGSEGL SPGGVASLLRLPRGCGEQMTIYLAPTLA ASRYLDKTEQWSTLPPETKDHAVDLIQK GYMRIQQFRKADGSYAALWSRDSSTWLT AFVLKVLSLAQEQVGSGPEKLQETSNWL LSQQQADGSPQDPCVLRDSMQGGLVGN DETVALTAFVTIALIHIGLAVFQDEGAEP LKQRVEASISKANSFLGEKASAGLLGAH ARAITYALTLTAKAPVDLLGVANNLMA MAQETGDNLYWGSVTGSQSNVSPPTAP RNPSPMPQAPALWIETAYALLHLLH EKGAEADQAAWLTDGSGFQGGPSTQ DTVIALDALSAWTASHTTEERGLNVT SSTGRNPFKSHALQLNQRIRGLEEEELQ FSLGSKINVKVGGNSKGTLLVLRITYNVL DMKNTTCQDLQIEVTVKGHVEYTMANE DYEDYEYDELPAKDDAPLQPVPTPLQL FEGRRNRNRREA PKVVEEQESRVHYTVU IWRNGKVLGSGMATADVTLLSGFHARA DLEKLTSLSDRYVSHFETEGPHVLLYFD SVPTSRECVGFVAVQVVPVLGPASAT LYDYNNPERRCSVFYGAPSKSRLLATLC SAEVQCASGKCPQRALERGLQDEDDG YRMKFACYIPRVEYGFQVKVLRSDSRAA FRLFETKITQVLHFTKDVKAANQMNRN LVRASCRLRLPEPKGYLIMGMLDGATY DLEGHPOYLDSNSNIEEMPSERLCRST RQRAACAQLNDFLQEYGTQCGQV</p> <p>SKYLPVITFQHEIWGNTIQTISDWVL ICCPGWSAVTQSRLLAAASTSWAQMSSS SCIGLSSSCYRHTPPCLANFVAFVETK LYTMLPGLS</p>

SEQ ID No: of nucleotide sequence	SEQ ID No: of peptide sequence	M eth od	SEQ ID No: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleo- tide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, =possible nucleotide insertion)
9266	23167	A	9335	338	178	EVDIKVSRRKQAFNCLLCKCPHNCL NLBGGSSSELKLCYCIPANATDQSL
9267	23168	A	9336	396	254	KLSTDUCTSKEIINRHPTENKIFANYAP NKGPTSTIHSLSCLMPPVLP
9268	23169	A	9337	454	359	SSWDYRHAPPCCANFVFLVETIFIQGEI GLL
9269	23170	A	9338	540	328	IKKKGAPRGVLFFFTKRRKKFVSYYKK TKERVSLFVAPGCIQGGKKKKPPTKKK KKKKKKKKKKKKK
9270	23171	A	9339	21	209	AEEFFDFKLYYKANONTYRGQNNKTETS EITPDIVYLGIQLVNSNWPQVILLPWPVK VLGLQA
9271	23172	A	9340	345	2	KIFFFLIYLFFNFNFFFFFFF FFFFFLENRWFLMENFIKRGHVKGPLG QARDHDISGRWRREOCRASQLPGVRR SLLQVQAGGVHIRISGLQDARQCPVRA GA
9272	23173	A	9341	15	252	LERVIRQSAALTDSPNFNILLILFIYLF FETGSPCVSQAGLKLGSRRDPVVSASQS ARIGVSHRAQPALTDFFPSISF
9273	23174	A	9342	484	276	RHAPPCQANFFVQTRFCHVAGSGLKLIR SRYLFSAPASQSVRI*CMSHCARPLYFLM FKRQLYSKPTKS
9274	23175	A	9343	464	326	LVEITGPHHVQAGPELLAPCDPPAPASQ SAETTGMSHRRAPPAFNV
9275	23176	A	9344	486	280	SFSHSHCSLFSMSDVRTCSHLANFFF KRWGFTILPRLILNSWPQVILLPQSHRH EPLCLETLKTINV
9276	23177	A	9345	276	179	DRDFTMLPRLVLNSWPKTILPLLPKIL RLQS
9277	23178	A	9346	45	143	RNNSRQENCLNLGGGDCPSESLCHCPA WATE
9278	23179	A	9347	229	73	PEPHMIFFFFFFFFVFVFVFVFVFVFVF FFVFVFVFVFVFVFVFVFVFVFVFVFVF VFVFVFVFVFVFVFVFVFVFVFVFVFVF
9279	23180	A	9348	391	139	PTLSKRSMLSLAKCDYRRHKPCQVTF SFLANRIYATKFLISPTLAWSKYWVLV FLSFLSFSKYYLITPSFLFLTHYVSSSIF
9280	23181	A	9349	53	191	IVVYTVKTSVSHVAYNSSTLGGQSGRIT GAQEFKTSLVNIAPKLLY
9281	23182	A	9350	373	235	EGEELLEPGVCGCSLSNCHCTPANGTE QDHCVSYNNSNTHNNVNY
9282	23183	A	9351	476	82	YLATVILPTVLTSTVLPVLPVLPVLPVLP GSHVIAQAGLKLFGWHVHGSCGL
9283	23184	A	9352	286	142	ELQPKRMFGWRHSQTTISGLSLLPRLIS NSWAGVLLITWPKVVLGIA
9284	23185	A	9353	3	102	FFETESHVSARLEYSCAISAKCTPVIKL VLYT
9285	23186	A	9354	3	270	TAGAPRPKANFCLFSRDSGVSPCWGWSR TPGLRCDPPASASQLLGRLRHENCNLIG GEGCTGAILAHCTSTLRAQAILQPQPS CAPO
9286	23187	A	9355	1	112	GGGSAHCNCLCPGSSNSPASTSQVAGIK GVSHRAPRN
9287	23188	A	9356	1	63	VALIQAYVFTLLVSILYLDHNP
9288	23189	A	9357	244	140	QRHTHTSHTYTHTHTHTHNKPIITL ILKCIA
9289	23190	A	9358	464	181	LGAGGTMGILFSLGASMLVGGVQMLAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KATRRITQTTDNGKNTYFSSLDNMVAQ QNVLPVLVGMVRVSGSRVVSQEISTADEG DGQVUVIGR
9290	23191	A	9359	11	469	IDLRCRFRHEERERERERERERERERERER ERERERERERERERGRAPPPPLFGGG GPPARAHALSPPHLGRPLTYTFYSYVR APPTERSARTQREARALKSVCVVRE THSLPRARCVCVSHPTGCGAPGARVSL QSAHCLVCVCGAG
9291	23192	A	9360	22	172	GLSHEERERERERERERERERERERTV CPLFCPTGGFILREARVKGCLCF
9292	23193	A	9361	15	345	PPNRPPAEFTTHLYISLLCLEGTYLSL FIATLITLNTSHLLANIVPIALVFAA CEAAVGLALLVSIINTYGLDYVHNQKK KKTWGGGRAPNSPYGGRNNPRPAV
9293	23194	A	9362	61	298	SCDSFLQECCHTHTHTHTHTHTHTHTHT LFSDIKHTWTREWALSLFTEEGGGT LFGQTLIFGHTLFWDKPLWQKEF
9294	23195	A	9363	430	2	GGAGFPFPWCQTGGPVVPPPTLSPRVNGP SLCSDFPSPKFKYKRRKKKGNTPKRRKG KTLLETETIVLHVSPGCKSPGAGSADR RAPGVRDGGSDASSGTRASELGDGPVR VNFVLGDGPEAGRGFSMLGHPPTSGPR TS
9295	23196	A	9364	432	291	GITGLRHHSQTLPLFLVETGFHHVUGAG LELLIHQRHPSKVLRVQV
9296	23197	A	9365	343	507	GQGLTLVPQGVQWGNLSSQLLPGLK QSTCLSLPKCWDYKCGLPFPASFCFVL
9297	23198	A	9366	417	128	MGWVPGRGAPPFLEMAAGQRRSSLSR GSAEGLLTSHTMGGPAETLLTSTGTWR LGRGCNLSLEGGQRRLLGGGCNEPSSR HCTPAWAPLSTE
9298	23199	A	9367	500	285	SLPSRWYRRAPPPANFLFLVEMGFHH VGKAVLELTSGVELLTSGDLPASASQ AGITGVSHRAWQIRE
9299	23200	A	9368	1	229	IVDLTTWGIPTHTTHKYTHIHXYLHTH AYTHHTHRHGHVITYIHTDMVLSHPHN LILNFSNHPHVSWEQPNR
9300	23201	A	9369	451	88	KQTNIVTCIYMYVYVITCIYTYYYIYR TYTCIYVCVYTCIYVCVYTCIYVCVYTC IYVCVYTCIYVCVYIRVYTCVCIYVYIR VCVYTCIYVYVIRVYTYICITYCISTY IQCIYTHIYKVKCSG
9301	23202	A	9370	1	208	ADETIORGGIPKPFVHDNYVIRRTAVDR GIPLLTNFQETKLPAAVQSKRVDSKS LPHYRQYSAGKAA
9302	23203	A	9371	354	202	PAAQREGITASARYSNKVNTPGDPAREF TMIQSAFLMLLADPDEFVSLQA
9303	23204	A	9372	1	336	KSLIKYKGQVAPAEIESILLQHPNIFD AGVAGLPDDAGELPAVAVVLEHGKMT EKEIVDYVASQVTTAKLRGGVVFVDE PKGLTGKLDARKIRELILKAKKGKSKL
9304	23205	A	9373	2	187	NILVTALYSLYITFTTQWGLTHHNNI KPSFTRENTLMFIHLSPIILLSLNPDII TGFSS
9305	23206	A	9374	96	240	ACWLMPVIPALSEAEAGRLVQPRRIRAA WATWQDLISTKKKKGPP
9306	23207	A	9375	3	293	STISAFSTSTSTATTSTSTATTSTIS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						APTTSTTSLPSTTSTTTTITSTTSAPIS SNKLHKKKKKKKKKKKKKKNDTKQD TITKIHSGGSL
9307	23208	A	9376	69	160	ERTHTHTHTSHHTHTSHLPERFFCVLN SL
9308	23209	A	9377	336	199	EGITASARYSKNWTGDPAREFPPIQS APLMLLADPDEFVSQVLA
9309	23210	A	9378	321	128	EPFGTMAWLASPTSSQVIRHGLPKCK DHRREPPHPAYHSLYESGPSVQNGEEKG INPIIKMG
9310	23211	A	9379	440	286	SSDPSASASKSAGFTGMHSHQTLLTSYS EGECCLSYLVFLVLV
9311	23212	A	9380	392	154	KGSSPLSPFPISLAGGKPPPPRKFLLNFF FFPNRDRVSPCLPRLVNSNWPQAILPPO PHKALGLQAYATTASFILIVTV
9312	23213	A	9381	403	178	GRRHEPCRDADAHLEGIIFSAPYPRNWE TTGDGAREWNTMSNSAPLMLLADPDEFVS VQLA
9313	23214	A	9382	303	206	DPVSTRICSLQPPPPGFKRFSCLSLPSS WDHR
9314	23215	A	9383	215	116	SNMFVCCCCCCCCCLRWSLTSLPRHL SCGTM
9315	23216	A	9384	2	285	ARHLLMQLSGGATLAISTIDLPLSTLIIF TLILLITLLEIAVALIQAYDITLLGSLY LGDNTYKKKKRGAFFEETKTSAGMQSK NFFGLTLNWR
9316	23217	A	9385	12	123	GYENFLLTLHTQTAHTHTHTHTHTHI HSKDPMEY
9317	23218	A	9386	3	230	KCWGYRPEPLRLADLPCEFFTPGGISLTS GPALLSNASALAEVGRQQCLPPTPFLPT LIAITLLLPISPFILIL
9318	23219	A	9387	590	396	ARVOWPDLGSLQPPPPGFKRFSCLSLN SNWYKCAPPCRADFCIFSRDGLVSCWPG WSQTPYVK
9319	23220	A	9388	224	79	GLGPVGHACPTLNEGEAGGSRQETELAL PANTVKPRFLRKKKKKKKK
9320	23221	A	9389	249	72	LVYLITVKKILFVPHVIRTFNKKIDHMHG KTCNLKLQMTIELQSVFSDYNRIKLEAS NN
9321	23222	A	9390	400	254	LKQPGSTNSPVSAIRVAGITGTHHTHTQI IFVFLVEMVHACNPSYSQG
9322	23223	A	9391	3	64	PPQKSDPPYKLVVHLDSIL
9323	23224	A	9392	266	106	LTANFLFLVETGFPVHTRVGLELLASD LPTLASQRAGITGVNHLQNFWPNGF
9324	23225	A	9393	430	348	FGKQCFPPKKGSPFRGNFFPKAPKG
9325	23226	A	9394	481	311	LSLSEKRSIRVGVTRFSRCCFSPSLITG KGNLSLTPGVSQEIHSPWFGIAYSVCTH
9326	23227	A	9395	3	136	VFPRLVNSWAQMIILLCPWPKVLGLQAC TTRPSHFLPLNLSKYK
9327	23228	A	9396	143	347	NFVELVETRPHHVGAGLTLTSSDDPAS QSAGITVRVRPEILTLKRYHFPSSGLLGE GMVEMAYLLKV
9328	23229	A	9397	2	231	LELLTSSDLPASASQAGITRSHHARP SFTFRCVIHLEFNFRGAREERLHFYCR WVIRRLTTFGRGYPSPAASD
9329	23230	A	9398	383	200	QHYLNRRLSLAQWMPVVPATQEAERG LLEPRSSSLQCAMMFLVNSHCTLAWATH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						REPHL
9330	23231	A	9399	3	416	GFLHVQAGLKLTLTSGDLPTSASOSAGI IGVSHRAGCLKSIYLTFFTRKFFVQMSI CDFKVEIEGKIGFISVPSILQSLIHIVN NFFFLFETGSPFPQWRAWEKFGLIAPLA SGVKGIFLPLPRENLGWRPSPPIPPA
9331	23232	A	9400	400	151	FGYPQVFFLPFPFLKPGGIFFLGLPLKKN FPFPPGPKIKFSFKRAPPPFFVVRKGLI MLLRVSNWSAQVLIIPPPPEVLGLQA
9332	23233	A	9401	324	154	FFFFFXXXXXLLFFFFFFFFLPYIFFF FFFXFXFFFFFFFFF
9333	23234	A	9402	413	312	PKLVINSWLQALLPRPPKVLGLQARAT ITQPK
9334	23235	A	9403	363	3	FKKKNFCLGGAGVVFVFFDPPPKKNIF YFPSKKIYFLSPASSSFFFLCPFFPIF FFFFFFFPLENRFWMENFIKGRGHV KGFLGARDHDISGRWRREQCRAQL PGVRPRV
9335	23236	A	9404	401	82	SELPHDPINFTGGIYPPKMKSVCFDI CTPMFTTALPSIAKINQKCLSKRITI FMPLTYSQCFTHYFLIYFPPFAPLS SSINVHYTLVLYENILDSYV
9336	23237	A	9405	382	219	WARWHGFLVFTSPGGEAGSLEPGKRRV QLTQISPLSPSSLGKVGVLPLKKKNN VLYSLVETGFPHVVGAGLELLYSRDESA LASESAEITOMSHSITQPSAFYIPIPET FWQPAFK
9338	23239	A	9407	371	1	FRRLRLKRLNLGGGSCSEPLRCHCIPA WETRAKLGRKKERKREKGTMYNKM MYLELNLTCPEPASPKMOTROLEVLSS NPSPGTQFICKQFKFSCCFALRVSIY LLMSVFEYCSC
9339	23240	A	9408	326	229	RQGLTMLRLVSNWSAQVILFPWPVKV GLQA
9340	23241	A	9409	81	231	LESASFPGKVAHTCNFNLTGRCAGWIA WAQKFKTSLGNMAKPCLYKIK
9341	23242	A	9410	367	256	HPGWEWLVSVIPTFLREAKVRSLEPRS LRLAWDTWG
9342	23243	A	9411	2	192	VFLVEMGFLHVQAGLELFTSGDPPASQ SAGITGVSHHAQALTFLNIPINSPHPK ACCSKOL
9343	23244	A	9412	3	83	KNCLNLGGGSCSELRCHCTLTWATE
9344	23245	A	9413	371	301	EDHFRNVILRLRYIVRLVWRMH
9345	23246	A	9414	486	337	AGLELGLSSNLPALTSHTAEITOMCHT WLAYIFVCAFGWLLDLCLAF
9346	23247	A	9415	378	254	IYAHCSLDLGLSSDPLTSASRVAGPTGM CHVWLVIVFFVC
9347	23248	A	9416	160	309	VVRYSSNEFLFLFLYFLKSNFTVFCFC YCCCCCNRQSLTLPKLECGV
9348	23249	A	9417	162	339	RFSSFCFLHDSVPELALPMKARFEKSR RSQVSWLPVPIPTFWAKVGRYQARSLI PA
9349	23250	A	9418	1	147	GGGGCSEPRSCHCTPAWATRVKGLFKK KKKINFLVPPPIFLKSKTV
9350	23251	A	9419	283	126	KMYKGGAGWLIPIIPAWFEAKERGLLE VRSRLPAWATEQDSTATKNNKMF

FIG. 4

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9351	23252	A	9420	133	3	ELNFSWAWINPVI PALWAEAGGSRGQ EPKTS LPMVKPRLN
9352	23253	A	9421	3	133	LRGLYSAGIIRFEAKKNALALAWADI AGDNCAICRNHIMDL
9353	23254	A	9422	409	291	ILILGGSGCSSELRSCHCTPAWATRAKHR LKNKSPINVI
9354	23255	A	9423	1	210	RFPHLGLSKEMDYRCESPHAGTRNEVLI YATITWMSNIIVPNEIIQTQRTNIVSFY LYQVGRIGKPIDRP
9355	23256	A	9424	479	306	GVPTNPWNSRVKTPSPPTKNIKISRPWW CMPCNPSCSEGOGRRIALNPGWRLO
9356	23257	A	9425	1	209	GFFLFQGGGHHAGQGLELLTSGDLFAS ASQSAGITGAGPNQGI FVALESPMESAA LLHLHVLLSPSCS
9357	23258	A	9426	628	433	RQGVHLFGMGCSGTITTHCSLELLGSS DPPASASQSSRLAVVSHCAQPSLLESVL CLKPIFCCA
9358	23259	A	9427	417	125	FLKQSLTSSPRLEYNGATPAHCNCLCPG SSDSSILASQSIRITGVNHCTWDAAVL RQNFFFSEKQPFYSSEFGQTHI IKNLL YLKSTKCTCYPL
9359	23260	A	9428	366	256	SFFYRDRSLATPLRLGSNAWSQAIPLPG PPKVLRLLA
9360	23261	A	9429	3	140	GPCHVGQAALKLLISDLPSTPSQSAGI TGVSHCARLTRLFSSE
9361	23262	A	9430	368	3	VRASQLCLPTQASANAGTFFPASPFPFC SSISDCCASSEQSGMGVGPSEPGAGYNL VVCSSRLTLEKCSIRVGVQFQRCHLSQ LPLARKGNSTPCASVWRCLTLQLML RGLYPLSCT
9362	23263	A	9431	3	131	LTMLPRLVNSWAQSSSHLSPPKCDYR CEPLHSLGKDIFLE
9363	23264	A	9432	384	274	LSFAMLPRLVNSWAQESAHLGLPKCWD YRHEPIGLA
9364	23265	A	9433	431	273	PPPLGYFFIVKMEFFPVVQDGFKLLNSS DCSTSAFSGRISGVNHSTRPPIF
9365	23266	A	9434	211	473	CVCTFFSFLSMHIFFLFVGEAESHCVT EAGVQWHDLSGWWPPPPRLKRFSCLSLP SSQWDRKVEPYPAFCIFSRTRVMSWCP GWS
9366	23267	A	9435	391	188	LPSSSDSPASASRVAGTIGGCRHTVLLG FEFKDNIRWIKLVEKANTQYGNIIYCVI KVMPLFPYVHI
9367	23268	A	9436	331	115	SRDRGFMLPRLVLSNWTQATCSLLDQ SAHLSLPKCNRYRREPLCPASGEILSFI KPSSSKS FHNSTKKRQ
9368	23269	A	9437	3	109	IYGSYSLPACFFPSFLPSFLPSFLPSFP PPFLSFF
9369	23270	A	9438	2	167	ECNGAISGHCNCLSGSSDSPAPAWATR VKLRLIKKKKKKNQILFFYPKRTLF
9370	23271	A	9439	648	310	VCPCTLRHPAPLFAKSGNPLESSLLDHS SPTPKLTDRENLRHVKTSHSQSLPTSG FQPGLPDSTLCAWYPTSPKLS PAGWVG GYRAPVGRRGPGSRNSRLHWTPTTSVG D
9371	23272	A	9440	1	170	YEIWFILDVGAGLELLTSGDLSASGSQS AGTGMSSIHARPLKFTISVSNKVKVC LFGYQTRGLAMLKLDNSNWPQAVLPQ
9372	23273	A	9441	133	244	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PPKVLGLLA
9373	23274	A	9442	365	176	RGSDMWVPSSECTGYNLMLCPLLRPLEK RSTRVGVTFRSRCHLSQLPLARKGNSLT PCASQVR
9374	23275	A	9443	368	231	VEAGFCHTAQAGLTFLSSTDPASALASRS ARITGVSHHARPIFLKE
9375	23276	A	9444	88	194	KMLEAKKKIEQGGFTFENKGVLSAFNF GTVPNN
9376	23277	A	9445	3	349	TRSGSYACYFCYPRECVALFHCYSMTIVS YGPYYFMNIDQRHESRLSTIYIFKFIIG SKHIVAQGLELLCGSSPPAFTSQSAGIT SVSHHTRPQKIFNVIYSCDLHFHPGIEG PQR
9377	23278	A	9446	3	141	HAECSSMMIAHCELELGGSTDPASASQ SAETTGISYHAQPYSTF
9378	23279	A	9447	2	282	ICPTSRFRFPVRLKNGRKKDRLECSGAI SANCSLCLPGSSDSPASASRVAGSTVAE EDSTRRAVRHQGSSRSAPSGRGSWAGKQ ERADRAQQS
9379	23280	A	9448	307	430	GLAWLTPGIPILWEAEVGGSLVEVEFT SLASMEKPSLYK
9380	23281	A	9449	2	253	IQCVVCVVCVVCVCLSVCLHFIATLGC SPWGRSLPCSVSSPSGRGGEDLSPLP PTMSVSPEADFPFLAAAPGNIMTAIT
9381	23282	A	9450	1	166	NTGGGGEIRVFSSCFADRLQRKDRP GAVAHACNRSTLGGRGGIVITRSIIFC
9382	23283	A	9451	1	123	NTRGLVMLPRLVSNWAQVILQPLPPKV LGLQASVTVHINN
9383	23284	A	9452	396	291	SLCIKRVCAACVVCVVCVSGAKRLKL LDPMRS
9384	23285	A	9453	1	147	FAIRARFSNIYTKIGTINTYIYIYTYI TYIYTHTHIYLSQVLMMEYF
9385	23286	A	9454	394	235	TRSCYIAQSVVGMFLFTGLIHYNLQLL SSRDTFVASQVQLQAHTTTPDSC
9386	23287	A	9455	1	85	TNFPVATLLEWQDALCFIPVGSAAFGSP
9387	23288	A	9456	339	165	KTHHWGKSLFNPFPPFFFTKSRVS TRLECSGVILAFKQKTKQNDKNTINKT I
9388	23289	A	9457	3	209	LLYLFSLKMRNRDPSALLSTQLPPIFI YIHTHIYLYIYTHYIYIYIYLYLFA YIHIYVSLFPLK
9389	23290	A	9458	374	156	QAGLELLTSGDPTFISASQSARITGLSQ AQLSELTLTVPTRHCTCLCAHPLYTYV FLEGRNDEFISIPST
9390	23291	A	9459	287	3	EAGLLWRKATHKYAHTHTHTHTHTHT RGLQNMINKYITYQEIIMTLAQAKNGV IPDSFPPTSSPPLTYPPALSFHQKHIP NKTITYHGHC
9391	23292	A	9460	3	72	KTELKMKFTNILESSFLMNNKS
9392	23293	A	9461	327	92	ISLFLVWGLFFPKKIYPPKRKSLPFF PPPPQENFNPPSFLAPPVFPQENPKF AGGRKIFCPPPPVFFYFFFFF
9393	23294	A	9462	3	173	ACRGDSGGPLVTRDLKDTWYLGIVSWG DNCGQDKPGVYTVQVTYRNWIAKTGI
9394	23295	A	9463	258	39	LKVLPSDPSSIFVCLPLENERSVTCQ GVQWHDLGFRFSCLSLLSSWDYRRVPP PPAKFCIFRKHGVSVC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
9395	23296	A	9464	104	336	NHVSQCEETFLDFEYIIFSRVASMFVW DAELGSDIYLDGKLKNSFLLSGLGFFFF FTLGGKVVFFFSQNGQLGRPGQ
9396	23297	A	9465	410	0	LNLLGGGGCSEPLRCFCTPAWATE
9397	23298	A	9466	254	61	KKKKDAFFTTIPLYPSSQNLFAFTQMDPD TNISQQLTWTVLPGQFRHSPTFLDKPF KQTSINFA
9398	23299	A	9467	403	255	PAPQLGGPPMPMMAPPPSSWMMPMGCA AMRLPIGGDIITWLCVPTQISF
9399	23300	A	9468	1	1428	PARFKDLNLAGTAEVGLAGYFMDHTVAF RDLPLVRMVCSSCTYRAETNTQGEPRGLY RVHHFTKVMFVGTVGPGLEQSSQLLEEF LSLQHEILTELGLHFRVLDMPTEQLGSL AYKKPDIEMWPGQRGEFVETVSAQNCCTD FQSRRLHIMFOTEGELQPAHTVNTATC AVPRLLIALLESNOCKDGSVLVPPALQS YLGTDRTITAPTHVPLQYIGPNQPRKPG PGQPAQPRVGYKALQWPAPQRLGPGVGR PCRPEGQPLSCCCCGCSCWGLRTRCLAE VVTETVLTVQVQGRPGCTALLHKLKCGTE PHGCASTEEKLLGLDFFKKQEAAGMRSS QEVREDEEEEAERTHSEVQEQAIRMQ GHRQLHQEEDDEEEKEERKRGPMETFD LWQRHLENGDLOKRVAKASDKETAQF QAEKGVRLGGDRSLWQGAERGGGER EDLPHNNHHHHPQEAEPQKEEASERE
9400	23301	A	9469	265	170	GTESHVITQAGGQNLNLSSLOPLDPPGFK QFS
9401	23302	A	9470	289	110	RDELASFLSFFPSFLPSFFPSFLPSFL PSFLSFLISFFPLPSFFPSFLSFLSL FFE
9402	23303	A	9471	67	210	TVTGQALTHAYNPSTLGGRGQGITRGQ DFETTLVPGDNLNFSRVLISS
9403	23304	A	9472	2	186	TSLWRAQKQNVKIKTDKRYTEVLKTHGL VCTQKSCSLKNNKAWLGKQANAPARK VEIRC
9404	23305	A	9473	417	265	FLSSLFFFFFFFFFFFFFFFTV
9405	23306	A	9474	430	120	ASQKKKKKKKKKKKKKKKKKKKKGAL
9406	23307	A	9475	1	150	PTRPVQAGSEFVLSQGNPPALVSQCPR TGVSHRARPHLLNLRAPLPL
9407	23308	A	9476	404	109	PPPLFFNFGFFFLVEARLHHVQAGLKL PTTSDQPDASQSGAGTGVSTRQPTLI TLV
9408	23309	A	9477	391	235	PPFFFFCRDRGLTMLPRLTNSNWAQVIL LPWSPKMLQARATVSGLNKRRYS
9409	23310	A	9478	438	277	KRAPFFFFCRDRGLTMLPRLTNSNWAQV ILLPWSPKMLQARATVSGLNKRRYS
9410	23311	A	9479	399	279	PPPPVFNKPPKKNKGAAPKKNISPPPG RKXYFFFKGPP
9411	23312	A	9480	247	26	LKAGDSDRTVLGKVHQSFCPSLLFFITQ VSCRDEGLTVLPRVLNRSRPAQLLPOL PKLLDHRCEPPLANHG
9412	23313	A	9481	2	176	HAPHPANFLFFEEKESCYYTQVTSIKLL DSSNPALTSQSAGITGYNQGHGHPNCL SG
9413	23314	A	9482	2	178	HAPHPANFLFFEEKESCYYTQVTSIKLL DSSNPALTSQSAGITGVSHHGQPNCL SG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9436	23337	A	9505	426	208	QKVYICNM VGHNLVPRFLSPSEKRSIQGVTRSSR CRLSPSLTRKGNLTPFASVRQCLTL LRLARAPTDLRPLSGTP
9437	23338	A	9506	441	189	CPANFFVFLREMGPHHVGQAGLLTSSDP PASASQSAGITGLSHCARPTVGSVDLSL PSGQCTSLTGTFMLGSTTVHNSAAAAA
9438	23339	A	9507	117	278	NKALLCPHGNHNIKKVNGRLGMETHTCN PTTLGGQQQEFENSLGNIGRPHLYK
9439	23340	A	9508	3	126	FFVEMGFRCVGRAGLRLITSGGLPVLAS QGAGITGVSHCI
9440	23341	A	9509	421	134	FLVERRSHHAAQASLEILSSSDPTSAS QCAGITGMSHCARPKYTSFFRLHRHMPM ATPTKLPFTLASASPQVKVCLYPLLPST SKGEIFTLQLY
9441	23342	A	9510	2	200	ICPPTFYPSTLPSTPEPPAFYPLRPST PASRLDPPAFYPSACHLLQPPTTFY SLGNRRLHL
9442	23343	A	9511	414	204	ERDRKKKKRKKRERERKKKKKKKK KKERKKRKKRKKRKKRKKRKKRKK T
9443	23344	A	9512	1	211	FHRVWGAGLGLTSGDLPASASQSARIT GMSHARRHRGFDNLSLCALASPPTLW RRHRRRGHFTVPEK
9444	23345	A	9513	390	265	VFLVEMGFHHRVGOAGLELLTSGDLPLE SQSAGITGVSSQFS
9445	23346	A	9514	438	180	IGFRHVHAGLDLFLPLGDLFSLASQNA RITGVSHRAWPAMAFVNCHGAGGSVAMRT TRGHSRHLGIGGWFPASLLQPVLSAGS L
9446	23347	A	9515	126	11	RNLDFFLSLGLAMLRLVNSWQVIFQA WPKALRFQV
9447	23348	A	9516	2	249	FLHVGOAGFVLPTSDDFRPTHTPQSSGI TGVSHRTPLRCYFLRLNIPLYVYAY ILFIHSVISQYVGCGTAHYCHPRKV
9448	23349	A	9517	403	57	PEGALVPQKKKKKKKKKKKKKKKKKK NIKI
9449	23350	A	9518	406	140	PHYNHTFVYNGVRLEDLQHMCLTVD REPLASNDFLVGRGVGTGEIPSPILT CLKASCLFYSYHSRPTQSSSVMTVVF FPFS
9450	23351	A	9519	3	75	GIEWMVNCVVRVHRPQRQDIT
9451	23352	A	9520	183	6	LLTHLILTSALIGEMVAPILQKNSGE RECRPLRLVNSWQGILLPWPVKVLGS QV
9452	23353	A	9521	89	339	LQCLQSGKLEPGMTYTKLIDADVNVGN ITSVQFIWKKHLFEDSQNKLGAEVINT SKQYGYKSTFCSQDIMGPNILQNLKPC
9453	23354	A	9522	3	329	PSLMFPLKLSFFGRPRGRQTYRSYOTL ELKKEFLFNPYWTXKRMEVFHALGLTE RQKQIWFQNRMRMKKXENTRDLNPEAQN EEKVEEGIEEKEKEKEKEENKD
9454	23355	A	9523	1	156	AKTSMNVNIEFMAIAKPLPKNEPQNGA NSARGRGVDLTPTOPTNRQCCSN
9455	23356	A	9524	1	272	AKNSARALLGILGYRSHLISLLCLLEG ILSLVLIATLITLMTSHLLANIGPIAIL VFAACEAAVGLALLVISINTYGLDYVHN LNLQC

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9456	23357	A	9525	1	62	GNDAWVCTNDMFRLAHNFG
9457	23358	A	9526	1	111	GDITHNENMRQGRDKYKTLRQIRQGNTKCRIDEFEAL
9458	23359	A	9527	427	340	ITPGNIMSCDSHSHHELVMASQALNAIFHD
9459	23360	A	9528	439	27	PRRTDKWLTVMEMIQDGHQVSLLSGELTVDKASITQFRDGRGKXVLPTNVARGIDVVKQTVIVVTFDLVPVKGQEEP DYETVLRIGRTGRFGKGLAFNMIEVDLPSPMKIQALFDGRKNQLNAEVPICQAAEMD
9460	23361	A	9529	1	236	REVLITTNVCARGIDVQKVTIVNVFLDLPVKQGEEDPYETLYLHSGRTGRFGKGLAFNMIEVDLPSPMKIQDHFRRKS
9461	23362	A	9530	437	240	QQVSSARPEPEAGSVSPFVGAGVNSNSWAFKYGPNGPKQSGPEPKQTQVSFLRRKGEASQPRO
9462	23363	A	9531	413	260	LFDQVVVVASPSGLRTSTVRYGDPEKRLKLEESLRQAAKEGSALESVRISNV
9463	23364	A	9532	431	260	ASSGQMFSVKQAAPPVRDLPPFGISLFGGQIYDNISPRPPQGI VAPPGGRGNIPNLG
9464	23365	A	9533	2	134	IHGVCVHMVCACVCVACVCGVGSYDGRIFLALSTVPSMVNIM
9465	23366	A	9534	419	53	LLLLTNGDRGTQREKIEACQSYFDFAVVGGEQREKPAISFYCCNLGLGVQPGDCVMVGGDTLETDIQOGLNAGLKATWINKGIVPLKSSPVPHYMSVLELPAALQSIDCKVRMST
9466	23367	A	9535	439	109	NCIVITDSTPYRQWYESHYALPLGRKKGAKVTPEEEELLYKNRSKIKKKYDERKKNAKISSIVEEQQKVLACIASRPOQCAPADAYVIBCKELESRLRKIKARKGK
9467	23368	A	9536	1	185	NTTSSHHFTTPELVLYSCTSTHTHTHTHTHTHTHVRVSYIPSQDVKEGCIAPSVFSW
9468	23369	A	9537	168	280	NPNISRLTSCCCCCCCKWSPPYVNVNRLRLTGTFEP
9469	23370	A	9538	142	324	KIVKNGFPHAGQAGLELLTSGDTFGSTQSAGITGVSHRSRARSIFLYPYLPSVYLPWRRV
9470	23371	A	9539	3	139	YTGGMGAQMWLMPKGPFRONDYLSPGVQDQPGQHSSTPSLQKGFKN
9471	23372	A	9540	383	318	MSTONNTQSYPTGEDEESES
9472	23373	A	9541	372	207	YGLNRCRCFRQYAKDIGIKVGVCRRTPCCLGREGCGGYFRERQTRDSLEW
9473	23374	A	9542	2	360	ARGDDHRSDDKDGVLLEQERLQEKVESAHSEQNLFLVLVFORVINILTEHLVRCETDGTSLVTPWYNKCIERLQOIFLQHHQIQQYMTLENLLTAELDPHILAVFOQFCALQA
9474	23375	A	9543	379	75	TNLQGFAMSHGSAQVKGHGKRVADALTNVAHVDDMPNTLSLSDLHARKLRVDPVNFKLISHCLLVTLAHLPAEFTPAVHASLDEFLASVSTVLTSKYR
9475	23376	A	9544	380	56	RDLMSVMRMSMFAIGFCPTALMGFNSIFDGRVVAKLPTPTLSYIQLSHRNLLGDDTTDCSFIFLYILCTMSIRQNIQKILGLAPSRRAATKQAGGFLGPPPPSGKFS

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9476	23377	A	9545	304	92	SKSRVTNNLTSTRKDTMTLTNTHSLLA NIVPTAIIVFTACEAAVGLALLVSI NPNVGLDYVHNLLQCC
9477	23378	A	9546	394	108	KEIDFSLVDVTDADAGNYSCHMYQTKSP FWASEPSDQLEILVTPVPGTSSNYSLG NFVRLGLAAVIVVIMGAFLEAWYSRV SPGESEAFKPE
9478	23379	A	9547	1	335	GNVAGNLNHRINFDKYHFGYFEKDKMKH YHLHRNQSCFCTVNLDKLRTLFSEQTRL NAAKNKTGTAPIIDAARSVYKVLGKKG LPKQPVIVKAKFFGSLIPCFRIWLLID
9479	23380	A	9548	326	188	NFLRMGTVAHASNPISLGGGGRIGAAQ EFETSLGNTTRPCLYFFKK
9480	23381	A	9549	381	152	VTIISLSLLQVIVGLVLIARLNLNE VEKWRNLNOLNNAATLIVFTVINVPFI TAPGAHKTGFLAARASNP
9481	23382	A	9550	170	65	IHRSKNKKFHLKDGIMNLGRDYTFISK AIGDAEW
9482	23383	A	9551	544	361	RRLRFENRLNPEGGGCSKPRSCHCTPAM ATEQDSSSEKKERKNLGNVTKSVPLP LTSHA
9483	23384	A	9552	369	181	GVLGATSGDMQIHTFGSMIGSITGMVS ELGYKFLTVSTADVMIQTLNLHLSHMS HQQKSEY
9484	23385	A	9553	1	516	SLVHVVEFGQATARRLKFPGVORFLYTG RQRPPEAAEFQAEFVSTPELAQSDFI VVACSLTPATEGLCNKDFQKMKETAFF INISRGDVTNNQDDLYQALASGIAAAGL DVTSPPLPTNHPLLTKNVCILPHIGS ATHRTRNTMSLLAANLLAGLRGEMPMPS ELKL
9485	23386	A	9554	386	56	LFFACVLNRQFASDGGDIGFVFLTKFM GEQOSAREMTEVLPSORYNAHMPEDGS LTCLOAGVYVLRFNNTYSRMHAKKLSYT VEVLLPDKASEETQLSKAMRPSPTQ
9486	23387	A	9555	375	150	IVVGKTSFPHVSIPLSLFFFGVDVLYDLLQ HILKQSKPRILFSPFFPHGNSIHTQPEV ILHQTHEEGTGRGFSFLA
9487	23388	A	9556	3	354	CLPTQASAMVDTTPPPALLFPCCSLISDCC ASNEQGSVIGIPSEPGAGYVFLVCRLLR PLEKHSIRVGVTQFSRCLSPSPSLTRKG NSLTPCTSRVRCLALLQLTSLSELPHCP VPSV
9488	23389	A	9557	463	40	PTKVEDPEVPKPKPEQKRSIKEMPFITC DEFNGVPSYMKSLTYNQINDVLEIKNK AVISYKILHQPKKSMNSVTRNLYHRFI DEETDITKGRYFIVEADIKETTLTKADK KFHVLLNILRHCRRLSEVRGGGLTRYVI T
9489	23390	A	9558	338	104	NFKKKKKRRTKKKIRTEEGRGANKKT FRGPKKKETRGSNRSPEGKNHGAKEG ERRPRKKKKKKKLARYDFTCL
9490	23391	A	9559	1	152	NTVCVCVVTGFCFVAQVAELSSSNLP SSASQSAGITGISHAWPGF
9491	23392	A	9560	517	238	SGPGESVPHPSAVRTRPAKKPQSQCLL QSAFPLWCSSRTTWAERKLNITFTGV SGRFLGRSSRGFRGGRNGTFRNPT SHRAGTRV

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9492	23393	A	9561	709	280	NTSPALTPCGRPRTIPMQCWARVPAP SSACPAQLPLSLCLRSTVPAPPAAH QPCELSCHHRGGLPALPCTQRCLCSRT WHRCVFLPQAQAEAGELGPAACTGRLP VSHSTDMEQAPGLTSLHQEPHSTARGGT ATH
9493	23394	A	9562	3	130	YRGFCHVGQAGLELLTSGDRITSASQSA EITGVSHRAQPMQS
9494	23395	A	9563	409	160	NPGVKRSFCLSLSSGGYKMPCLAYY KKKKRRFLDKDGLTMLPRIASNSCAQOF SHFGLPOSWDYRHEPLHIAQFFFLSL
9495	23396	A	9564	1	241	GTCLGSGNIGSGWMGTSSLCPNYSNTLNQ NLLSTTKPPFVPSVGTGNCIEPDMGSVT SGLGKMLFLYYYYLLFLFSQMTPOS
9496	23397	A	9565	2	215	IHNWNGNMDGWMGWSGSCVRAVTPGT SSPHTSTCGHAVCVVCVCTCAHVFL ALFGVEKNYFLWKA
9497	23398	A	9566	244	117	DHQLNNSVFIISFSFKVIKARKNKKGIL NPDSMETSPDFFF
9498	23399	A	9567	414	77	FGGVPGTLVPPPTLPPVVPVPPAPFCL GELSPPPFFWRKGLAPPLNFFSPQGR GFPSGGKGRPLRPAGPGFVAKPPF RPPGFSTSPDCGLPFFFFFPPKKVF
9499	23400	A	9568	418	198	PPVSLTEIVTSKSKAELVFWMNPGTLE HPEGDNMYMEFIEVLTEALERVLLVRGG GSEVITIIYSYPTLNARA
9500	23401	A	9569	549	415	ROENRLNPGGRGCSSEPRSCCCIAAWATE GDCLLKNINNNKPKMEQK
9501	23402	A	9570	546	1	KLECRGAIHAHCSNLNPGPDPTSATQ AAGTTGTCH
9502	23403	A	9571	415	215	SLRLKKIYIYIYMCVCVYVYICVYICIY VCVYICVYVYICVYICVYVYIYVYIY WMEFTTFSI
9503	23404	A	9572	374	138	LAASATQRLFKRISEQETPMFRKAPL HNYTCBGMDENEFANENMNGLVSEYQ QYQDATAEEDEGEFEAEAEVA
9504	23405	A	9573	370	233	GSPFVRSVHQSQSVLSGTQVDEQVRSGS KRMVAPPGRYNTTSL
9505	23406	A	9574	3	399	YSSFGPTALALEPCAHGSPNSSLSP AQGHPARAQGPQPGQPPSHLGSDLRP HVAHTRGALHGPAPAPSPAGGSGGV AASMCAPRPGRAGGTGLSVLTAHPAS AGCAHRDAYVCKAPGRAVF
9506	23407	A	9575	314	48	SILPHSDPERCFSTIQEETIHTAAPLD REARAWHLNLTVLATELDSSAQASRVQA IQTLDENDNAPQLAEFYDTFVCDASAAPG QVSN
9507	23408	A	9576	505	264	IFVVEVEFHFGQAGRLRLTSGDMPPASA SQSAGVTDMSHCTRPDTFNFKELPGAV VTLFLCGMQVGRDELDDWNGAWS
9508	23409	A	9577	508	314	PATWKGCLSNFSSYLTKPADETEHQVLS WEQVPDGFIFNERFKSTVVVLNNVAE FVCKYKLL
9509	23410	A	9578	512	1	RMREAFSPGRLFRGAAPLRGPAGTLVP NMPTPGCWLSSLVSAAGEKPKYKSCVCE SAFNRKDKLKRHLIHEPFKKYKCFST HTGCSKEFNRPDKLKHLIHSKGMKLHK CALCSKSFRRHALEHQRAHTNGKFR

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						CAGCAKGFSRHXYLKDHRCRLGPKQDKD PV
9510	23411	A	9579	3	487	WDLIYVGRKRMOVEHEPEKAVPRVRLIVE ADYSYWTLAYVISLQGARLLAAEPLSK MLPVDLEFLPVMFDPKHPVSEYKAHPSLRN LHAFSVEPLLIYPTHTYTGDDGYVSDTET SVVMNNEHVKTIDRAKSGMRREQALS REAKNSDVLQPSLDRADEL
9511	23412	A	9580	1	840	SKVLYDEGESEEEVFNDEWCAAGQAVFT LNALERGPLSAMDNHLYTDPREIFVLS WLESCVAEQQRWRGHTYTTDLCVLLEQ PTWQLALGSLCQRLVKLSCLLAVAYVSS VALAVASVAVIHQSLGLSCTPTGPPDL GLTSRCLLEPCTPSVPQCLPSLANVSSC LEGSMGLRSLWGLSLASLTPTPLPBPDP PAPPTLLHNCHLCQKLQDPSPTCHACLI PNRTVPTALSSPWHTYGLAPPWPSPFV PLSLPQPOCCSLFSVMEIARLKSFFVFG
9512	23413	A	9581	2	158	IHAGFISVSVLNDITYICMCVCVCVCVC AHMCACISEHITHAPRLPEVFYTP
9513	23414	A	9582	3	144	VTAGVISVSVLNDITYICMCVCVCVCVC AHMSACFSEHITHAPMLP
9514	23415	A	9583	503	3	GKCVCLSAVWGLSLSAFQGLSVCLLQ FVCLSAVRGSFSCVCCPGQVCLSAVRGS VSVCLSAVQGNVSVCLSAVRGSLEFVCLL SGAVCLSFCLLSGAVCHLCRAPTPCLSR SLAHRRCNVNCEMTOLISVSYFFCWGW WRHRNNIHLQKCLRLILMAYTGGGPP
9515	23416	A	9584	2	1358	AGLDSLHKFQVKIEKEKYVVRASQALQ LQRRTKVMACISPSAGYSSSTNVLIVG AETLRQEGFSRDRIVLCTLDRLHSYDRPK LSKSLDTQPEGLALRKEFFRAYGLEVL TEAQVTVVDRTKKVFQSGFKLEYSK LLAPGSSPKTSLCKGKEVENVFTIRTE DANRVVRLARGRVNVVAGFLGMEVAA YLTEKAHSVVVELESTPFRFLGERVG RALMKNFENNVRKFPYMQTESVLRQEG KLKEVVLKSSKVVADVCVVGIGAVPAT GFLRQSGIGLDSRGFIPVNMOMOTNVP VFAAGDAVTFPLAWNRNKNVIPHQMA HAQGRVAAQNMLAQEAEMSTVPVYLTAM FGKSLRYAGYGGEGFDDVIIQGDLEELKF VAFYTGDEVIASVMNYDPIVSKVAEV LASGRAIRKREVELFVLIHKTGDMSWLT KGKS
9516	23417	A	9585	360	239	QCRGLGKLVSFGLGINSILDVLLIGV GYVGPVHGSSVY
9517	23418	A	9586	160	1156	MPRLTFAPKGNPFPPTLSLHFGQVTDOTT WWLFCLEPTPSENMPGLSTPTASQEG AGVPDPSPQTRRQIRLSSPERQLSSL NLTPDPEMEPPPKPPRSCSALARHALES SFVWGVLVPQSQALVAMEKEEKESPFSS SESEEDVPLDSVQALQITFAKTSGMT NMYTWRFTLLRAKEEMRCKAQTI QRRNETEALRLEAEVLEKLEALRQ SSSPQOKKLVNGQLLQIVDKNSLVAE EASLMTITVQELNLEKQWLDQLRGVM NREENLKTAADRAQEDQVLRKLVDLVNQ

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						RDALTRFOEERRLSELALGTGAQG
9518	23419	A	9587	419	130	RRDPHLPRIMGRTRLNKNAETTRINAQL PLTDKGRMARHVLMDNSGEWSVTKROVL LHTELESLLEYLPRLCGVLTGLAAIASL LYMLTHYLLPYA
9519	23420	A	9588	2	399	PSCEFNMEANQCPVLVPEVSPDLVINVG EVLGDEENRKKLQKIQRDQEKERVMAAA CALLNNGGGVIRMAKVKHVPVEMGLDLE QSLRELIQSSDLQAFFETKQQGRCFYIF VKSWSGGPFPEDRSVKPRHV
9520	23421	A	9589	19	205	LYCLVEWHDLCSLQPLSPGFQFSCNLN LSSWDYRHMPRPRTIKLSSYSIKLIYY LFMLVL
9521	23422	A	9590	500	407	KLTVNEVRSVKRSQLPFESFMCKEKLNT NII
9522	23423	A	9591	727	236	RRSRGLGREALALCPDGGSHLLCRRTD SSFSFMAFFFTFMAQLVISIIQAVGIPG WGVCGWIATISFFGTNIGSAVVMILPTV MFTVMAVFSFIALSMVHKFYRSGSGSFS KAQEWTTGAWKNPHVQQAQNAAMGAA QGAMNPQTOYATPNYTSNEM
9523	23424	A	9592	381	278	HPSVYKVASGLKEGLSLFGILNRCHCKW GEKLLR
9524	23425	A	9593	412	156	SQRCLSLGCEHLANAYATIIDCNFGFSA LLGPPPLPGWIYDIAQKYDFSFYICGLLY MIGISFLLIQPCIRIEQSRKRYMDGAH V
9525	23426	A	9594	263	50	KHAAPFASLSLLELLHHGQKACFPFFAF CRDCOLLEGSAMLPVQPAKLLVLEQV CLLCALLIPPSGSR
9526	23427	A	9595	432	309	GTFSERGFPLEPRSQTVTVDFCQEMTDK CTTDEQPRKDYT
9527	23428	A	9596	457	29	TLLPGWITAGASEGEIGASLPSSLPLLL YLFWSRSCSPSGALTHPAACPTGQRSSA LLPSLPQAPPGFCMGITGLRPLPSPVGC CSAPSPQLLCTPLPPAPSPSEGGCSSES RCVANVYKTRDLGDFLEKCTNGEASALE YP
9528	23429	A	9597	864	407	PSRRLSPGTGRTTHGSSAACAPPPRLR RSRTSRPPWGPPhSASARTORACTTWYS RSWACSCSWITSRPSWMTTKRTCMIFST IPTTPRTALWRGLSLWKDAWLLTRLKLA PSSPFSMPPTTCTACSSWTMTGSPAR WASTPMRPSSTT
9529	23430	A	9598	421	145	LTQHNGDAAASITVAEQYVSFAFKLAKD PNTILLPSNPGDVTSMVAQMGVYALT KAPVPGTDSLSGSSSRDVQGTASLDE ELDRVKMS
9530	23431	A	9599	1013	604	PGRPTRPDICLLERMEEQKVNVMKTR EELYNIKAFEVERQELLASNKKKWEQA LOAHNAKEVLYNNRMKRVEDYEQKLN QRIWDCEEYNNMIKKLEQDVQILEQQLO QRKATYQLNQKEKLEYNLAGAEER
9531	23432	A	9600	409	191	HHVGAGLELMTSSDLPASLQAGITG VSHCARFTVGLSLIVFPSSHRGFASVRT PSNENFPDRPISIAHP
9532	23433	A	9601	367	1	PRYSYPLGGRVGVGPFQGVLPAPFPK GKPPFPKPNPLPRPGGAPYSNPPFGV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						GRGISFNFPGQGGSPGQKKFPFGPPRRGT GFFSKKKKSTKLPVTSHTTCWFLPE ALDLELDPLY
9533	23434	A	9602	1722	394	GWNGSWNDNLVDTSPFLKRDPLQDICRRY MEDLKKICFYRELNSKTTLLKFVHTSPHG VGHDYVQLAFKVFQFKPPIPVPEQKDPD PDFSTVKCPNPEEGESVLELSRLAEKE NARVVLATDPDADRLAAELQENGCKWV FTGNELAAALFGWWMFDCWKKKSKRNADV KNVYMLAITVSSKILKKAIALKEGFHFEE TLPGFKWIGSRIIDLELNSKRVLFAPFEE SIGFLCGTSVLDKDOVASAAVVAEMASY LETNNITLQQLVKVYKGYHISKTSY FLCYEPPTIKSIFERLNFDSPKFEPKF CGTFAILHVRDVTGVDSSQPNKKSVP VSKNSQMITFTFQNGCVATLRTSGTEPK IKYYAEMCASPDOSDTALLEELKKLID ALIENFLQPSKNGTGGSGSCIGVPPNTV MTLCGAYGNRATRNCHTLEPCG
9534	23435	A	9603	14	356	DFVERTQYTHQTTHTHSHAVRLSPRP VQSRPEASQTGPTRTKPAIGPAHPSPRG APCPDDPGSLRMLGYSRASHNSRRGR GHGRCKDQRAMGPHSHMWEALPPGALS SP
9535	23436	A	9604	477	264	LVETGFLCVGQAGLELLTSGDPPTSASQ SAGITGVSHRTWAALSTFTVLCNYHYLF LEVFFHHPKLLSPH
9536	23437	A	9605	1	378	EGINFSDNLRRCVVMVGMFFNIRSAEL QEKMAYLDQTLPRAPGQAPPKALVENL CMKAVNQSIGRAIRHOKDFASIVLLDQR YARPPVLAKLPAWIRARVEVKATFGPAI AAVOKFHREKSASS
9537	23438	A	9606	417	254	MVSLTQELCPVAHKAEGHNKMLSNVAE RVTVPRNFIRCALLEGAGQDIQNKLE
9538	23439	A	9607	404	272	PFKLESGSPRVVDNWSLGAALYDMLT GAVGAOLKACIIGLC
9539	23440	A	9608	409	205	HMNGSLGSGDIDGLPKNSLNNISGISNP PGTPRDDGELGNFLHSFQNDNYSSSL PCSWSLFPYELFP
9540	23441	A	9609	449	263	VNITCPDPPASASQAGITQLSHHLPKC WDYRLPEPPRPAPHCFCFYSFTMNRNLLS LVKYSR
9541	23442	A	9610	366	75	TPGLKRESSCLSLMRNGRYIEKKRTIIR SVVEAIEQDQGREVDWEYFVGLLFTSEN LNLVHIVCHKKTTKLKTCDSIIYPQT RLRKQPVKRO
9542	23443	A	9611	1	801	PGYCGSVVFTCGALRLSGGRDLRSGAR MGNSALRAHVETAQTKGVFOLKDRGLTE FPADLQKLKSLNLTIDLSNNKIESLPPL LIGKFTLLKSLSLNNKLTLPDEICNL KKLETLSLNNHRELPSFTGQLSALKT LSLSGNQLGALPPQLCSLRHLVDMDLSK NQIRSIIPDSVGLQVIELNLNQNIQSIQ SVKISCCPRLKILRLEENCLELSMLPOS ILSDSIQCLLAVEGNLFEEKKRLRELEGY DKYMERFTATKKKFA
9543	23444	A	9612	179	329	KGLAFCCPPFGRGGGPPPLWPPPPSYKK IFGLKTPKSGALSPPPPPPGNF

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9544	23445	A	9613	410	298	PRFTFFSCLSLRSSWDYRCPFPPRANFL SLSSVLHGT
9545	23446	A	9614	1	130	NPGSHCVAGAGLQLLSNGNPSASASQSA RTTGVSHCAWPNNTTI
9546	23447	A	9615	1	146	NWRLHNVRLVSNFVWAPGILLSWPPKI LGLOKRATTMFGPEIYTSIN
9547	23448	A	9616	552	26	RLSIRNLLTHAFFAEPTGLRVELAEEDD CESNLSIAIRLWVEDPKKLGKRRKDNEAL EFSFNLETTDTPREVAVEWKSQFSESD CKAVAKSIRDRVTPITKKTREKPAQCLK ERRDSQCKSMGNVFPQPONTALPLAPAQ QTGAECATEVDQHVRRQLIQREPPQHC SSVTGDL
9548	23449	A	9617	420	48	FSQILRASVEFDPFFNDDISESAKOFIR HLLERDPQKRFTCOQALRHLWISGDTAF DRDILGSVSEQIRKFNARTHWKRAFNAF SFLRHIRKLGQIPEGEGASEQGMARHSH SGLRAGQPPKW
9549	23450	A	9618	190	285	RQGLTMLPWLVSNSWQVLLWPLKVL GLQV
9550	23451	A	9619	392	308	SPFKPKIPLSAPRKNTINSVKYRLKFRFG
9551	23452	A	9620	166	23	FCNFPSSLPSSLPSPISFPFLPCFLTFF LPCFLPFLPFLSFMLTTF
9552	23453	A	9621	49	374	DRRGIRIMAAALFVLGFSLLGTHGPSG AAGTVTTA*YLGSKILLTCLNDSATQ VTGHRWLKGRVVLKEDS\LPGRKPEFNV GHPFPNGDKSFFVPPSPCPRLTF
9553	23454	A	9622	85	472	SHVFFPLRLTLTLHSMVAPETRPNTHTY INNLNDKIKKDELKLSLYAIFSQFGHNL DILVSRILNMMGQAFVIFKEVSSATNSL RSMQGFPPFYDKPMRIQYAKTYSYIIAKN KGTFSC/DRKLIK*TPQ
9554	23455	A	9623	170	2	IFFFFCFERGSCSVA*AGVQWRSYLL* S*TPG\SSNTASATSVAGTTGL\HHHAE
9555	23456	A	9624	2	469	RRLCSDRGLQRLSGSHSAVATGAKLARA RADPQKAGVPGVAAPGAFAAPFAKEIP EVLDPKRRRYVRGRFGLKQSPAKCEB ILDADTKKEFAGKIVPKSLLLPYHR*K MFMEIFIHRSIGHOVL*FHGYF*EHD MSELEL\CRPRSFLF
9556	23457	A	9625	661	1393	ASPPPSQTTTAAAGPGCSAGEVSLA/GLCL QERRLDVDVAGFSIFIPSRYLDHPQPSKA EQDASIPPGTHEALQTLASPPPPPTRP VSPQKAKEAPNTQAPISDDEAS/RWG RNP*CS*SGSPHWPFLP*GRL*A* PSPCCPG*VG/FVHSPQARRRPITTSIS QRSWFKWPKPTVRETSGGPWAMPSPSM PSRASISLSPRTSRKQPRELTLCGCCW HVVHTDGERATCGDVRRAHHSR
9557	23458	A	9626	1	286	PTMAKLIALTLMGMLALFWNHQASYQT RLNALREVQPA*LPNCNLVKG*TGSED F\EILPGLTIFISSGLENPI*RLDP\N SPGKMLMDLNE
9558	23459	A	9627	173	491	EGPLPLESSSNWQADLDKKSRELLWKT VYLL*LNQLPYPNPVNPILGINPRETH C\HQEMCTRIFIATLFTKAKA*K*PRCP *AREW/IK*/IWNHIEHY
9559	23460	A	9628	351	1	VLGDATQRRRSGRRAGSVLYLSRSP/CS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to last amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
						EGGRGGCWAANNLGTMSVASGHGAWVPER ELTS*AWPEPGPAGQREGRRPPTPCPPT CAHGPPAQP*PRGKAAYPG/CLGLQWPD *SAFNP
9560	23461	A	9629	599	11	KMWR**H*AKSQIRNAIPFTIARK/RDL KSLKIQLTKEAKDIYENYKIPL/NEIR DVTNKNWIP\CS*IGYLYSTYKYKCIC LVNIYL
9561	23462	A	9630	226	1	KCDNLGYSTFFFFFFFFFFFEIGSYFVA QGVG*WHNYSNS/DASAFQVAGTTGVCH HAQLILFNLFVEVESHYVAQA
9562	23463	A	9631	241	1	VSGCPLPRG*RPFPQPSPPSTPGTSD HFCPCRC/PAIRK*SP*LPCLDLPPAS GPBSTSGNSTWQTT*KLNSSSS
9563	23464	A	9632	201	1027	MTLTPAFGQCGOSQCLRRP/L/PLPFG PDSSEPGSAAQ/PSSSL*SPDLPPAP PKP*TSS*EMNTVGSTQEGSGLAQTTO HCPVPPT/RVDILGTCLQFPALCLTS APWLVRMPSPSORSREIP*RLEAF/SLR TPIPAHSAQPSHQEKEP/PSPR*DHGD* PPP*PPKPTHQTLAQAPRSGGGLARPT LPYPPSPRLVTPICRVHV*GHLRRPRG PPPSARRPTWDRVGLPWEDLEVVLGR GPAWLLARTSAPFSSLPHTACTGKKTMT PF
9564	23465	A	9633	103	379	YHCITIIYLKCIFFFFFLKFLCLISLPR EARGIILGH*NLCLT*SQLRLRLKSP LTLEGGVCDPRSPhCSPAWPTKGNFFS KGGKKILD
9565	23466	A	9634	155	405	VPAFRSVTNISISVSFFFFTEPGFVTO AEMQGLDIGNQPPCPKLSSFA*ASQVM GTTGPRH/HC*ALIFLVKTGPPHVAKTW F
9566	23467	A	9635	4	423	GAMRGDRRCRGRGRFGRSGGPRGRFRFP VPHIPLDFYLCENAFPRVKPAPDETSFS EALLNENQDLDPNSEQASILSLVTWMT YEIDNLTVAAGTLDVLIIEERQGGPYIK GTMTT*RH/SVADLTVLQILTWESVA S
9567	23468	A	9637	2	492	GSRAIGFGLAHLERHLTYTWLASTVR* DLA*LMNWSG/SHKDLAGKYRPILEKAI QLSGSEOLQAFKAFESMVNENVSIVS RQMLDTDFCTHLPNLPDSTVKIEYHFTLE KIQPIVISFEEQVASIROHFASIVEKEE DWRNAAQVLVGIPL*TGOKQYNVDYKLE TYLKILARLYLEDDDPVAY
9568	23469	A	9638	1	417	VVQGLGLVMGSPSRRLQTKPVITCFKSV LLIYTFIFWITGVILLADGIRGKSVLEN YFSLKDKATIVPFI/LIASGSAILLFG ILLCIFSV*HYPV*LLLVTFLL/LLVFL NKWNISPHFLILTFNYLLFDIIIDNS
9569	23470	A	9639	125	451	TYRKLPLSIRRVGGLHLNKIFFFFLQKI WGVARGLMPC*HFGRLKGDCLTLGIGD /SRG/RDYDHPALQPRQSKTSLKINK IGWAQWLMPGIPAPWEG*AGRSFGAGI
9570	23471	A	9640	670	927	GHVLLPRRAGCAQPGTGPARRAAPAQR LPFGGVQPSGPGGRAGQGQGLRGT*AGG NPGTGF/GGPHASALLPSEAPGSLPLS

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						QPR
9571	23472	A	9641	115	460	ISNIFLIITCVGFFGGGGGARVPLCHLSP RLECCSAIRARCGDFDFPGSSDP*ASAS* VAGTT/G/SCIHVQLIF
9572	23473	A	9642	1	431	AMRAEVLVYCCRGALASGCVQAFRARY\ WVLIIVDVPDNEQANASIIIVKLTDSFTE QADQLTAEVGKILGE*KVDAILCVAGGW AWGNAKFKSLFKCNDLMRKQSIWTWTIF SHLATMHLKEGGLLTLAVAMAVLDGTFG MIGD
9573	23474	A	9643	154	408	INNAQSVVEEDSILIIPTPDEEEKILRV KL*EDSDGKYGSKI*PNWHLPEPENRLL FKHVGYLD*SGLY\ELITKF*ILCVLCY Y
9574	23475	A	9644	3	403	YSQFFGGPKLEDPIRPGVFSQGEHRGH PPQIF*KVGLNGARPGFPVLGKVKCKD NLKLGQGCSSVEMHPRTSANAIERDPV LKKKKRQREHQCSNEQKHTN
9575	23476	A	9646	3	399	ARANVLSPADKTINGKAAGKVGGAHAGEY GAEEALERMFLCFLTKTYPHFDLSHGS AQVKGHGKGDADSLTNAVAHVDDMPGAL VALSLDHAHKLVEGVPVNCILRH*LLVT LGG\DFPAWLTGSGIAFLFKEP
9576	23477	A	9647	22	407	AFSAWGHCHFTBEDKATITSLNGKVVNV EDAGSETLGRLLVVPFTRPDSFGNLL SCASAIMGIFKVAGHKALTSGLDAI* HLDDL*GTFAQLSELCHDLKLVDPENFK LIGNVLVTVLAIHPGKE
9577	23478	A	9648	243	2	QIATTTLGPGESEGVKKRDLGSSSRHHSQ VESVKH\PRDLAQDA*GHGSAPPFLCPS PAQSWHLGRGFLAPLHPTLCEPSR
9578	23479	A	9649	283	196	SYFI*ITTTTHSL\ISITPLFFNQIN NNLFSCSPTFSSDPLTTPLLILIT*LLP LTIMASQRHLSSEPLSRKKLYLSILISL QISLIIIT*ATELIIIFYIFFETTLIPTL AIITR*GKPTPLIQ
9579	23480	A	9650	10	354	QLRVITRLTVVNN*TSA*SRGVSY*AH \SSDALHL*RELTEORFIVSVNCAIAHC RHQSASEDHVKLRNEVTEFAQTWDADES AENCDSLHLLFGDKICTVATLRETYGE MAD
9580	23481	A	9651	2	404	AFGTTKWVYISVFLCASSAYSRGVRL DAHKSEAAHRFKDLGEENFKALALAFPA QYLQCCPF\EDHVDLVNEVTEFAKTCVA DESAENWDKI\HLTLFGY*LCVACFRE T\YGETAAC*AKHEPVEDE\CFIR
9581	23482	A	9652	83	396	NIPGVGGGGVPIPLVWKNYSHTQR*RE PYIQLSRSGNWSERMSHMVAR*QRHHP YXI\LLQAQLSMA\SDPANVMDSVITA GVLVA/SRRARRISKLGHR
9582	23483	A	9653	67	954	REGNNTERNCCKRPQDPTIC/RPGPF PEEVPWQDASAPTPAAAPVKLLPS*G PGSASCQGR*TLGSHVHL*GSLPSPS AGGRALPYGPAQGGSGHMENTGRTPL PGSRET*GHELTTGVZHQHKAAPREPQA GQPRLCPMWQSLPPT\ARSPSWSQGERP
9583	23484	A	9654	1	252	RPFOLLASDSLPPSRPFPPFLLLSLR PPLSRSLCLSHVLCPPLSLIQQLTSFPD

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						TFSPPKSTTSGPPQPEDSPSS*PPTPSP P\PPSLSSLLPPSLSSAPPF/VYHSVSP TISAPLYP*YNS*PHFPFPFPRKVQHL ARPSPKTARPPWTIRRI
9584	23485	A	9655	1	394	SLRIYCFVIEVTCFLYLL/FIMYSIS*G I*LLMNFILICIGY*LLQYFFVUVKSF YFNFRIPRIFILPLYLICLLVF*LIFFDL SYF/MCLRLIIINLFY*LFLLYSICLWN MVLILLISKLF*F*FCGRFALIQ
9585	23486	A	9656	122	371	SPYLLLLQGGVSWIWMNLVNSTSSFL FPETGSHCAVGGVQWQGRSLQS*TPG /SQS*VAGITGMCHAS*LEKFFVEMG
9586	23487	A	9657	425	3	KTSMNNSIVPHISTPTLNVLNGLNVLKR YRAE*IKIHQPSICCLQETHPTKDSH KLKVGWE*IFHANG/QGVAILISDK/T DPKATTVK/EDKEGHYIIIKGLVQGENV TVNLNLCAPNTGALKFIK/QLLLDLRNEI NANT
9587	23488	A	9658	179	373	VHSWLLMGSSQSFVLEFRLTD*MLTH/I MKGNLLESKSTLSVLNLIKQIPHNRINQ V/AQNIWVSWNS
9588	23489	A	9659	103	373	LKHVLRCLQSKERKLHYENIDWQKFX TWDDLYECISSKFTTHFFSFL/FFSF* SQGLALSPRLDCSDAIIAHCILEFLGSS HAPTSAS
9589	23490	A	9660	216	424	TDINVTTKTIKPLDENIGITLYDLGLGS GFLDMT*T/AQVANKEIG*WDFIRNLKL TCIGHYHEVKKNTPW
9590	23491	A	9661	276	2	PRIGKLPINNIEPIYIKEMLINLAMRFH LSPVMAI/IKIKKSNRCW*GCREKGI/ IYHYWNECKLVQPL/WKSSLK/FIK*LP IDLFSVPAIPLL
9591	23492	A	9662	239	356	ICIKRRK/WSGTVAHTCNPSLLGGQGR IA*VQEFQPGQ
9592	23493	A	9663	1	340	RHELMTPHAFGAMKRVTFISLLFLNLA YSRGVISRDAHSEDAHPIDKLV*ETFK ALVMIAFAQHLQRPFDHVLLE/VT EFAKTCVAEESAENCOKSLHTLFGDK*C TV
9593	23494	A	9664	759	1039	KRIFFGRPRRVDLHRSRGVDPQGLHDET PS\LKIQKLAGGGICL*SQLLRRLR*E NHLNPGSGCSEPRSCHTANATE*DS ISKKNKTKS
9594	23495	A	9665	1	355	ITDLYSHFHG*VDLATITSLWKGNEQ KAGR*TLERLLDVYPWTHRFDSFONLT SASAIMGNPIVKAGKKVLTSLCDIIMH LDD/LKGTFAQLSELHCNTLHVDPENFH ENPCDGS
9595	23496	A	9666	364	3	APNIPPSVTRIPALLAFPSQCLGSCPL PLATEPVGLLLSMSFOAAPCTWWTEA WLTGISWPPDFLISLLCI/HINYNVAVF RKYPVRVGAHAHCNPSLGG*GGNIA* AQEFETSLGN
9596	23497	A	9667	1	357	PISNAMHRLGOEETATITSLWKGKVNVED AG*ETLGRLLVYIPWTHRLFDSFGNLS ASAIMGNP*V\KAHVKGALTSGLDAIKH LDLKGTFQAQLIELHCKFLVDPENFKL LGNVLAT

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9597	23498	A	9668	24	369	APFDAMGHFTDEDKATTITSLWGKGNVE DAGGETTLARL\GVVPTW\RLFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAI*H LDLKGTFQAQ\LSLH*DKLHVDPENFK LIGK
9598	23499	A	9669	12	365	LLMDGERK*FLETDSAPCEDAMNTEM TTKNLE*SNLVDKAVA/SGFERIGFNF EKSSTLGKMPNSIACCRIFHERKS/S MQTSTLSYFKLRQA/PAAATLNDHO PSALRODPSP
9599	23500	A	9670	346	2	YVYDFWSLNNMFFLKFRRFNFLLKEGT LTPFFKGFRGDL\SFVWPYKLPNLKSF L/CKFLEI*RYFFG*IIFFPPFFFFFL RQSLTSLPRLECGNTSAHCNLCPLD*S NSP
9600	23501	A	9671	121	364	HKKKTAGRVQWFLVLPALWEAEADCL SSGVQGPQGHKTPSLP*PSKSWDYRC TPPHLASFCNFFSFFGRDGVLLCCPGW P*TPELKQSA/CLGLPKWDY/RARATA PGLLFF\FMLKYVLVKPAVNIANAN*KE LSEPDVKNICFV
9601	23502	A	9672	437	223	EME/FSLLPGLECNCTCLAH*NLRLLG SSDFPASASPVAGITVGR\HAQLEYFL NLGFFFIISLVVYLS
9602	23503	A	9673	100	338	KSRFSAVANTFVLPALWEAEAGGSP KQPSLSLSSRDHRFATPC/RG*FFIFF VMEFHCVACQGFELLDSSSPPTSA
9603	23504	A	9674	161	1	SFLWLKCLRGAPSCNRCOLAYL*DVSO LGY/SGVRDPLEEAVCPFSLDKLRGR
9604	23505	A	9675	304	1	VPLASQLGKRRIFFGKKKKKKKKDK IHIIISII\CKFDKI*YSLIIK\TL*KL GME*TYLNIKVIYDRPTASI\LSGEKL KSPPLKSGR*QECPLL
9605	23506	A	9676	111	346	SKEGSKGSLIHWGFLVLAFFPPFPFPF SFFFF*RQAGRPRLECRSMITHCNLE LIGSSDPASAS\QVAGTTGPTSP
9606	23507	A	9677	3	349	ARAGRIKDLWLGFVFFVFFVFKPTPL PTRDKGGKQLQAKGNPHVREKKKP PPGGTRGGKNPGRNFWGFGPQRFVFGG KTFGGGAHPDPTLG/ESPQS*KR*PGK RGPPF
9607	23508	A	9678	38	368	QASLLKESESERKSPTSLTSLQKLMIR LCEGMSKAKAD*RLGLH/QVQLVNT KEKLFKEIKSAISVNTLMIRK/RNSLTA DMDKVVVAWIEDLSSQNNFLSQSLIHSK A
9608	23509	A	9679	187	345	PFILFFETESYSVA*AEQWQDCLGSLQT PPPG\SNPPVPSALWEARAGGSSQ
9609	23510	A	9680	192	468	ERTSLFTIHLKLLTITNSAAMNHV*V FV*T*IFSLGQMPKSVTAGSNQSLFR FFK\NCQTLFHGGCAMLH/SHTQLNAIP LFRNLWQHL
9610	23511	A	9681	141	367	GSWAASPCSCCTMDDFAKESFTVVDDYVLL ENCPNMGGDYVAPQFMTDNYVRVTQLNW DVGWQ*QDYI/SSERNL
9611	23512	A	9682	193	3	IFGERRLIKYIKLTGHVGLRL*SQILR RI/RLNLGGGCESEPRSCHCTPFWATER DSISEKKEK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9612	23513	A	9683	1900	1988	NLVHFEHFPSLFTSPSLCHIF/CSRD RVSPY*PGWSRSPDL/RYLPL/CLDLKPC WDYRRESPCPASSRFLMNFLYF*NTTLW Q*KTIPLLE*SGDC/S*FF*YNFLAHTS STMVNSGISRNSRPVFKLADKAPSHSPL SILAFGEVFF/NLGSLOPQLKPK*ASH LNCLSSWDNRHAPPCPDNFFNIL*RWG FPLSRMVLNSW/PLCSLSTASQSSG/ ITGVSHCAGPILVF
9613	23514	A	9684	69	358	ILIVKVFPPHTOKPNFVLRSLQSIQQM LLPERKNTHAQKTCVSSENTERCHEKQV ITSHWLGWVAHSCNPSTLGGGGWIT*G QVFET/SLANTVKP
9614	23515	A	9685	66	344	IGEKLLTCDKHNWVLETE*APGKDSVN IDEMT/TR/DLEYIYN*TDKAVTGERT DNFKNSSIRGOQL*YSII/CAKGSQQKQ QISLVVPYFKKLPO
9615	23516	A	9686	269	1	PKIQNGHCRTLPKPMSQSDTTPFLFETS GSSPQPHKLSFCFSGAGTLPSSKTLKIH L\WOQTVPHAYNPSTLGSRRGRIT*QGE FKTIQ
9616	23517	A	9687	229	361	DRYYYYKSHFKPGAEAHAC*LVLASFFMC YRAIMINK*HLYHKL/VYQVIRH*KYR D/I*THVTLTTTL*DRYYYYKSHFKPGAE AHACNPNLGG*GG*II*GQEFKTLAN MA
9617	23518	A	9688	318	46	KLYALNDMASNTCKEYDNLQYRYRYKIY XRLIQHD*VEFIPEME/NWFNI*/RKS I NVIHYIHSWEEKNYMIISLDVADVSDK IKLTFLIF
9618	23519	A	9689	168	3	GNSNTMIFFTILYLFLLYFF/LFFIFDM KSHSVARLECSGVILAHCVN*LPGSNS P
9619	23520	A	9690	192	3	WHKASLNSPQAPCGMOPRMALHAQHTF VNFLKTLWAG\PAHAYNPNTLRGGR IT*GQEFK
9620	23521	A	9691	388	1	CRSAGVCWRSTPDPVCLGITSSGCRTA EIVACSLFWLKLHSGAPARCQPELSCMC R*V*TL*CVSOSGCTGVDRPLKEAVCP LAELENGARRSTALFRASQDLSLLKL RQPLPLPGALSQIEGI
9621	23522	A	9692	226	3	WFLLEQVKLAINTPRILYPPNLPFFFF* DRV/CTVAQAGVQWRDLSLLSLGSS SSPTSASRLTGTIILOHAE
9622	23523	A	9693	305	1	NHAITTVN*FGLIRHLVTKAARNSEVD IV/SIKDPLIALNYTVMFHDSHTGKF RGTVK
9623	23524	A	9694	320	1	PRDPFASASQAGITGTISHQAWFDMILY IENPKDSSKNPLGLINKYKSVAGYKINT QKSAFL*TNLYLN*P/MRTIPTFIAT KKKYLETYLMEVKDLYTENYKM
9624	23525	A	9695	263	1	VKILLFSESLSLSPRECSGVISAHCFL CLPGSRGALSLLSRVDY/Y*VFLVKAGF RHV/GQAGLEFLSSGDPTVPSLPDFWDY RCKPR
9625	23526	A	9696	262	359	IRKIKHIWSGVVARTCNFSTLGR*TKA HEGSLYCLRVGKIVSNKVGRS*FFRTQ K*V/HLFFS*VYHNGSH*SRTSL*IRK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						THKIWSGVVAHTCNPSTLGGRVGNIT*G Q
9626	23527	A	9697	166	473	TQDTSQPQKNINISWFSGLKVFNVDIHK LYLELDNRHRSWMTDILLFFYP*DGSP VT*RLCNCNGAILLAIICNLHLPSSNSPAS AS*VAEVGCTLEPRRLLO
9627	23528	A	9698	456	59	LYFLKWLHRCAPGVVRCRLA.LLQGA SQ LGYSGVRDPLLEA*CPFSDILKLHAGRTT TLFKAVRYGHLCLOKFLPLFPVRLCPAPT GGVFT*VRQASMSCDGLLIV*\VSERH*L PKPQQFVELVPKFPVRLGKSL
9628	23529	A	9699	4	375	VFCSSVTITVSEIAFLMWLSAQLLLVVRN ASDFCMSSSLVPETSLTKVTQQAQ/H*N G*L.T.*EQYVWKTOKAVI/CQOSTGSS GQSSQAREIKGPGAVAHTCNPSTLGGRG RWIT*GQEFETSLA
9629	23530	A	9700	239	361	RNDTFFFFFETESNSVA*RLQCTGVTLAH *NLCLPGSSNSPA
9630	23531	A	9701	169	1	IFYWKATFFETESHVSAYAGVQ*SNLGS LQLPSS*GSSDSPISASQAGTTDAHH
9631	23532	A	9702	37	348	HAKNFVDSLLPYTKTHEHFVKEDITWAN KHVKRCSALT*VTKELPPQS/TLKWLKH* PPC*QNGRTGSP/P/C/WVEKIVOLW KIV*PPFKLSLYL/PY/DPPIILLGI
9632	23533	A	9703	16	339	ARLNTFAMAAC*KSERKS/RN/SLTLNH KLQMIKLIBEGLMKAVNGQKRLRLYQ/T SQFANAKDELMDIISATFATV*MIG*Q NSLIADLEKVRVV*LDQ/TSHNHLHS
9633	23534	A	9704	276	2	GISRGGLSKPPFFP*DFPLDYLGQSPFC KVKRNS/RFRFTTKSPDLFFIPLPFFFFF EKVSAISAHCKLHLP*CHSPASASRV AGTTGTGRH
9634	23535	A	9705	352	2	CNSRSDFFQLMNCNFCRLWAVSPRVECS/ GVITAKCNLPLDGVDPPTSTS*VAGTT GHTPAHWLLIIIIIVAGIPLFLFFLPS FFORDGVSPCCPSWSQSTSEFRQSACLSL PKCWY
9635	23536	A	9706	6	351	INNSRPRRPIGGQGGRIQWFKLHKTR SL/LKKIKQLARRGRASLWSQVKKRLRL TWVDCLSGG*GCSQ*SH/IHCSPAW
9636	23537	A	9707	76	359	CFLFVCLDFVIFLAYFCN*YLFPPFLSH TFFFLKGLIPAGVNLRDQNKFYFTL FDVFVNIYYC*IFIF/CLVLLFFIFFF FFYCFVMRFIVL
9637	23538	A	9708	342	3	GEEILLMDEQSKWFLP(TPGENATNIVD LTTKDLEYSISVVDKAAAGFERIGSN*N STLELKTVN/SVPHAR*IFCKRLQSVWQ TSLLPILRN/LP*SPHPLVSAMLIQQS STLK
9638	23539	A	9709	211	350	RQDIALLPRLE*SGTITTH/CDPOLSGS SEPPTSASLVAGTTGACHYV
9639	23540	A	9710	253	3	VKCFSRHEMLIKRSAGGKKHIEKGTILI MSFVVVVSQSEH/NLCNHYAYSHIKK VWLGTADVYNPSTLGGQGGRT*GQEF E
9640	23541	A	9711	80	324	LITLTAMSCSNERKSHSTLSNQLKLEM SKPTPEGMLKAKTS*KLGLFHOT/SQV/L KTKKKFLEEIKSTTPINAPLMRK*NSL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, =possible nucleotide insertion)
9641	23542	A	9712	246	3	QLAKHGLFFLPFFFMGSH*LRLECSL(TALLSKISAHCNINLPGP\SDPPTSASQVAGTTGACLLAQLIFKNFVETGSHYVA
9642	23543	A	9713	2	359	AAASTTIKEQDMLKFYFLFYFFETESHPTVOGVQVQCNLCSLQPPPP\GPSDSPAWVTEQDSVSKE*KRKKLIKINVLQVTHP*HSPQHIVRVLSVLN*LNKINRRVTKSSSKEKDR
9643	23544	A	9714	278	53	KLFRGLNHRKFRQTCRGGFLFFFLFYF*DGA/YALSLLECSGTIMAHSLDILGSSHPFISASLAA\GVVRTCSPSC
9644	23545	A	9715	166	402	TLSLKKENISIRANWHVPVSVGVNKAER*GLVPRSLRL\HCTPAMA
9645	23546	A	9716	168	1	VDCITMRKSTAKSPRRKCRGTISARCKRLSG\SGHSPAS*EAGVTGVGHDPR
9646	23547	A	9717	1	553	TSIRLFLSLISFPFSRARRRLFKFYCNQVRAKRGCGWTCRGRHTWBPQGLLLSWGRGMKRPQCGQSGRQGBDTACIPPPPGSTSRPWTFRSPWFLRLHLFSAAGPGSSSSCSP*LFPLTDSQVGRCSGPDFNPPYHLMKVQFLPALLPLLLKPHRFPPLSQ\Q\PDPPSSPSPSP
9647	23548	A	9718	13	364	PPNR*RNPLIELTHNSHLYLPTPS\GISA**NFGSLLGACLLQITITGLFLAMHYSPIRLQLAFSSIAHITRDVNYG*IIRYLHANGASIFFICFLHIGRGLYGSFLYSQT*NIGIILLLAT
9648	23549	A	9719	82	351	GEALEPELPMFALSH/HATILLAPLPTPFVGTKVITVGQAQW/HQAL*SQHFERPVRVDYLHLFSRNGQNPSTKNTIRISWAWWRVPVIPA
9649	23550	A	9720	179	365	FSLFLASLKAQIIDS KPFFSNTLENT*KYEVINFFLYI\IKLHFMNLSLFCYCHSVCTILL
9650	23551	A	9721	2	320	PIPPNGESSPPTAQEDMQAANKH/IRRYTSLAIRET/QL/KTTTREPYPITMATSTESANTCWEYEGSGSYCWGCKTLRPLCKTINWQFLKKPSM*LAYDPAITLF
9651	23552	A	9722	1	344	PLPQKNWPGQGSFLHYVLLPAVSVLWSSPFFFWKQILLLPFRLG/NGQNSG*WKPFLPGSFLSCSPSTGSGNYGPPQQAARAFKWKFKIKTGFHGVTRBGLNFLTSGSAPLGS
9652	23553	A	9723	156	3	VTEAYFIFLYFFETESHVS*WHDLSGLKSPPG\SSNSPASASQVAGTTGALH
9653	23554	A	9724	76	337	YLSIYLSIYLAIVYSIYLYLPIYHSTISIYVSSIYSINHLPIYVFSTHSSSTHSSIYLLSISILSINVLISLISISYLSI*LSIYDSSIHLSIHLSHLYIYLI*YLSIYLSIYLAIVYSI\TIYLSIHLISMYHLFILSIIYLCIIFLPIY/LSTHSSIYLLSISILSINY/HTSIYLSIYLVFY/HLYIYHPT
9654	23555	A	9725	249	436	ELAG*IQDHP/GQHKTKLSLQGTINLARGGRRHL*SELFLRLQEDHLTPGVRGCSBL*SHHSTP
9655	23556	A	9726	177	3	HLN*FSNLIFETESPSVT\RGTIISAHRNPLPGSSDSPTSASRVAGTTDT
9656	23557	A	9727	272	233	RKNQRTYQIARKRLNEMARISPLRSMIT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LNVSGLNPLKRCRLAEWTEKKK\DP1I CCL/QKTHFTG/KDIYRLKIKGWKKIFH ANGSQ*Q
9657	23558	A	9728	368	380	RKGQRISIEIAIKRLNKMARI SPLISITII LNVSGLNPLKRYRRAEWTEKKK\DP1I CCL/QKTHFTG/KDIYRLKIKGWKKIFH TNGSQ*RR
9658	23559	A	9729	294	2	KGNLSPKKKNNLNKFNKVTQNFGLKQK TOGKPTLKVSONQKKPKFK*NLGKRPL KLFPKKKKLNPSRQWFYKKKK\INKLD GTLVRQINKKRKNQ
9659	23560	A	9730	7	284	SGQLGRLRRENYL*FETESHSVARTGVQ WRNLSLSQSPFPG\SSNSPASASQVPI T
9660	23561	A	9731	1	322	RSLLKKKKRREKKGKNGPQGHGKTLFLPK TPKI*KIKKIYP/RGGTHNSQLRLNL RKENHLNSGGKGNCDPKLGHCI PAQMTK TPFKKGGAKQNGKKLLQLIYGIK
9661	23562	A	9732	168	2	GFYRKSLSCLSVVICFKDFFFFEMVSR SVA*AGVQWHDLSGMRPFPFG\SGDCPA
9662	23563	A	9733	43	317	LKLOPRDTHCIWLSTTSFFIYFFETES CSVAQ*MQWHDLSGLOPPSPG\SGDSP ASASCTGMHHTWLKMCINSFDVDPDML GLGLNSHI
9663	23564	A	9734	8	296	NVVSACSLNGLVKGRLSCLTLNQIL*MI TLTTERFLKAERGQKLGSLHQA/QVNV /AKEIFLNEVSSATPVYEGIRKLSLI ATMEKACVWVIEDQT
9664	23565	A	9735	3	300	TRPSNSPAALSKCSRRRT/R/TCLTLN QKLEMIKLSKGLKAERGQKLGSLHQA A/QVNV/AKEIFLNEVSSATPVYEGIR KQNSLIANMEKA*VVWIEDQ
9665	23566	A	9736	352	1	PFFVYLNFPTFFKGPPLIHFFLESFLEN FGQGAFFKLQNFPAFLFSLNGPFLFN PFFYKFPINC\KFLGQNTFYCPYLFFF* RSFFFFFFFFFFESRFPVA\RLCSGAIS AHCKLG
9666	23567	A	9737	130	3	KIFFFFFFFFFLRQSLSVQAQGVQNC/N* LGLSQPPAGLKRFLV
9667	23568	A	9738	167	3	ISRSVFCFFFEFETESCSVTQV*EQWRNIG SRRPQPP\GSSNYCASACRVARTGLV
9668	23569	A	9739	140	419	INVKYLRSRHHFKGNIQSPNKRKATREI QIS*TDNNKCW*CGGEVQYFIHCCMC MVHSLWKIVW*LLTGL/HIELSDDPAIL LOGIPPEEMKT
9669	23570	A	9740	93	371	KLCNGYYQESKREPTERN*IFANHKTG CISKTYKELQNLNKNNS/NPTQKWKADLD ISPQTMKQTAKNQVKRCSTSLVIREMQI YTKSILPHIH
9670	23571	A	9741	1	288	GTRDHLRSQVRDQ\PGQHGETRSLLKIO N*CGCHGGGCLSSQ\LTWRLRQVNCIS
9671	23572	A	9742	296	563	FIKHLNSYMLGQNLATKLSEICKLPFYI EK*IQAGYGGTCL*SQLRLRLRHDNCLN LGGGGCSEPKI\HCTTPAWATDGGSVSK KKKSR
9672	23573	A	9743	32	400	DALVPHWSSSYSPICLDLNLVGLYIFLSR VSLIVPRLECSDAIMQHSLDLPLRLR*S SHLSLFPNWLMFVILVETGFCRVA*DGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
						KLLGSSNPALA/PLKC/WRNMRKSQL* PLLGLLSADHSD
9673	23574	A	9744	60	356	HSEVDSIIIPILQGRKQISEVRPQRMCE REGGLFISETLFLCPAPSCS/HFLTPA Q*SYF*KNVSWLGAVDCTNPSLTGGRG GWT/RGQEIKTILANMV
9674	23575	A	9745	2	446	PMVNKHVRCRCSLVIRAEQIKTIMRSH CTPNS*M*KTONTKSW/*GCGATGTPIH C/WMKYKMWQPLWKKQAQFL/KHILHPY DPINLLGIS*EK*NHLC/YKKTIVRI TARLF
9675	23576	A	9746	257	1	VMLRLSPFSPFLPLSPSSQGDLVCCFL MVE*RDGVSLPIPAQCVQLDRSL*P/P SPGSSPPASAS*VAGTTGMHLHAEFYA SC
9676	23577	A	9747	148	3	IKLCEQPHK*TIHVLNHK/L/WPGWVAH AYNPSTLGGRGWIT*QGEFDC
9677	23578	A	9748	769	1	YPQLFKTKAKKKKSINVTKSINVSQVGH *ENKKVNLNHKGATLO/EGKNGFQDTFK VTLKDKIAVAVKTRQERLPQELKLFLL EAKILQYNHPSNVKSIGVHTORRPIYV IKELVPGGDFLSFORKKNELK/VKFS DADSGWCISKKCIHRDLAVRNL/VGE NNVLKISDFGMSROEDGGVYSSDLKQI PIKWTAPALNYGRHSESDARSFGILL WETFLG/VCP*PGMTNQPPQEQVERRY WMSVSWQC
9678	23579	A	9749	607	986	SFSSSSPEFISVGCDDLPMRDHVFIT HPAFNLPLFLALGMFFSLFSPSLFIYF LPPPPRPPC*HSPP/LPPPPLTNSLFLV PPPPGVSPSPNTSPPHLPVPRPPSPSP TSTHLSPPPPSPTH
9679	23580	A	9750	313	339	AR*GLSCSG*ST*PGFMQSSCLNLPKCW DYRC/RATVPSLCFVF
9680	23581	A	9751	213	453	NLAIVNDEINLFFPPLFIIVTLASKFCS /HLNVGR*FIQCHYFLFIIDTESRSV TARAEMGATVLAHNLGFCSPQSA PLSSPPLPPLPDDSYFLISISSTFL SPPCYFLCVFLISGWSFLVSQGDSDL SS*SAFLGLPKCWYRL*PHPAWRELS FFFS/SFFYLR*GSLSPSLECSGMIIGH CSLDILVSSARA
9682	23583	A	9753	2	335	ARAGPSGDWNVNQSTASGLSLFHCFI S*GELFIIYLILLKYITL*IN*LMFGS FYFRDLQHFRLP/TSIVGKKRPGTVAHA YNPNTLRGRGGWITQGEFETTLANMVK
9683	23584	A	9754	467	120	SOLFGRPROTDHLSGCV*DOFG/OHCET PSPLKIQKLAGRGMV/CAPIGRLLGRP R*ENGLNSGGEVCSSEPRSRHCTPAWRE RDCLKNQNKTKSGVLFHSPHQCLISNT SRNLL
9684	23585	A	9755	137	368	DGVYLVTHRPYCGLSLNFSGSVIIVLP* VKAYGMVLTSLGDAIQPLADPECSFG QLRELRCMLHVDPEDFRLLGK
9685	23586	A	9756	172	267	SKSGNKPNDYHLMNGSVRWCTRTV*QLL KRLTTELPYGPAAVFLGVYAREMKAYVH MKTYSLQKMC*IFIALLFGIVKWK*A K*LSPDEWISK/M/WCIRTVEYLLTIRE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
9686	23587	A	9757	56	318	QFMGFSFFFFFCFIDTETCSVSQAGVQ WHNQS WLTA\ P*SDPPAS\AS*VAETIG MCHHDOLIFFFFKQALCPRGWSAMAQSQ LTSSS
9687	23588	A	9758	179	1	KDTRVSRGN\TDTLKPPPPGSSDSPT SAS*VARIIGVHNHTWLIFCILVEMRPH PRA
9688	23589	A	9759	219	208	NFCNFOMPLVQKILEWVVRVSLSPLEEC SCTIITYCSL/RTPKPK*SS*LSLGVQG CSKL
9689	23590	A	9760	133	371	AMAYQLYRNNTLNGSLQESLDELQ\LR NRVNFRGSLNTYRFGCDNVRTFLNDEVEF REVTELI*VDKVKIVSL\DGKGTGF
9690	23591	A	9761	813	3	CGEGWAAGDQGRMGSCLPVPRAGROL GSLFPAPGVYCSSCGTORSSQSMHKT RSLPGNNPAPQDS/ASAPKYQTPGPVLG VQSPNLNQCSHTALSPEASSAPFTTTP ATLLHQARTLSLTQGRPTTWPVLLKMP A*RPRESRH\GR*EWTKRSQARSQEA INARPRKALGLSDPAPSLHPGSLSDSPKFS LGAPKAPPLPASSPTAQETQOSHISQOP TATGFLGARLCPSPQHICQGGFFPGVTP LLLLGEWGVGHSFPDVLV
9691	23592	A	9762	96	377	RYHTNMAAQIPESDQIKQTGFHHVQGAG LELLTS\FKEFLGTYNKLTET*FLDCAK DPTTRERKSEETTLSEHCLPKYSTMT\H RISLT\FTDNHI
9692	23593	A	9763	164	399	TDEELLLRDEQ/RKWFLEKIESTAGADAV NIVEMTTCDLE*CNMLVDKVAARLERTE TNEE/RCSTVRQ/MLSKSIACCTE
9693	23594	A	9764	225	25	KCKITNIST*IE/TVEKDIYHELVCKL KNLEKTDKVLTIHNLRLNQ*EPEVLTR AKMYKIYNDIE
9694	23595	A	9765	128	218	FFKDLDFCFFKMSHCFTLLAVYBGEFTF ST*LVIREMQIKTP*YIHFSNRMVIM KKSINKCWQGRGESKALHC*ECKTV *PLWKTUWQILKKLIG
9695	23596	A	9766	194	551	KNFFLEMEF/SVLLPRLCNGVISAHR RLRLPLSSYPASSSQVAGDYRACTTTA G*ILYF**RQGFHHVGOAGLEPTSGDP PASASQSAGITGVSHCPQLKKSILHETP KGLTGVT
9696	23597	A	9767	238	3	SFLWLKCPRGAPACLRCLSA\LLGGVS* SGYMGVRDPLEEAVCPFSELEHAERTT ALFRAVPGCCSLQKLSAFCSC
9697	23598	A	9768	343	1	RGAHHSRGDCVRFTGFCAPIPVLNHPKP LFFFFV*KSPIERSSSLGPPPLKSKNR PFLR/VPRFFKNHPEFFFKKILFFPPFF FFFMESHSLA\RLSHGAILAHCNLSL PGSC
9698	23599	A	9769	191	2	FRINH*TSH/LRGQRKKKTKNSKATGRK QITKIRA*LNQTPPESIORINET*S*F SGKIKLI
9699	23600	A	9770	165	2	GKPPNCFYILNPKKKKQDVFNRT/WLG VVAHACNASTLGSQGGWIT*AQECKTS
9700	23601	A	9771	97	912	VILSTGCSGGLPGWQSVLHHSLTRCPF SFFLSSPTPEME/FSLLLRLCNGEIS AHCNLLLGSNSPASASGVAGNTGI/C

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GLHAC*AS*FLYFHSVETGFHHVSGSLG LELLTSD\RPASASQAGITGVTPRV* PLNSFSRHGLSCFFKETRVLSCCPSWT* TPGLK*SSCLNS*E/C*GYRHTPAHPAQ DMVFIFITY/CPFFVFPPL/VYIPRFLF LRWSFTLIVQAGVQWRNLGSLQPPPG\H KQSETPSQI*INKY*LLN*LITFFFSIK
9701	23602	A	9772	3	363	HELRSANHEHVFASPTGPTILGLFGVLL IILYPLLIARTSYILISN\RL\VTQQ* LILKLSKLMITHNSIGRS*SLILGSLI IILINTNLGLLPYSFTPTQLSINLAM AIFP*AGAV
9702	23603	A	9773	38	385	YLILIDSPEKGLICGLCNCMHSSLLDH LNLTS*SS*HCLYANHIIHVAISCIFYI* F*SI/YIFII*YFHSIAYVYI/YIY MYTHAHIMCI
9703	23604	A	9774	13	1350	DRVSLILLRLCNCSTSAHNLGLLGS DYPASASQVAGTIGVHHHTPTALFLV ETGFFHHVQAGLEIPTS GDDPPL\ASQS AGITGVSHCTWPHLSTTGKILSSGTICP GIWGORWNAFLIL\SLPWL*LWHPCLS IMCLSLFFLFCQ/RCKPLISD
9704	23605	A	9775	376	1	KYFELMYIPVIAICLFSNEVFLENK*QFF NLTSSSGICQNLNRIISNEVESIISKLP TVKNLPGDGIATF\TYKEQLTLILKLF QKHEEARILSNLTSETSIILRKQQPK KVPNEHTVKILV
9705	23606	A	9776	192	2	NVYQPPFVFLYPGVAGGV*PF*SPFVF RVK/LGF*GSLFFF*FFPETKRSRVTRL ECSGVILA
9706	23607	A	9777	77	350	WLRKPGSRNSGKLTLYLVVYLQTSFFF FFFKIGV*LSPTLECRGPWVN*NLCP G*RDFFPLTS*VL\GPRVILEFGFLEKT GFSHVQOL
9707	23608	A	9778	133	325	PRWVRFPYLGDCPTPRVSEMLGLQGVVPS SSPFFVCFT*SCSVAQAGVQ\NWCGLG SLQLPLG
9708	23609	A	9779	145	362	RLAFGSCSTCFEPLT*TVLYYLI*PNIFI VFEMBSLSV\RLSCGSAISAHNCNCTP AWTTERVDAANSRSMN
9709	23610	A	9780	260	1	QKQNEKKKKKIFERNIKQRDYNEQ*VG /NKLNDPDMNKE*ETRIT*/PNLHJEE IGMLNRFPVINKVL*LVIKIPLTKKSP DGVF
9710	23611	A	9781	230	1	SSDSKTGSSVVLVACRFFFFLETGSGSV TQAEVQWHDHSSLPQPPQPPK*/PGT GA*STLAS*NAETIGVSHHAR
9711	23612	A	9782	20	322	SQHFGNPKGNKFTFRNLNFFFLRNAD HMIISTDAQVFDKQHLFI*TS*QT* TERIFNLNIKAS*KKPTANIILNG*RLN I\FPKTGETKHC
9712	23613	A	9783	158	379	LVKIICNSFQYISFFFFFPLETKFCFFP QVEVQGGNF*NLPLPLGNHFS\ASAS REPEIPGPPHPG*ILVF
9713	23614	A	9785	54	312	KVDKSTKIGRNSCKMAKNSKQNGASSPP KDHNSSPARKQNTENELDETVGFR WVITNSKLEKHV*PN/GKETKNLEKRL DQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9714	23615	A	9786	13	613	PGAGWARQHHGV* DQPGQHG\KRPSLLK IEKLGHGGRCLLS PAIGGGLKQGESLE TGGRDCEPRLCHC\MPAWGNRNKTL SQ /QNKTR
9715	23616	A	9787	794	164	FSFLFCFFFLRWSLTLSPSLECSVTSF HCNLQLPGLSHSPATVS*VAGTIGTCHY TKLS*FF\FDDSL*APFLGVDTTETYP DPSSKGLLPHSGQHQGP PAISRRAWL SCVLPPLRS /STSLGQP /RIW*LSKVE V*RGTFSPQNTPTNMGCS IAPGRVD* SLLID*LOWCDHSSLOPQTPVLK\HPPT LASQAGITGISHTTRD
9716	23617	A	9788	256	380	YTFRQKTKQGLFFCRLFREAVGENTP*V FAC /PKNVLFVHP*LPG* I* IYQLKIT F*NYEGMV /FVFPLEPFTTRSHLSPRLE CSGTITTHCSLELVGSSINSSISAS*VDG NTGVRHNASC
9717	23618	A	9789	22	226	TKNSKGNKELNVRAKTIKLEENIDRN LCDLGLGNCFD*YCIL*TKNSKGNKE LNVRAKTIKLEENIDRNLCDLGLGNCF LDMTPNAQTTKGR\IDKLDIFIKI*NEWL DT
9718	23619	A	9790	288	2	QVWQE* AETESAHCWNERKAIQLL* KM RWQFLKMTNV\ELPYGSAIPLVGIHGRE LER*ST*NIMPTAPLFGVIG\T*NLFKW PSPYEQITKMHSC
9719	23620	A	9791	142	361	PPGEGKRVFPFTTEPSPRIPSKAKSVSQG DTCTPMPTAALFTIARMWNRSKCPSFEE *IKMRCIT /MECYSA
9720	23621	A	9792	305	346	TYEYTDYGGIL* *LITFYDHAVALIIFL ICFLF\YALFLTTLTETKTGGDAQE IETV* TILPGIILGIALPSLRRLYITD DAPDASLTIKSIGHQWY*TYEYTDYGGIL ILNS
9721	23622	A	9793	2	317	SKDRFVRDR*LFSTNHKDIGTRYLLFF A*AGVLTALSLILRAELGQPNLLGND HIYYVITLALFVILIPDLILILSSF G\SVVVLILGVPCTAIVLHSS
9722	23623	A	9794	384	1182	RIGKIKG\LCPLFV*NFLKFFFKMEFL PRLECNCKI\HCNLLMGSSNSPTASQ VAGITGMC*F\VFLEMFHFVHQAGLK LLTGD /FPRPPKVLGI
9723	23624	A	9795	205	1	GLQIKCTMYRHPATKMAITVFLKKGK G\NNKC*GS/GTEIGILHCWMECVM QLLWKTADAWADAW
9724	23625	A	9796	307	348	QSARL*EAVCFPSDLQRTGRTALFRA VRQGHLSLQRLLSFVCLYPAPRGAY RGRQASLSCGLHPVRASRLCLPKQAW AMVGAPTPASLPFCSSISHCCASNORDS VGYDPSSP
9725	23626	A	9797	193	381	ILLI*THILLSMISSPPFFETGSHSS/V SRLCSTASAHCSLDLPGSGGSPTSAF *VAGTTGA
9726	23627	A	9799	153	359	EGTYMCFADSYQLSYLFPVVGTFSWLEEE GV*WCICGSLQPPPRVK* /FLPSLSLL SSWDYRCAPSC
9727	23628	A	9800	2	396	ARAARAARELEELIKIFFFFFFFWGQIL ALMPKGGGGGILTYFNPPLPG*NNFPG

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						LTPPTGTLNGLPGRVNFPIFKKGGFPFGARGV*NPGRGTPPPGFPKGR/DKA PHPGPL*TFEKVPRPNPFQ
9728	23629	A	9801	256	347	LYILLNSLK*LVEKLW*NVVLASLIIR YKVT*TKRF**FSKPAQSEELQLTSA LNF*RYIIISFFWQSFALVA*VGQVWC DQSSPQLPFGFKRFS/CRSDYRHEPP R
9729	23630	A	9802	109	401	HLRRCPPTPFFALRTSGDQPLSPPEARFD SGILLHSLTSPRGLNGCQPPRGSTLNFN P*ASIPASPPFSGGQFQASQEPFVASEH PBDT*GDPAQPPF/RPQDFWGPATVPRS QACQWPSDPLPSDFS KGAQWVPVPTR/PP PSTSTQSRWT
9730	23631	A	9803	371	2	FGFLPFSFPEGNGSKRQTGD*TRCLF* DGKWECSPPKKKKTKKKKAVIF/CV PVQTKCIIVVEGGETLVGDV*V*P*GS FKHVVAMFPEK/DCLCTLYEASPKTKES RRVDGFVCVRVGT
9731	23632	A	9804	188	1	FLFFFFSET*SQSVTHAGVQGLEQSLP G\SGNSRASASQVAGTISRRHSHIIFV FFVETG
9732	23633	A	9805	112	383	VFINIRVFRLLPTFSFFFRKGFNLSPVRK CNG*TKGHCPDLPGRV*SFPSLLTNW DYRCAPPNKNKFF/SFETGSHSVTQA
9733	23634	A	9806	599	237	FRDRSLTLRLHCHCVTIAHCSLKLGL SSELQASPLSSWDYRHSPPCLANFLFF VETRSHY/ASRNSLGSSNPT*A/FPKCN DWQV*ATAPSLAYWFSAEKLIIRLLAL KVDENICITNF
9734	23635	A	9807	168	2	POODVFFFLFETGYSYVTKAEVQWCDHG SVQL*PPG/STDPPTSASQEATGTHHRA
9735	23636	A	9808	225	3	GLGLYLPYFFQPLISRG*NPSDFLKIS RVFYGT/HKFEFLFLFFETESRSVA/ RLCSCGVISAKLCLLPGS
9736	23637	A	9809	541	3	RLTGTYSGRRCFGFQMSRYVILYMDNM IILKTKKSNKYWOGCEKTELLIHLME CKMVLVWKT*Q/LNRSIDIEFHPDGI PPL/GYKRKKMKTCLPKKLCVLEP/RM FTAALFEVAK**KQ/PQTPITR*INTM RIYTMYYSAIPRKTPLIHPIA*LDTES II*TEKIQSOETTY
9737	23638	A	9810	213	1	FLCVDVFPCNFAELKALVGLFVCLLPG SVTQAGVQCNL\GSL*PPPPGLSBLPT SAF*VAGTTGVSHH
9738	23639	A	9811	54	388	PARPLPRQ/WDERPNOQPTKKKKRGRN LPTKKKTQNYSHONPVAQRNPGGKTNQK KPKTNPKKKGGAL*KKTORGPKQTGGR K*KISPNKGGK*NPCGKLEKNPFSGGE K
9739	23640	A	9812	429	24	RSKGAEFFICPCRSSKFSVLQQRQVRIV FQHPELGESVAR/CRYSQLGLRLRQ*SH LNWGGRGSSPEPRCHCIPAWATRASSIF CNFOASSVEVRRSARKKLFSDILKRHNT INWRVSGLLLVDSYFGRLATVPRTQ
9740	23641	A	9813	149	350	CHFPCHTTL/CE*EPGBDVTPGIGTKF FPAPGRTDGHHTHTHTHTHTHTSDHP HLCVWNTLHHV

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9741	23642	A	9814	66	401	PENKKTUVRKTIATIFNCERLNALFLKLETRP*YLLY*LFNIMLEVLASVVRQEK EINLSIFT*DIVIK/MKIPKNLENKLLKLLSPFSKITGYKISIQKLTSSFLYYGFTV
9742	23643	A	9815	82	1	APPPARFFFFFF*EKFSSPPFGEVQRGVFCPCNT/CFP*G*KIFFL/KPLKKVGF WPPPPGPKNFFFY*KKGGFPFWARGFFI PTFVFPPLHFPKKGVKRG*APPPARFFF FFFFFFFL*GRVSLCHPGWNA
9743	23644	A	9816	256	2	QHFF*LPHPFIQT*QHFPQTRSPPFG PPLCQKPFSSPWGSKVVILLSSFFFF* DRVSLCHPGWNAVM*SQLTAASNT/VK*SSHLSLSS*DYRCVLS
9744	23645	A	9817	53	411	TIYCSNVYVNFVQHFRLSY*KNCGLC L*FHLFVLQS*NFQFHM*FCLKI*VDP IITFEV*FTYI*FF*TYSSVSPFDAYNF VKPHR/VYRGGAHAHICNPSTLGGGGG WIT*QGEFK
9745	23646	A	9818	100	417	DEHSEKQDEPLQRPSKLLPFPPTPSS LLLMHGQESGLTHVRLASCLNRRCGF FEMKERLCLLPLERCGMISDHCSL/R PG*DKPPASAYQVGETTGTYHRA
9746	23647	A	9819	136	2	TYKMGQAGVAHACNCPSTLGGGGG/WNI T*QGEFKTLANMVKPC
9747	23648	A	9820	257	426	IVGGLFLGTGSCSPTHAGVQ*SNCSVQ S*TPGP\SDPPASASRVAGTGAHHKAN L
9748	23649	A	9821	151	416	LHKLCLMVMESGTAKTIFSLSPFNSVGL ILLLLEYSIDSLC*SVLCCYKEIPBAG* FIKKRGL/WLGVVAHACHSLT*LGGRGGW ITRSGN
9749	23650	A	9822	50	513	RGDPRVPRVRIITKLSEEGMWKAEIGRK LDLLHHTISQVNSKEKFLKEMKSATSV NTRMIRE*NSLIADMEKVLV*DOTSHN IFLVQNIKSKGIGLFLKMLRAKRDEES/ AEGKLDASKGRFVRLK/EKRSHLHNMKV QDEASVDIETTASYLVK
9750	23651	A	9823	48	406	LIIVVYTLITRIIGHGSAVSPYLLRPYS LRHNIETIRPINPTMASKCSERKSLTS LTFHLKIKMIKLSSEGVSKAKT*KLGL L/R/QTVSQVNMAMKRYLKEIKSATPVN T*MIRKQNNL
9751	23652	A	9824	143	444	WNKQNKNELADMILWGCQDKTIFMRKL TRDETKYIGIPQLALRGHSHFVRDGV I\N LDGQVDLS/G*WDGTLHLMDLTSGSTTR RFVVK/TKDVLSADFS
9752	23653	A	9825	297	2	HRSPTKETILIASIKKTKITKDLNRQP SKQDKHLTSEVMKICPTLS/LREH*AKTI MRYHLTPIRAPITKNMK/NKSKCW*GC GETEILVHCW*ECKMVP
9753	23654	A	9826	175	400	GGKGGKNFSLKGGKKTNLGIFGKKKPIF GGTNGANPPPKIKGSKKKNFVTFPP FPFKNFFFP*NL*FLGGWPHLSPPQK* V/CFPKIPKLVFSSPPLREKFFPPLFP* NLGPPGF/SFWGPPPLFFFFFP*RDKF SFYHPGKAVIAAHFSLLELGGSNPPTS
9754	23655	A	9827	64	622	MFSFFFLFDLILNHLFFCFV*MFSFFFLFD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in ISSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LIINHLFFCFVIRQOFSFLFF/ISFFFS FFHCNVNTPELDCFSVCIHSDNSFRFLH LF/NF*HMTLCISELR*TLQSCSYTYK IC**FYSVQLSFLTILY**CKS*QALSI ALQNEFLSV\QYHKNNYITLTIEFSRN KFLSVTFLFLFSIFSHNFGISASISIFIL HVYIKNNPQGFK
9755	23656	A	9828	298	1	MRNCLTDDERKWFPEMASTPGEDAVNTV EMTAKDLE/Y**YINLVDKAASDFEMID SNFERCSTV/NKMLSNSTACYRENPFER *GQSVOQTFRVGRV
9756	23657	A	9829	361	1	PLTGTQNGK/DSFPNTWC*DH/WNIHRN LDLYLIPYIKINLKQLTGPNLRAKTIKL PEQNGENLCLD*LSRERYSTKSTIRIR KL/DLGFIFIKNNKICISDKITIRK*ATD WEKIFAMHVLKQ
9757	23658	A	9830	402	2	REHHRFSFVLFGQPAKFAVPTGAKNFIS NHVWAGVFPFWKEKNKIDSFLPPPSKNP ILGELKA*P*NFLE*GFOIFF*SLFFCP PGGK*IPGVFSFPFFPLVFEIGSHSVP /RLKCSGTITAHCSLDLGLSSN
9758	23659	A	9831	2749	3215	FCQ*TKMYVMCIYINFRFVLCIYTYL HTHTFTHTKHTPTQIPEKDS/QCSLSD LKGHSL
9759	23660	A	9832	3	386	KLRGLQNLTSAMAAC*SERKS/R/THL TLNQKLEMIKLSBEGMLKAVIGQKGLGL YQ/TSQVNAKEELLKDKISATPVTA*M IGKQNSLIVLEKV*VV*IEDQ/TSHNI SLSQSLION
9760	23661	A	9833	1	370	RRCRWFPDPSRTVGRQIGKLVTHRPVFE QERGCFFPLTRQAGSHHGGGAFAQVISP TKSISPCGRGGSR*SQHFGRPQVODHL R/LGVODQ/RWPICGQYGETPA\LLKL KISAWWLAAPVIPA
9761	23662	A	9834	125	409	GOENRETWKIVHLV*VLYT*HIKRLNCF SHFI*CYQPTASQAHVHSDNSSTHV\ N*NSRWFGTVAHACNPISILEG*GGWIT* GQFETS LANM
9762	23663	A	9835	223	1	PKPQRMGT*PFMEGS*MGPFHNEKMGF FLKKKGHGFPPFFFFEMESRSVT/RLEC SGA/TISAHCNCLPGSSNS
9763	23664	A	9836	377	515	FILFLRQVLTLLPRELYSGAIVAHCSL\ AF*G*SDPPASASRV
9764	23665	A	9837	274	1	AGENHDQTCVEKFLPMKNGLHCAVQGE SWKERNQOV*DRQCKQNLSD*IQT*R/ M/WPGTVAHAYN/FTSLGGQGEWIT*GQ EFETSLANMVK
9765	23666	A	9838	553	114	GAGVKTHPGHKGRTLEFFKFFFOKLPQV GGKTLPSPLSRLGRENSFHPGGKGSNK QSSPSPFP/GWKKGGGLPFOKKKKKEK RKKGKNGVAPSEPLKYSN/WQATWG* RKLLNDTRMVQPTKSRMQKILQDKGPVN GIFTKTGRL
9766	23667	A	9839	36	434	LPFFQCVTEFTIVLISWCYIREDACKNL KHVAITINVCYIVCVCPCSTLYVMY MLP/HLSDTLTLN*VTLVEMLSFQCL MFVYHGI*K*HELDVVAHACNPSTMG QGGWIT*QGEYKTS LANMKPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9767	23668	A	9840	268	1	RFPFFFCFLTILFWAPGVVFSNFLGVRA PQPP*IFFPI*KKPSPLIFFFFFEKES RSVS\RLYESGTISAHCKLCVSGSQHSP ASAS
9768	23669	A	9841	463	86	LYNHFTISGLFLLEFCWST\WSVLQCVKN CPDDKVVGLDYGNTSQVFT*NSKLIKLY TLTWYSPLCINQTTIKPSEMIQATKANI DK*NYMKLENFCTAKETVNMKRLKKN EKVPSIHIPOEVNI
9769	23670	A	9842	37	400	VHSPFFKFSWLSVSLKFPFCSLYFKPL ALYSIFLQMCQHLV*AFF*KGINSV T\RLRCRGAISPNCNLCL/SGSSDNWAS LPRKAEAGNSFT/CR*SQVAGNPISIS TRLNQKTPFES
9770	23671	A	9843	42	407	NCLSFLLTFFFFFLFENKVSFCQG*G/ RGGPFWHGTLPPRG*GNPP*LPGRGE *RGAPPPPGYFWLPGKKGFPPL/GQGG KPPALKEPPPLGPKGG/NYKRNP PPP GNFF*LPYQVV
9771	23672	A	9844	113	379	LGPVVATSLRGRFLGYQLQSKKH*NYP TVR*CGEMRTSVHCW*ECKTA*PL*KT VWQFLKLLNTGLPDAETPL/LAETPKE LKA
9772	23673	A	9845	284	528	PLPRTMEIMLDKQIQITILPFLFKMGHK IAETTRNINKAPGPGTANE/KCTAQWMP KKFCKA*E/SLEDEKA*GHPSEVDTN
9773	23674	A	9846	888	1295	LEQGCNLFLLHKHS*LGEVFFVFCRRSF TLVAQAGVVKWRDLGSL/HKLPSSLPLS SWDYRPPLPRLA/NFFVFLVEMGF\IVL ARWVIS*PRDPPTSASQAGIIGVSHR AGPVAGILMPCRWNI SNKPGAVFKKK
9774	23675	A	9847	88	387	AYRMKIIDRISLSLYTALWTLFLPLF LFFFFKTEFCFAPAGGQ/WQGFKMDP NPPPP*K\DFLVSHPRDLGIKGAPOQC GQNFVVPYKEGGWLLTAT
9775	23676	A	9848	298	438	KIPRGAPNPPGGGKIFSPPLGGGIKTPR GALEKTLF*VRGPWPGVPKESPRPKX LG*QIFWPPGKKPNPMMGG/SLDPPPL ILSRDPDP*KKKKKKKKKGGGPKLNP PGGPKFPRGGKNFFPPFRGAYKTPGGS *EKNPFLGGGKKRKQP
9776	23677	A	9849	251	498	AIKKMESKKFW*RHGEIGTLIHCYWEF KMW*PFWKTV*QPLK/D/LNMGFLPDSA FQLPDI CLGELKTVIHTENTCQMPMAAL F
9777	23678	A	9850	478	37	ESRNKHSWLWSINFQKGLR*LNRGKQPL NK*CRHNSISTCKRMKLDPLYLTPYIKI\ KSKWTKDLNVRAKTIKSLEENIEVNLHD LG*GNDFLDMTPKAQITK*NID\LDLIK I*NFCSKDTINKVRQSTE*EKIPANH VADKLK
9778	23679	A	9851	2	378	RLEGLFLCALFCSIAICMFFFFFFF*K KRGPFGQGGDPGNGNPROLDPLPGIKO WGP\PPRKAGKTGGGGPPGANLGFWGK KRVPHGQKGFK/RNPRGSRPGPPG GVAFVRPKPDQ
9779	23680	A	9852	229	3	FGPYKIFPKKKGACPLENPPVF\HQL GLGFFFFFFF*DGVSFLLLRLKCSAA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9780	23681	A	9853	108	420	TLAHYKFLLP*SGSASAS GPRVCVRLSRDDSDLLATEDSLAHTEG DEVTAASSHSQAPSLSVHPGAALBGVCWG TGAIAGTPEPQKPPQLTGGPRPA\PIAP GLTWEPSPHPPPQ*RSPPPPP
9781	23682	A	9854	2	256	FFFLPRYYLYCARFQFLSPILYLK* MD*RRVPQEKWEQAYFFVEV\SPMCLII CNQTLVSXKEYN*ACHYTNHGENFD* TEKMIIDENTLLHLTDP
9782	23683	A	9855	323	3	ITQANKHKKRHHQSO*VVVMOKKRIIM IHRYIPQWLKTSKSDMIKCCSGVGTTEI FTHYLWECKLLHLWRRWML\ILLKFKT DTFHDPAIPLDGTYPACMHMYPRRA
9783	23684	A	9856	28	385	DGVTQAGTQWGSKETA*TA*YQGSIFN AMSFFSPVPVLKTPPPPPQK\YPPPKKK KIPPPKKK
9784	23685	A	9857	436	518	AANRLNTYRHLTYDKD/EHRYTVGKDD LFNKWCWVNWNI\ASNKEKNLDSYLPHT K/LNSR*ITQLDVKD*IKLLEENLYLH DLGDRQKFLGRI/PVFTTKKIGIKFDDPM LKLSTFVHQKTPC*RLNSA
9785	23686	A	9858	133	492	RLAGSDPGVADVVSQLOKQEKSPCSWK AVSQAESSSSSAGVSLFLRLLADMMRP IPIKEENKL\SQSTDNLNFIQKHCHRN TONSV*PGGVGPPTGCGPFRQSSP
9786	23687	A	9859	2	419	TTGKLQVSHKKTSTVSHFSKKTPTHTNKD MKRYSPSL/AIREMQKTTG\MRHYFT KYG\MNKCVLGCGETETLIYGV*ECKMV QPLWCAVWHFLK*LNIES/PIY*NYYS YISYSWRKTCITIVDPVILLGLTYPREV KTH
9787	23688	A	9860	88	419	TTTTFFGFWFLKTKLPFLVPQLFEGGPI LG*WNPDPD*KNFS/GNPPGGGE*RA QPPPPGFFLFKFA\GVSPWGGGSKPP TEGNPPGPPKIRIVIGGPPPGGKHF
9788	23689	A	9861	301	401	KRA*GGGQETKVCFFYNNKRVNGSPK KFKKGRRAAFGLRANKGLFVVKCKKI WVGKVGEPIT/DPKPEFGR\LPKDG LV
9789	23690	A	9862	220	415	KIMGGAQIFRGGGGFFFLGWEKKNFG VSFRKFFPPGGGVFLPPDP*HKKNVSS QROYISLGGGGRKTPPPKKNFLKDKTP LEFSDPSKKKKNPPPRKIWAPPMIF* I PPPIPIFFFFFFFVFVFVFVFVFVFVF FFNFKKPIFKTFLSPFKVFPKPKKK KKNPISYRRWPLAI
9790	23691	A	9863	116	366	GGEPETSPAMFCFETESCSIA*AVQVWH DLSSQLPLPG\SGDSPASASRAAGELL EPRIRRLQSVETPLHSLSGNRVRLHL
9791	23692	A	9864	619	295	FFFENEFSLLPRLECNAGTSAHRNRL PGSSDSPASAGGLL*SQVAGITRLRHHD *LILY/FLVEMRFRVG*AGLELLTSDG PPSSAQGAGITGMSHSAHYGKTF
9792	23693	A	9865	12	432	IADRRLLFFTNHDKITGLYLLFGA*AGVL STALSLIRAEGLQGPNGNLDNDHYNGI GTAHAFGIILVIVIPIIIGFGN*LVTL IIGAPDMAFPRINNISGGLPTSLLLL TSAILEARAGTC*TVYVCLA\GGVSHLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, =possible nucleotide insertion)
9793	23694	A	9866	30	380	LFSTNRRGIGPLYLFGA*SGVLGPALT LLI*AEIQPGVLLGDHDTYNDIDTAHA FV11LFIVIP11IGGFGD*LVPL1IGAP DMAFPRIN/NISF*LLPASLLLLASGI REGRSK
9794	23695	A	9867	256	395	EVLREKSEKSFETVCI INNK/VWPMVAH ACNPMTLGGRRGIT*GOEF
9795	23696	A	9868	458	2	PKRFRFSQKPPRGFYSAPLKGNFYFPP PVNFGPKDFKGPPLFFFFFFFFFFFP RFFFFFLEKG*KF*NFFFT*NMVFFYIS /CSKKFPQFVLTP1PF*KVPKPVWFN DFPIFFKK1FFFFFCDRVSLCHPGNSA VARSLTASPRV
9796	23697	A	9869	144	425	IFLCRSIYFSGPC*FSLISSSSCLSPFL S1PLCVLS***T**YLFFYISMREIYKTR TKGIYPGAQRNSLYTH\FSIEVQSTIKA ERFWPGAVARACNPSTLGGRGQITWQG EFE
9797	23698	A	9870	138	401	DLRLKLNLSKNIIRLQGTVESSLTIE MQIKAKVRYNLI PVKIR/SGNDRWK*G CGERGTILIRC**ECKLVQPLNKT VWSFL KKKKK
9798	23699	A	9871	179	441	PSGKGIGKPGPPPPKKIPGNFFFLKKK GVPPGPPGGPKRPLLETTPPPNPKGGEY GGGP/WPPPP1P*FKGPFKKKGPPWTN RGMP
9799	23700	A	9872	57	435	FTCMRKLNKNNSGNKKK*GSTTLPKDH NFFAVDPCNCFNMF1PGKEFKK/SDY*V TQCDTRERCCKPT*VLKTLTLDMEKCSKE MDLLMNQSELEKKDTFRELQNAMESE NNRLDQVEERITELE
9800	23701	A	9873	228	443	FSSKFILISVFLFLFLETGSCSAQAGV QL*DYSSLQPSPG/SGNPPISASQIAT TAGAC1HALLIFVFFV
9801	23702	A	9874	349	2	KKPKKKNLFPPKNFGFFSPFSP*KFFFF LKGFNFRGFFNFPNPKKFFSKNSQL VFFLPPLKKKIF/CFPTPVKFGP/SQRF FLKGPPLFFFFFLLDRVWLCYPGWSA VARSRIS
9802	23703	A	9875	405	2	KKASRMENVKKKKLEMIKLESEGLKA NIGQKLSLLAKQOVVNAKENLLKEIRSA IPLNTQMIRMQNSLIADMENIL/VVWI/ EDPTNYN1PLSQSLIQSNALT/FNSMKT ERGEAA*EKPDALS1G*FMTFKERS
9803	23704	A	9876	355	394	THPYYSHQEQSP*P/LTGALSALKTS GLAM*GHFHSITLLILGLLNTNTIYQ* WRDVTR*SAYQGHHTPPVQVGLRYG1IL FITSEVFFAGFLP*AFYHSSLAFTPLQG GHWPTGITPLNPLEDPLNTSVLLASG VSIT
9804	23705	A	9877	47	85	TIYTHICVRIYACEVCVCAYIHICGVP AHLTEQNLKPARTQSPAPQKNPELPV DLVSSLDREAGQVSNHRLQNTCTD VLFPKNTLCLEL/NFECLEPLLELQEL P*LENIPLFPOPIDYIYTVMAVICV
9805	23706	A	9878	2	389	GRGQPPPEFFYFPGGSLVSTPNKKKP LGEVLGGGWSNRAPKGWGGFPFPIALF

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						KPKGPFPGKFLVLFKSNVPLFFPKMRG PLPKGGGLPFFFFFETKRSRVTPQGVQ WCNFGSL*PPP\TGSSNS
9806	23707	A	9879	351	1	FLGFSKNFNPFPQKWPFAFFPKSHRAR VNEIFS/RLSVINF*GLTKPQRLFFSLL NFSS\PIPPFQPSRLIKEIRFSTFLTP ENSKIKKPLFFF*FFFF*DRVTLCCPGW SAVVQSR
9807	23708	A	9880	123	387	SFLWLKLPFGAPTCMRCLLA\LLGGVSQ LGYTGVDRDPLEEAVCPFSELQRHAGKTT ALFRAVRQGCFFFAFYF*IELFP CY/CSG RVGG
9808	23709	A	9881	341	659	SLGRVQWLHACKSQHFGRLROVDHLRS GV*DLPOQDHETSLNMPK/QKLARHG GMCI*SOGLRLROEHNLCGRCNEL RSOHC\PAWATEQDSISKTKKK
9809	23710	A	9882	216	1	PKFFVWLRSQIFPKFGFGCGFF/CGFG NPQGGKKPGFWGLG*KKKGFPFFFFFFF LRDGI SFCCPGWSTQW
9810	23711	A	9883	2	244	GRVGAVGRREGENTKCDLEPPFPBEGK QONLCKFLTGSLPCQDKK\CFPV*KK KKKKKKKKKKKKKKKKKKKKGGGA
9811	23712	A	9884	310	2	IFLQTLFPNPTFENLSIEYCITFSEYSPT **KQ\TNFILSSILLYI*PSGSYISNL *Y*ELFSQNL SYQHPLWI*KKWGLGVA HTYNPSTLGGQGRWIAWSPG
9812	23713	A	9885	242	358	KTVMVLYMNI*MANNHME*CSLPLVIREM *IKTPVTIV\TVGMAAI*KK*NITR/C W*ACRETAVLVYCWGFYTOPL*KTVM YMNIE/IPCDPAIPLGLMYLKE*RFQTV AHTCNPR
9813	23714	A	9886	360	2	LLKLGFPPWAKKGGKRLWVEGPLKFPF GGFCQRLFFSPGGGPKGSPSIIILPGK *PFVWGPFFREV*KKRFLKKKFRPTFS /Y/LFFFFETESHSA\RMESGAILAH CNLCRLGSSD
9814	23715	A	9887	236	347	TKGFFFF*TESHSVT\RECTST/SAHC NLCLPGSSNSP
9815	23716	A	9888	310	3	NFFFFETGSCSVTOARVQMSDQ/GSLQ FSPGLADPPTAS*VAGNLKFLSLGLC SSL*SLGIS*ETKKSQVITDLCYTVV LCLFEMESHSVUQAGVQWHE
9816	23717	A	9889	119	391	AFAYVNHARDSFFFFFF*TNFFFPFQVG QWPNSSGSPQAPPG/SPPP/YASASAK ISGAPGAPPPPGNFFSFSSPTFFSR DGVSPYEP
9817	23718	A	9890	195	3	DGVSLTLPRLECNGLTTHCCLSPV/SW DYRRLP*RL/V*FFFLVEMGFHVAQA GLELLTSGDHP
9818	23719	A	9891	3	378	RDGERNMLALGTASAKALKYSLALS LPR LECSGTII SHSSLNPP/GLKWSCLSTT SSWDFRAPPPLAKTKQ/HATFF*EG ESPVYVQAGFKLLASSSPPAFSLPKCWD YKLDRHAW
9819	23720	A	9892	231	1	PKFFFFPKFFSP*N*KPFFQISPAKIQKI RVYQS\HKKFFSFFPHGVSLLLPRLE CNGTISAQCNCLSGSSSDSP
9820	23721	A	9893	2	347	APARQENVVCVYVCMVCVIVLHRRHC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9821	23722	A	9894	28	382	EVLFCYKMLGKKRSIYAY*LVY*YIVIH MCVYIYI/YIYV/YMIVITYVCIYTH TAHLEAGATGYRTFLPAIGLLCLPWL DDGAGQTAQ*SMLLDHAMLAHRAHELF I/DITYEFTYIPKQOKYSFLHDSQTS FCFSDSIATPSKMEETQOKSNLELLRIS LILLIESW
9822	23723	A	9895	93	386	FWKIIISHYYPKYFSCSILISPSLPITC ICMFHLLKLCQSSSEFLHLLFLVWLVFET QSHSIKQPECS* *LSAA/CHLPSSDDPP
9823	23724	A	9896	174	1	TLDWGPRKKNPPFFFPETRSRSVTEAGV Q*HNEGLPQPPAG\SSDSPTSASQADAW
9824	23725	A	9897	251	386	LQRLCESGTI/SAHCNLCILGSSNPLAS AS* IAGTTGTLTGDDVST
9825	23726	A	9898	127	393	GHMGTLTGSPATLILALFWGGRISTQ LDGINKS\FSLFLYFLRHCSLSRLLE*S GAIITYCRLELIGSGDTPASASQETGTA GTCHT
9826	23727	A	9899	3	334	KLRLQLNTSAMAAC*KSERKS/R/THL TLNQKLEMIKLREBGMKAVIGQKLGILL YQ/TSQFVNAKEELLKDKSATPVTA*M IGKQNSLNCDEKSCVVLIOQDTG/HNI FLS
9827	23728	A	9900	356	1	GRKPSFSLPKATLLPMPGVLGRRALMG PDSRPGVPFSCSVLLTLPALPLTARE SLCPCPFS*TPQPSVNP/H/GKLARRSP CVVSGRQSLP*AEIVPLHAPALGDRDE TPSQKKKK
9828	23729	A	9901	118	343	IPVAKKKKQENVLPFTHVNLCISNNFW FETGSHFVTQ*VHMNCLNSLP/PNLQ GSGDDPTSASRAAGATGVQH
9829	23730	A	9902	321	50	SLRTRV*RPFSAPG*NPFCCLKPKQKIFQG GG/ESPLSQILKRVKQENSYNLGGKGFN *PKLPCCPLTWTAKTSPPKKKKKKNYR TWETSVS
9830	23731	A	9903	317	8	NCYDFNSGIVIFLLGILPKSTK/T*VRT KTCT*MLIVALCIIITKKK*SKCLSTDK QVNKI*YIHIMEYYSPIKGRKY*HTLQH /WMNLENIS*KRLDIKKPHII
9831	23732	A	9904	287	3	RGALNCRGGPRGVKSPGPAFKLQLKPP GTFLNPK/QPPFFPNPP*KKGAFFHFF LPLF*SFRTWTEFYSVT/KLECGAISAH CNLCSCSSDSRA
9832	23733	A	9905	2	406	PRVRTSSRRATALFFFFFVFVFWGKG EIWAPPLKNC/IPEKFCYFGGAPGAG LPPPPGVIFSLCRVVKKKKKKAPGPPG VLGKKKKTFFTPKGGTFLTLGGF*KKSL FGKKTLLWVGGLLLKNFF*EKER
9833	23734	A	9906	1	296	IWVGATECIPKNNFTIWHQBHTFTCKD TYRLKV/KGWKKIHTFHTNGNQK*AGI AIVISDKTDFKSKTIK*KGHY/IMING SIQQSDLLDWKSSCSF
9834	23735	A	9907	474	41	FMEYLTLSFTHVLIQ*FIHCFVHLFTHS FFYALMKSIIQ*FIHLYSCF/ICIDLLI SCCIYSFIYALVKSILANLTHSIHTFL Q*FVHLFTPLLCISFTHSSIH*PSHSLT FIQLHLFHALVSGFIWSFIYLFCKINV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
9835	23736	A	9908	286	84	FLIDK LKPPPPPPFFFOANFLCFIRD/GPHHV QDGLPLLT*SASHGLPKCWDSCRALR PASPLISGPHQTI
9836	23737	A	9909	316	63	DQLLVRSIGFEALMSPIFFQMEF/SLS LPKLECGAISAHNFCLLGSDPPASA AV*/PMANLLKLCASVSYCIELVLNELH WIK
9837	23738	A	9910	370	461	F*F*FLPSETESHSA/OLECSAMISGR CNLRLLSGGDSPTREAGAQESLEPRRQ SEPLCHCTAAW
9838	23739	A	9911	294	28	PGKNSTVQKEPKWFCMKFTPGENAVN IV*PTTKDLEY/WINI/DKTVAGCERTD SNFERSSTMGRML/SNSIAWYTEIFRGR KSQLMGI
9839	23740	A	9912	307	463	CKL*TLNNDNVIGSLIVT/TCTTLVGV LIMGD/RLCMCGEKEYLGNLGTPLSIL
9840	23741	A	9913	377	28	REKLTIVKPLAPSPFRMSRAYRAIFFITP TWKSKGVTGPLEFLHIFPPGP/CPGL PIFFFTKTKTRFFFGWFFFERVSLCC PG*MECNGAISAHKLR/LPGSRYSASA SEFHR
9841	23742	A	9914	384	725	HLTAIRMTVIKDTENSKCERGC/KTLMH SCWEYERVOP/LWKRN*F/LQVE/LPS PCDPSIP/LLRMYPK*LN/D/CKRMC/C IPTISIAALFPVTK/SWKQ
9842	23743	A	9915	187	3	QPHKHLGLDNIYIFFETGFCSSVAQTGVQ *RDHGSLLQPRPF/GSRDPPTSGSRVAGR PRQENG
9843	23744	A	9916	15	167	DGVLSLSPRLCNGAILAHCNLR/LPGL K*FSCRLRLPSSWDYRLPPHPAHV
9844	23745	A	9917	345	477	YCSRTSLPL/TLKKGSA*FGAVAHAYNF SILGGRGRWIT*GOEFK
9845	23746	A	9918	460	42	HORPKVDKTTKNGEKRSRKTGNSKNQSA S/APPKERSSSPAMEQSWTENDDELRSQ EGFR*SNYSKELKEEVRTHGKEVINLEKK LDEWLTRI/SNAEKSLRDLMLTPKA*Q LPPERTNLSS*FNQLEERVSVMEDEINK MK
9846	23747	A	9919	282	21	AAGYLQPFSEWLHSLGSRRLPISVFPV

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9851	23752	A	9924	254	3	RGKQAWLSCDGHVPRPSRLCLLPQTQA PGGFYPPGFLPPPLGFFPKGL*RLWFFC PATFFFLYQISKPPFFFGKYNQNF FFFFPEKSKRSVTARLECNQIAHAHNL
9852	23753	A	9925	309	1	YPTTLMLLGIYSNLKINVMKT* I*MF TATFLIAETWQPCRSSLSWLI/QQLW YIQTI/EYYSVVRNRIK/LMKT/MKLG YILOSEKTOSEKTTYI* POLYDI
9853	23754	A	9926	237	2	RWNFNFTOLLKCLFLRTKFFS*VSK*N FKYFLGFWFFFLRQGLTPVT\RLCSG TISAQCNLRLPGSTDFSSASAQE
9854	23755	A	9927	244	1	KPQCLWRK*D*WHNTQKLDVEKGKPLIH YWERKLV*PLWKTVMRLM/NLKIPLP YDPVPIPLWGNYSKEM*LCQREDSRA
9855	23756	A	9928	2	644	IVQVDQIRLNIHCLQETHFKCYTYRL KVMR*R*VYVHNIHQEKALVAIGAYFR ARKITRDKERHY/IMINGSMLOKD
9856	23757	A	9929	1	364	GTSGTRPINNTTVFSCSSSEKTR/R/TH LTLNQKLEMIKLSGGGISTDMG*NLGL LHQTVSQVNTKEMFLKEIKSATPLNT* MIRHQNSLIAAIGKVLVWIDQ/TOHNT LLSQRLIWNKALT
9857	23758	A	9930	88	374	ILKACGCPGNPHPWGFL*GGGGLGLNP SKSPHPHPRGDPDTWGGTPIGDVGPKPP KLPHGAGLPKPKCSGGQNN/PKISGP
9858	23759	A	9931	384	2	LCSPPFFYRKINGGGQSLRLPPFWFKP GGKDCSPGVLDPPGEQAGAPCFP*KKI RWG*GAAPVVPVPOEG*/VGRAPLTPKI PAPVSGCSFALPGEQGETPFFLKKKK KEKSEAMIPPPPGPRA
9859	23760	A	9932	32	359	IFFFLFFF/C*KGSPFPVQAGGGGPKT PFWPIHAKTKPLSKKKKKKGAGFP PPKCGPPLKNGGGLKRRFLKKNNG ENFKKKIWAGGGNPREPPFGGAR
9860	23761	A	9933	138	1	TGFFCC*EFALVAKGVQWCDLGLQ PPDG/SSDSPTVASCSC
9861	23762	A	9934	103	355	LAGQACCS*STSNRCHVNA,PGYANGH CTDITCLIFVIRNSWLITPAILTMFCY HVG*VRQEQAPGNRVSLDLL\PPVT C
9862	23763	A	9935	29	363	AWSHNAFLFFFKRELAFVPGORENN FVSLKPPPPG*SPSAPNPDKGNKGP PPPQLIFFY*/GEGKGSFPYNPEGPKPP TLGKPGLF*NTKKICPQPRGLKGGQHI W
9863	23764	A	9936	173	363	PKKRPIISLKRAFNSNPGD*QKFLKRL PPMGSQPKRGNYPYDKNLEKLCGGGNK GSG/YHYGL
9864	23765	A	9937	360	3	NQMRKNQSSKTGICKNQSACPPPKERS SSLAMEQSWMENVFDELREEGSR**NYS ELKEEVKTHGKEVKNLEK/NLDEWLSRI S/N*EKS KDLMLKPKAQELHGECPSL SSQFNQLARA
9865	23766	A	9938	194	370	VSNFFFFFETEFCSFAQVGAQGNFR*L KAPP\NCCLFPT*ASRVVGTGTGCHHS WLI
9866	23767	A	9939	426	1	SQEFKVAVSYDLTMHNSNLSNSETLSQKE KTKQTKTKQKRTY*EGRHGIRKCPPLI

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						IREIQITQTVRYHPTHIRI/VLLPQKQNCWCRVEKLPVRC*WECETVQPLWITVWV/FLKILNLIKLPDLATPVVCYQMEFSC
9867	23768	A	9940	255	16	RVYINVIYIMYLICIYTPSRLLVEIGFHHVGQDGLDLLTS* SIRLSLPK\CHDYRYEPPCVNIYIYLHIYLYMSDGVKY
9868	23769	A	9941	206	355	FLOGHTAIRNGRG/NPGAVAHTCNPSTLGG*GGRII*GGEFKTSLTNMVEP
9869	23770	A	9942	3	402	HEELNPRSTSSPALVLHVHTIAHVITAF AEGCFQHDFFCPSQPENRHIPLVFTTASKVRNIFYLLCRGRGLRFFLVCLKIDPAIPLMGIPYK\KSLYHKOTYIHMFTAAEFTVAKIRYQSKCPSTDV*IKKICV
9870	23771	A	9943	79	328	CIKILLKFLCLFCILPPCLNFFLRQSCSVARAGVQW\SLQP*PRLKHTFTSAS*SASTRGTHHHAHLIPFSNPL*R*VSHVA
9871	23772	A	9944	321	414	VPSWAG\VAHACNPFSTLGGRGGRIT*GGEFE
9872	23773	A	9945	142	480	QBAKSPFDSSTMEVMDLKKQIRVIFLFEFK\NORAAETTCHENAFAPCAAND*QMRWLEKFCCKGESELEDECSGRPSEVDDQLRAIIEADPLTTIQSEVAKELSIDH
9873	23774	A	9946	191	3	FFPLPRGGGDSVFKKPKKKGPFKIPFFCPGPFPLAT/INFPPQIFPPFFFF*DGVS LCHPGWNAV
9874	23775	A	9947	451	461	K*INK*VKVGW/RKEHHANINQKVDVDTIFISDNMNPFRKKNKITGDREGRYIIKQPIHQENIAILNVYVPPNNRVAKYV*KIILEKKEIHKFTILVGDFTILSTIDRTTR*KVS
9875	23776	A	9948	186	405	NHTLAISLF*PYKP*ATLKGIYRKERRKLVLC*RDICALMFITELVTAAKLWNQPCRPSTDK/WKMWYICTMEYS
9876	23777	A	9949	18	412	PEFRITITLPEKKNLL*LTN*VSKFSGYNINI*TSVAFF\YSNNKISGTGKIIVFTILSNRMKYLG/TLTKNMKDHTENYKMLRKENEEYQMGNGSWILKINIVKISILHKVIYRVKFLSNFNAILLKK
9877	23778	A	9950	1	396	LAPDGRAERLKTGFHRVTQDGLLELTS*SVRLGLLKCWDYWRPE/PVPGLWD
9878	23779	A	9951	307	405	GIRVRR*PQGLRPPFDALVFKKMWWPPTN\PRGWSGKGWEPPOGPODPPGQAAPQDLPETWROPNNSLFTRGAWPPNSNLPWPAPASRHPAQRAPGPGS\AAPPPGGGGEQMDPPGRV
9879	23780	A	9952	2	402	YGRPKGGSLRFVLLTTFGPKGFTFFFLKTQKITGGGGGG*PFLPRVROENSEYSRGGGN*PKRAPCALTWGKKFFLKKKNTPOKPKKLPQCRIQY*YQK/SSSLFMGGTPGKRQ
9880	23781	A	9953	249	1070	SSFISRFYFICILPETSRSHTVARQCCDYN*LOPQPPGAQELLPQPP*SAG\ITGVAPNTPQLIFYFFVE/SGGSTHVAPRLALNSWAQNIAL/RLPKVLYFTF
9881	23782	A	9954	75	396	GFKGRKRGLPLPLNGKRLTNLSBKGLSKANTGQKLGLL/RPVSVQVNPNGKFLRE.

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IKSAF/PIEK*VI*KNSLIPDMEEVLG V/WTKKYSHNIP/LGLSLTKRVLT/LF
9882	23783	A	9955	181	458	RLWNDGLYNI/FDLK/LQ/SHV*SLLLLF ILEPESHVS/RLECSGAVTTCCLNIP GWSDSPPQAFQVAGTTGVCNANVPFAF L
9883	23784	A	9956	67	430	LAPRLIYSPKIFOWSFMSVROIQVQSLA IGNFNRLP/LILICHVAFHRLLPQWV RNFILYSISISANKQESKILKYLILYI NLRNLWLGTVAHAYN/PSTLGV*GGRIS* AHEFETSQGN
9884	23785	A	9957	77	422	LPLALWASCRLPQCLD/DFIHGPPTSGA ASQFLCFTQMOPPTCSSRLYNL*PALV LDHTTSNVVCFRSP/SFFFLPLPLPLPA PLP*/FFFFFFFDRVLLCHDGSAAVARFO LTAAS
9885	23786	A	9958	3	422	LHSSLVTEQDSISKKKKKKIFLGGTRK GGPSLGGFFFGPPGPKIVKKRGALIG FPFPCPKKKPKKLPFFPKPLGKPPRKGG F*IGEPWKT/EGPGFPKLNLFVFFSPWG GNFLFPQKPGGKVGKILLQPKKPPGK G
9886	23787	A	9959	370	2	PFSSWVANFREGDGKECSVLQGIKRCMF CRYINVTPLVHFPFPIKSGTSFFPLVFF SPEVM/HFP*LPY*FGWALLSRF*/MSL L*LFFSKFPFPPSFFFF*RFHSSPRLK CNGAISAHNCNCLP
9887	23788	A	9960	256	2	AWEETAPLHSHCLGNQARPNWHRAP/ P*LIVFVFSVETGFHVAQVLELLASS DPPTFRNLLSSWDYRGLSPQPMRKSQAQ EG
9888	23789	A	9961	269	3	HRQACQVRSPIQCCWACKIAQFSLQIV RSSLK* I*SPYDPVPIPLLVIPRELKT \SLHTKTCT*RTTAALFIIARRWKQLKC PSIDE
9889	23790	A	9962	268	324	SGTLGH/WIFS*VGIEITMWLKVDPDTK KISLRSAEAAIKYPLTQATASIIIRRAI LFNNRLSEQSIITMTNQYSSLLIIMAI AIKVGNAFHF*VPEVTQGSPTVSGLLV L
9890	23791	A	9963	341	2	ITFLPTKIROSFNKFGKRTSDSNLNR HFREDTQMANKY*FI*IKMQIKTMR YYFISKRTTISRKTSNIQC*DTWSPTGT INCLLECKMVRLLWKMTWQFLTVEHIL VY
9891	23792	A	9964	250	2	YHPVNLYFKYISPIDV*FGCFIYIFDYP LCSCFSLHPLVYLQ*/L/LFFFFAESHC VARLECSGVVSAHCNLRPGSSDSPAS
9892	23793	A	9965	3	334	RTLRRHIWLDPSFE*HLSCFHLLAYN SAAINIP/HSYV*THF*YS*MYRGRTA GSYAT/SMNLNLRNCSTLLHRNCTF*PF YH/WE*VPISQSCQKLDFFILIAIS EG
9893	23794	A	9966	179	352	NQE*TEILNRPMSNQIESVIKYLPTRKS HRPIRHTAELQTY\ILLKLFQKVEGEG LL
9894	23795	A	9967	2	350	THPSINSFIHVIHASMNSLIHLTHPSF SIYLFTKSFIHLFIHFFSFLFLRPSFT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						PVAIYSFIHFHTYSSIH*FIYPCVYSCI DEFTHSFTHAFIQHLFIH*II/IFIYF ISFLFF
9895	23796	A	9968	228	558	CHQLRQELAIPTSFVILQLFSGHLDVYM QAWAQRDPDKYEYDNK*FIEIKKIQFTL ISKRMK/YVGINLIR*VKDLHNEYKTL MKEIEEDTSEWKDISCSWNGRINSVKT
9896	23797	A	9969	196	2	DRKVFFRFLFIIFGLKKIIFLFWFFPS /IRGRG*IFFFFFFFFPESPSPRLECS ETISCHCTP
9897	23798	A	9970	245	1	TQCDMCFVIYTHIYISHICVMYIYIHT RTHTGILFTP KREKNSNTCTCATKDNP/ CMTLC*/HKRRQTHIHTHTHTHTHT
9898	23799	A	9971	163	380	NHRRQKNGR/HNGNKYKTVMKINSNP PITRNNLVNGLKTPIKRQKLSDISKQ YPSIYCL*KT/YLKYKD
9899	23800	A	9972	328	1	AKCGFLKKLNIELFNSIPGHSCKT*TM FAAALYII SKKYKOPSCPSNDE*MNEIW HLLTIGYSAVKKIISWG/RWMNLENIARL SGRQRGHIQDSVDMKSP*AIQC
9900	23801	A	9973	200	3	MASKCSSEKSRH/S/THNQLEMIKLS EEMSKAKIG*KLGLCQ/VIHVVYTAG KFLKEIKSATP
9901	23802	A	9974	111	517	NLEQGLIKRTIANPKIKINTTILITLI NVNGLNTLTK/RQRMSD*IFNQDPTMI /C*KKN/HCKYKDTNPLKIKG*KNIYDA NMLTQIKKKAGVAILI/DKIDFRA/TDI TRAKEGHFTMIKGSVHQEYVTILNWSAH AS
9902	23803	A	9975	342	3	FLATKRIFFFFVFPQGPVPLVAPFF WAFGGGPPKAPKKEFGPRGPFENEF F*GFFFFFTKGGFFFLRFSKKVFFFFFF SETESCSVA/RLECSGTISAYCNLCPLG SR
9903	23804	A	9976	13	326	ILDHSNRPSSTLTKTPNAGKDVEQKQFL /LCCW*ECKIVNLYGR*L/WQPLTKLNL L*PYDPEILLIGIYQELKTCIHTVACT *MFIEALFVIAT*KQPRYSVG
9904	23805	A	9977	74	396	LAPRTQFLPCSPAPLRQCHTQSLLLPFL LRLIFYFPCFLKTRAHSAQAQAQ*RDH GSLQT*TPTLACTPASA/VARTTGTHHH AWLIVFVL/IEKVSHSLVCDKT
9905	23806	A	9978	287	2	QPHNSYTOIFTPKIIKTTPPNLKNQNN TPIKKTQ*FP/PSNTP/SYPSTHPT HLFIYPLIHISPPFSTHPRIHPPTYLS THPSTHPSHPSSR
9906	23807	A	9979	97	332	GNNDLFYFFLELTGSHSAQAQVOWC DHSL*PQPSGSSPSTC/RLGLQAC MCHAWLIFNFFCKGRLLGLLR
9907	23808	A	9980	168	2	STWLRLWDYKTFEFTSKS/WFGTVALTY NDYVLGGQGRHIT*GOEFTKSLANTVKS
9908	23809	A	9981	267	1	LKREER*RRAN/SKTSRRKETIKTRAET TATENRKPIEK/SNKTNQ*FFEKTDK/I DNPLERLRKKER*ITKVRNGREDIL*N NDLIKVKKD
9909	23810	A	9982	230	412	CHIVLC/D*PIDGIV*CHIVYFYGKKT HTYTHTHTHINTHTPT*VSKILLKKRR TCSVCA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
9910	23811	A	9983	229	415	SYVFCIRFCPLDSLNKEIVA/SQVQWC VSUVSTT*VAEAGGSLEPRSLRPDWSQ RDPISKX
9911	23812	A	9984	2	288	RGYDSTSSAYTVGHFT*EDKATITRLSG KENVXHAGGETLRLRLLDVYP*TORIIDS VGNLNSA\SAMM\GPRLPKVLGLQAWT TMGP*KYTHIFF
9912	23813	A	9985	246	3	FLLDQYQCALCCHCFLENFANGCHFNIL LQGVKHTKPKYS*KFSVL/WLDAVAHS CNSSTLSGLGWITRCQFETSLAMVK
9913	23814	A	9986	342	1	FLNFGSLTGFFPKGPKFLSLGGLD PPQFLGVFKRGAFLGTO*PH/LEGFK FWFEPKAFYFFF/CCTISAHCNCLP GSSDSAASASWIAGITGAHHYARLRRLL RQCN
9914	23815	A	9987	330	1	NRPLNNLVMAKSCSERKGYTFSVLRSK /LRKMKLSEESMLTVTTG*KLGLLCQT /VQVNTKEKFLMEIKSATPGNKGTVTKS NTLTADREKV*VIWIKNKTNHKIPLSO
9915	23816	A	9988	209	2	IKGSHFFPLI*YRKITIFGGVKGKGGF YSY/LFFFFFEKGYHSVTQLKCSGMILAP CNCLCPGS*DSPTS
9916	23817	A	9989	236	357	QHRWMNTMLNLYL*IIYVHF/HTHTHT HTHTHTHTHTHT
9917	23818	A	9990	263	1	IQRVFNHSLWPSYVHFFPHGSYLFCS L**AFFRH/G*FVLSVHFLKIFNLKKI FFETG\SHSVAQACSGMISAHCNCLLGG SSDR
9918	23819	A	9991	3	368	SLDPRRSLHLAKYVPPRSSLGDRARFC LLKKLELFFETGFCVCAQGPVRWCSHGP LQPRI PG\SSNPLSAT*VAG\IAGMICY HTOLOLAF
9919	23820	A	9992	294	391	SGTVAHACNSSTLGGRGWIT*GQ/ESQ TSLTNM
9920	23821	A	9993	317	3	TDKELLRLDEQRKCFVEMEFSPGKHAMS NVDMTKDLEYSINLVDKAAVELERADSN FERSSTLGMKLSNISICYKEIFLERKSO LM*QIPLLM/FKKLPQP*PSA
9921	23822	A	9994	193	395	IFWYFCSSLSVLAASFCTFWLWRQLLS LNLMO*DHLSQSLQSKSATLFWV AERGDSEAEKLEASRNFMFKERSCL HNKVKQGEARTDR/EAAASYPENLR/V KDEGGYTK*RIFFVDEIAFCMKMTSPSKT FIAREKSI PGFKVSKDRMTARCGRCL
9922	23823	A	9995	82	420	SFLWLKCPRGAAAYVRCSA/LLEDVSQ LGYTGVRDPIDIEAUSPFSELKRCRETT AVFTAVRGHLSLQ/LFLPFVOLCPAH RGGV*RG*ALLCCGSLSPVQAPLPLCLP TQ
9923	23824	A	9996	376	1	CGRTDAPASTSPYAMTVRFLRPQPCVL DGLNENCPARAPQEQNSLGEVDKRGPREQ TR\PATAPPRPLGSPSWICPGDW**CR NSLQGFSLAASVARGRDWALAGLPATVS ARFQEQQMNTV
9924	23825	A	9997	495	982	VOKFLRPNLAPKHKORKLAPNSLQGRRL SLPSPVTWCMTAPPTGLVSLLLLVITIA VCLWRMHSWQKNHW*ASPKKTHD*TGLA EP\SCARKQCSEGRYSNAVISPNLETT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/15,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
9925	23826	A	9998	401	341	RTMRVSHTFPPVVDCTAACDLSSCDLAW /WFEGRCYLVSCPHKENCEPKKMG IASKCTSERV/SRSHTLKQKLERFKL*E KGM/SKNEIGQK*ALLYQ/VSQVVNAKE KFLKEIKVD/LHAQMIRK*NSLTADVKK VLVVKIDQTL/PLGHSVITQSKALTFFSS MKAQ*GEEAA*EKS
9926	23827	A	9999	30	393	DTTILKRLQITGAVATKHWSEKSLTS LNLNKLGTIKLTEEGMLKAKKGQKRG LSCQTVGQVMN/SKEKFLKEIKHAI PGNT *MISK*NSL/IADMEKVLVG/WSKVIF *DOTSHNIP*SQN
9927	23828	A	10000	133	1420	EQRRLPVTPGVASLQTLCCFLPRRGCSH G*ESAATHPPGPPELVLLLQGH*AGYL G/DFG/PRATATGSPQ/PAGVQGPCLVPQ LSKRAAAAG*PDPT*GAIFS YHCKALRA LSAKHCPPGC*WFG/PAGSPPGTSRPLS HPSPPSPFWGVSSFFLLNLVLC*ASDA QGHACYPGPVRLAGQGHDSAGRLGDP GHHWQQAALHG/DQGPSPHQAHKCTPS AQQLGC*ATHPGEGG*VG YQQLPAG*GR SHPRFPVITRPMGRSPVATVRPGPGSG QGTPPGLV/PRGEAGONGPGAAPGLSCT QEVTVGRWNW*GKKPLGHYPFGCAVRCP S*S*PHDPTMFKGTGREGCLPPTSPGVGT G QMS/EGSRPCEWTLTMSPWGE*SPRASC AMLHFCGSRVGGYHGCPLPHHWGPQST AGAQGPHTLDIKAS
9928	23829	A	10001	1818	6682	IKFPFAEEEEIQEVLVLLFRVAEEKENF SRVGNSSQREYENQVVLYSI CNQLRYRNN L/RHVKKDERGYEELLNYSRDHMLY P YRLLDIMVKGFSITPFSYTTGIMENIMN SGHNFTAADCLRLLG IGRNCGYIDLMIQC RSSKKFPRKRTAGDLLPIKVEIAIEAW VVVQAGYITEDDIKI CTNPEKCATDKTV DSGPQLSGSLDYNVHSHLYKKGFTYLDV PMSDDSCIAVAPLEGFVMNRVL/NFDYF ETLLYKLFVSVDHNTVAELANVLEIDL SLVKNVSMYCRLGFAHKKQVNLQGL HSSKNVPSINRLKSLDP*KMLLSQGG GESRRFPVQEAASATDTDTNSQEDPADTA SVRSLSLSAGHTKHIAFLPDSLTAFIL MGNLSPVQSTGEGEAGRYFDHALTLRNT ILFLRHNKDLVAQTAQPDQPNYGVFPDL DLRCESLGLDPATCSRVLNKNVYLLVSM APLTNEIRPVSSCTPOHIGPAIPEVSSV WFKLYIYHVTVGQPPSLLLSKGTRLRKL PDI FOSY\DRLLITSSG\HDPGVVPTSH VLTMLNDALTHSAVLIQGHGHGIGETV HVPPFPDETELQEDSC\NMGVHKALQTL RNRVDLQHLGCVYVMTLNASSQLANRKL S DASDERGKPDLAGSGSDV\NGSTESFEMV IEATIDSATKOTSGATTEADWVPLELC FGIPLFSSSELNRKVYRKIATHGL*EKR AFKNLLHSSRKLSQLVNFVHSFQEGAS TLDIHTFSPFSSLLSQSSPADMGVPLPA KKFN/SLKIVSY
9929	23830	A	10002	439	1135	MAVDFFNFVTKLVVTTGYLRISFLAYKF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						FSFFFLDSLS/LLSPLRECSGVIPASLQ PLLPGFKRFL/CLSLPSS*GYRRAPPPC PALLYF*VETGFHVGGAGLELLTSGKL TRLGLPKCWDYR
9930	23831	A	10003	216	572	LTLVSIIFAKQSVTLPIICMLEMRKWL NDTSAP/PII*KVLPFKIFFFFFF*KG VLPFGPGREGAQGLTKPSPSGLKEIFL PNPFGKQKRRVPPFAGYFCFFIKRRVS LLNRGLPN
9931	23832	A	10004	3	354	YSNNPKDRKGEGTINKEKTNNKMDLSS YTSVITLN*ML*/D/KIN*KPVKSP*KK PTLCCLLETIFYKYGIGGLKVKRKKI*H ANTIGKKTLLVAILITKQTSLS*YPNKE EHYILIKE
9932	23833	A	10005	187	455	ASHYSLGVRICYYIPGCTHPGEKSKC NTCGKNSTQKPELVN/HR*LKGHRCKM* NEGGKTFTRVQSL/ACHKRVYTERKSYK C
9933	23834	A	10006	134	456	IWNLPGLGKCAWKQVTSDLISPDIAFIN AAIHSLSFFFFFETKFLVPQVGSGPWH NLN*LKLLPPKL\SDFLVA*VSKKVGIT GPPHHPGLVIWGFKKGGSPMLPR
9934	23835	A	10007	210	451	CYTTIOTTEQAPNDSMLGKIPHSILTL NVNNLTTPPKRLGVADWIK/TQDPAFCC LQETSLTCNRTHRFKVG*/WKKIYH
9935	23836	A	10008	169	462	YPCWVDMAKNTSYNKNQGGGEIRILPH CRWEYKMASPLWK/SQPLNK*NMELP*D LPIPLDIDPKWKTVQTKTCR/RMFI AALFPTSRS
9936	23837	A	10009	490	724	EMFP*FMEKNFLAPGG/VTPPGVNITRV NPKTAFDPKRSSSPFLEKSQKPLIEGL THLTKLILNPLKKDESGLPVLV
9937	23838	A	10010	306	588	KQFTRAFIEMSWLTPVPIVLWDTKADG SGIRDQPSCHGETPSLLKIEKLAGHGA GL*/SQLLERLRQENHLNPGGGGCEPR SCYCIAWTE
9938	23839	A	10011	473	53	YSLGQDSTDISTINIPMAFKLSSKRS HMSFSLNOK/L/EMIRLS/EAC*KPRS OKLGLLSQS*PSCSKFLKETSATPVN TQMI*K*NSLITNK\LKEVLMVWIKDQI KHTISLRQSVI*CKALPLFNSMKAERGE ESAKC
9939	23840	A	10012	184	455	FWLSLIIKKPLSSVTKKINRET\ILTT KKKKDCNFLEGLLIGGSVCRLVYRHY ATLYSVFCVDSSKSERGSVDTPQVFET *DKCFDY
9940	23841	A	10013	203	453	KEELYISREKRSSTSLLNQSQK*LILK SEOAMPNANIGDRLKARPLSPNSHLIKT KQKFLKEV/KCATP
9941	23842	A	10014	237	483	TLIRYIILQGLFSYIPFFHFETESRVA QAGVQW*DLGSLVPGSRHSPSSASQVAG TTGFHY/HAWLI FCLFCATGS
9942	23843	A	10015	157	875	DDPVKRGGEESAMPSSGGRNRSVSSSW GSMAGITITIEAVRKIQVLQHQADDAE *AEHLQ*EAEGKRWAEQAEVASVNG RIQVBEELDCAQCELATALQKLEAGK AADESERDTKVIEIWLKQD/E/EKMELO ETQLKEAKHIADEADGKYEEVACKLVII

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EGDMGCTEERAEAESESR*EMDEQIRLM DQNLKCLSAAEKYSQKEA*CEKERKIL TDNLNKSMPMR
9943	23844	A	10016	579	30	CGISTKRNKMKIKQNSSELSTCVHNGIT LHKIAMATQWG\KNSFNNK*C/W/EN*V ST/CKIKLSPSVTCTI*KOYLKWKIKYL N I K I * Q T S \ I S \ N G K Y D I G L G T N F L L Q K T K N L M S F S \ L * N Q M H K E Q I E K W D Y I K L Q N F T C S K E K F S G V K M S P K K W / D E I F E N H I E D R S * E S Q Y I N N V * N S T K S E
9944	23845	A	10017	44	228	EFVCRVRGLMW\CVVLASQLLWAEAGG SLBPKSLRLQ*AMWADCTPPW
9945	23846	A	10018	471	40	EGEGRFQCTRFPPFLPWPDPKGGFFPKK PKKKKKRKKMIKLS*KRQANQ*LCCLQ /TSQVNAKEKFLKEIGNATPVNTOEVR KLNSLIADIEFVLVVGTEDOTSHNIPFG QSPDIQINILAVFHSMAKAEQSKEATEBEF EARS
9946	23847	A	10019	217	486	KKIS*PVVLSVLSVLSVLSVLSVLSVLSI YLSIYLSIYLSIYLSIYLSIYLSIYLPV YLSINLLSI/CLSPYILTYHLSYLLS YLPTYLP
9947	23848	A	10020	327	1245	TENQOQVLAALAKSRIMMFRKLKFLN IDYTKFCBAFHVFKRKKKKINKINKQL KMPLTKRIYLAFTYSTQ*QONTH\FFL SADETHGKIE/HVLGPKTRHNKFKR
9948	23849	A	10021	329	490	GESPTDNHCPSKQVEKVIYITFFETES RSVTPAGV*KNCLGSLQPPPP\GTSDD
9949	23850	A	10022	3	394	YRVLEVLYGMLNIRFVVLGSSCGQAQ FREGRSCTTACRHPAHTLHAQMSRRKV SSAKCR*RETPKRSARMSAKPAP\QSE TKPKKAAGDKSSSTS\FSSSSSLKAEK GGKEKQAEVADQETKDLSAE
9950	23851	A	10023	448	477	SQVFETSLAS*MSKNIL/WAGTGAHTCN PSTLRGQGGGIT*SOVFETSLAS
9951	23852	A	10024	198	455	SLKTNRRIEPDPFHGQPGKLVHSEKPR VRMQTESKYASVLSFKVILRRGGVRA S/TRNLIMLFCQTEIQFCLWFPE*GTLDL KDW
9952	23853	A	10025	469	26	PBRAPVPPFLSSSLHITCVPLCKTVFSA TSRPDLSLLPAQVSAKMSFVL*SSLLLP SLGQCFPMASIAPL/PHRLSRCSVJA AHSRAELDRHEAFLOCSLGQWPRNDFL SFRRDRVLLCHPGWSTAA*S*LTAASNS GAQVMFQ
9953	23854	A	10026	222	489	KKKKKKKKFCFIARVKSNGAISAPNCLC LSGNSNYFPASTSLVSGNTGACPLARVNF FY*NL\FLVKMGFHHIGQESI
9954	23855	A	10027	313	2	QDWEISKLYSYCHS*VRRL/IFPKIRLS LYYILQHSNLCNII*QFESCYIKLAG DKIAFRFLTKTNHQLGLVAHANSSTL GGRDGIIT*GOEFKPSLANM
9955	23856	A	10028	49	388	TPKIRGVFFPFQWFLGVGFAFFPPQKDY FYFPTPMGTRLVSPGKCKKKEV*RVLY GLKKAKKIPVLKVKFSHKRFGFGEIQPK KLFG/HLKRNPFPKKKKR
9956	23857	A	10029	394	231	GRQIASAQEFKTSWGNMAKLCFLI*RRR VSPCCPSWS*IPELQKQACLSLPHY*DY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						RC/RNTTEGL*HLLFRCLLIILPSYLFCKSPKLLYMDI
9957	23858	A	10030	265	2	HDNMRGSDYFPASNGLAVPFKRQVFTIASNFLEKSPRLAPT*QVD*ERKWAG\ PVAHTCNSTLGGGGWITRGQEFKTSLANMPKP
9958	23859	A	10031	235	413	KAGKLFFFTEITFKKKGKAGGGGSFLKP HLPGRPGGGNHRVLI*KRIFYKMGKRV LKSLPCDSPLASQKQGVSRKPPRPF CPE*RLFP*KKKAFRLPIPKV*ALV/SLPFTIGEOKTLFFFP*DRALLCRPGNNA VAPSGKLKSSCLSLRS*DYKHVPPCLAMF*KFF/CRN
9959	23860	A	10032	167	424	GREFDLNRGMHVKPPLSFFFFPSETMSLSVTOAGVQW*DITALSASWTFVISDSPVSASRVAG\IGTTGVRHHTQLIFL
9960	23861	A	10033	252	3	VEGCLSSGVQDQPEQHSFETPSLQKRIFF*LAGHSMCL*SQLGLRLRWEHDHSSPGG*SCSEP*SCHCSPAWATE*DPISKKKK
9961	23862	A	10034	175	492	CPTCPFWNIFLCSEQPVQLYMVVHTHTHTHTHTHTHTHA/HLLFSLFSFLRQGLSLPTLWRSGLMI/CGSTQSQSPRLKQFCSPRYSRG*GWRMA*/DPGGRGCSE
9962	23863	A	10035	200	448	LYLHLVQLSLDFDPTPLFRVCECVLSLCLFS*FP*VCFFLVSLGLF*GRVLLCRPGWASVAVQSLTD/SDFPVLLKHSSCL
9963	23864	A	10036	229	463	MILGISKISFSLATITLANFPPTNLNLFILDGTGSCSVAQADVQWNNQSSL*/SELLGSSDPPTSAS
9964	23865	A	10037	164	422	GLSSQLTDGHLALLRVGGSEVSGREESEREAGREGERRDRSGG*REEREESGAREEREKKEKRER/ERDREK
9965	23866	A	10038	1	490	PNQIQNAVLIMISFSICFVSVIFFKSEITYNQPKFKSFFFF*DESCSVAQAGVQ/WCG/LQSQQPRPPG*SSNP*PTSASGVAGST
9966	23867	A	10039	255	446	FFLRQSCYVAQARVQ/YAHRCSHSHTLQLPALASSNPSALLAPRVAGTAGMHQHNGL*YVFRHS
9967	23868	A	10040	157	390	DHTCPFFSTADYRLS*FLYFLLLLFRSLALPFMLCECSGAISAHTCLCQVSTRETDAAHFAARTIRAPHPAQLTIAFVQVTHVYQDGH/DGSWWCDLRLTHPPRS
9968	23869	A	10041	290	30	TLKKRKEFSSVLCPRGYIVLLLLVHQFLFFQTGSCSVTQAGMQ/W/CDQSSLOP*TPG/SNNPPVSASQVAGPTGMHGHFLHTEYESRGP
9969	23870	A	10042	190	929	NHRYISYLTRLVKIKNFANKSWSLESLSPTLKHS*/W*CK*V*SLWKTVWHYLVNL\KDDLTFDPAIPFLMIYLIEMCAQVHPEIYARMFIAVLFEIFKHQ/NNPNKLWYIHTRESYKTIKIKE
9970	23871	A	10043	457	724	HFGRPQGVDCSSSGVQDQFGHQHVEQSVLKL/KLAGHGGHLL*SQLWRLRHNHNLNLRGRCSEPRWCHFTPAWTTEDQSV*NNNNNN
9971	23872	A	10044	111	429	KPEDTTGTRENYRPVFFNTDANLSKIKCMYPCISVH/HVNNYKIKPEMFT*Y**

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
						*LFLSFFVEMESGVPRLCESGVISAH CNLSLPASSNPPGFPFR
9972	23873	A	10045	30	220	LGVLVKKNSVFNKCYWDN*ISIWKMVG LDPYLTPHTKINFKNIKDLNIIKTLLIC CSWMKTKA
9973	23874	A	10046	203	361	TYKLLVIFIVIDHF/LFSFLSFFFRDRV SFLLPRLCESGAISTHRLN*LPGSSD
9974	23875	A	10047	198	358	IQRKCTFTFFFVEV*SCFVAGASVOYCG SPG/SSNLPFASAEVSKTIGVLLPS
9975	23876	A	10048	270	272	RKNQRFFKIAKRLNKMTRISPLISITII LNVSGLNFLPKRYRLAEWTKKK/DPIII CCL/QKTHFAG/RDIYRLKIKGWKKIFH TNGSQ*QRSEFF
9976	23877	A	10050	256	1	GVTITNLVFNKNFLNPFPLVKKCENCNPN KVFP*KPPLLKKTLPFSKKKFCGV/HPT EKFFPPFFESLALSPRLQNGTILAHCN LR
9977	23878	A	10051	112	359	SKVSEPTENEVEHNLKV*SFILPLKQY SM*QKKNIIH\ISFYKK*ELTWGMV AHACNPGRLGTAGRSPEGQEFETSLA
9978	23879	A	10052	346	2	FVSSYTLITLNLNKLVALKRYRRLNGF FYLKKP*PN\ICCIQKTNLIYKSTYSLK VKGMNHNH\HAGLKKQAEVAI/LPISD KKDFSKIVKRDKEGHYVMTKGSIQQ*D RTIL
9979	23880	A	10053	376	6	TRPSQHPDFILANKCLFEATPELVICY SGHRKLRVPVPPIRGSKSQIIPMPAVL PRWHLSCLSFRIPSSFF*LRLPLCKSR /SANGPVSPHLPQFLFQAISPPFFL*D GILLCHPGWSAVA
9980	23881	A	10054	102	347	FLSFFVDGKLCLEAKIHWLAPAVFTVIR VLLLLSTL/RQVELRNIVLCSNVHIFH LYFCIYLSAYILOQMSLY*HL*YHSNV
9981	23882	A	10055	251	51	ISLVNHLFLENMKLDVLSFYTKINIR /WQ*DLNVKNGTTKVLN*GTIVVMVG WKRPIALCQQPKS
9982	23883	A	10056	169	342	SQKQYSTCONVFCVFLFLETRSHLV/TT LECSGAIMAYCRDLPG*RHPPTAS*V DG
9983	23884	A	10057	1	586	AAARPAQGRKARPGLLLRGRVVELRAGF LTAKGAFRWMLSQKHVKMSYPPQSRGCG GGMGAAAGPPSLTVHQLCEGAYSPDGTTE ALPLASWPRARPSAKAPAYDTAKLPAL IGCGSRPPGVNPGASSLKPACVSEGA GPTGTLESAGSRPPTPLFPVPV/CCPGPP ARADH*FCHVTPOCR*/PPRPS
9984	23885	A	10058	393	43	HARPGAECERPAEGEARADAFSGRHAC PHSLYCRL*RGFFVHKHLNKA/RLIKR RKADNKCWQRCGAPGTLMH*WYETM GLLEQTQVFSFEIRSHCAAGVQRNNHG SLQRF
9985	23886	A	10059	228	466	GLLHGFIYDLPEFVSTTPSLYLFPPVDP *ASPLGFSAILTLPHSPPPA/PLFSPFP HSLVSGSGSPRLSP/SPHLPPLTPH
9986	23887	A	10060	293	9	DILQFYTFSPIQ/CFVYTLHL*YISLQR L*FHOKYLGIFYIETWNSCVARLECSG RITPRCNLNFPGPTTPTPSASVAGTTG VCDFLGLPWSR

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9987	23888	A	10061	199	428	TAYCR TLPLKKSNTPTSGSFFFFLEITGPRSVPG\RAGG\DLMAHCSFDLPGRSDSPASPRQVVGATGPCHHPWLIFE
9988	23889	A	10062	191	2281	LQTRGKLFYRKEKIGICTKLHRSEIITIGKQWKEAVCPPTGQAQSGGLDPKSRREALRGHGFVPVGGGVCGHQEL*LHSDGLKAVHPAGSEPSDPGGVQAAACQDAATGGTLPLOPMPETARGC/TATASSREAGPGMDP/RE A/GPEANQLGKARSWSGSSSTSGGPAMVFLRDPFSWGIPIGTVPSPAGRPCTPPTRPQWEOLOGSCRPG*MQTTAETNAAPRACQERTPSRGPSADPGVQHVLSHRRSCPKCERRSVPPNG\AGPTLTWELHPDSASVSLTFL*GDVEVPGY\CEGYIKPGRRTHQHNWLDLDRPAASRTRCKMLELPRV*FLLRLPELAETYSSTPPACAQRPRGTGGG/PQRCVLMGSGSHGGAS*KGDRAPSLGSGLERPREGGPGWLS/RQPSPHAVQPCCKHMLCLGPAF*RRRGARGVPVVRASHFPHGAANWPGDHMSQP*WQMSLRPARGHRPSWQVRRQCTVLGALKFGLPDLCKPGPTAFLPG*GVS/EENGQIPNVSTQLYLQNLPLPREQN*RRFPRLSSGGAGPGTG*CGGGGGHALSPTPSRRLRAHSDKNSWAQPLCCWMPAASGC\PGICNGVPPVAAS*QAA*TPPWSGSLPAG*QPSAHRCVTRVPGGRIPHLLAQAVPPDDRAPFNCQASGQLLGVHSHRPSLSAAGCRQPLAVSGICNGVPPVAAS
9989	23890	A	10063	65	453	ISREFLFLETKSLTILMKSGIQQEDITFVNIYTLMTGAPRY\IK*ILLELRQIESDTVIPEDDNTPLSALNRSRQK\VDLIC TIEQWDLIDITYRTFHTASEYLFPSAHGSPSKKYYMLGHKICLETFLN
9990	23891	A	10064	100	466	LGILFLQSRPSGPGGQCTFLPFWWSLFLPVRGCFPLHLCWCLPYSGALGPSCHTGLVCWHIPCF*CCGVSP*RYSCLEVHLYHTHTHTHTHTTRFVLM*MRTPLRKXKROVMRLCGGGGRA
9991	23892	A	10065	226	377	GLAGSPCISGSVFCSGGCIY\RGHGIMFICNDCKVFRFCKSK*NCFKHEHN
9992	23893	A	10066	292	458	KVSSICLKMSFLFLFFRTGSHC*KVSSICLKMSFLFLFFRTGSH/SSPRLECSGMIIAHC SLKLLDSSDLTASAS*VAG
9993	23894	A	10067	252	36	TGFNPLHFIIYYYYYYYFESKCSHAQAGVQCCDHGSLKQP\PSSSHPTTAP*VAGSRNAHQANSTAWPMVS
9994	23895	A	10068	56	481	GYLKNCHNLMIKLEMRSCVLMEQRK/WIY*DESTPGEDTNTVETINDLEYFINLVKTVAGVETVDSNFERGPTVGKIVCYREIFHEKKSPSMQQL\YF*KFPQQLQPSAATTLVS*QPS\SKQDPLSARRLQFTAGSD
9995	23896	A	10069	263	435	HFSFLSFFF*RTESHSVT/RVEGRGGISVDCKLCRPGSRDSFASASRVPGTKGISQGRG
9996	23897	A	10070	116	474	RGAGAGVSGRSSPPLSALFIQPPPHLS TPPPLETP/PPVLH*PLDLGGWGALLA

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						Q*RLPG*HSPKKKKKKKAPPPYK*GP PKTPVDPDPGPFLLDPPFLGWPPPP/VFL PGERPPPL
9997	23898	A	10071	159	377	KSHMPLTLNQKLEMIKLSEE/GLMSTAE IGQKL/GLLLPNSQVNAKEKFLKEMKS TSPGNT*TIKKWPGAVADA
9998	23899	A	10072	180	473	AIEIQLLSRPLCLNPSGRFPDAQVANIR VRVAV*GNPLR*VGPAEPEQRPSWGF PSIS/WDISPTWSSASPPGLSADCKFT CHYRCRALVCLDCG
9999	23900	A	10073	98	440	GQLNLKSGPYPENVGYYLPLVLINPLAQF VIYSTIFAGTLITALSSH*FFT*VGLEI NMLAFIPVLTKK\INPRSTEAAIKYFLT QATASILLIAILLPNNILSGQKKKKGR PF
10000	23901	A	10074	358	404	PCLYTYHLHNSNST*SLRLVSMIRIVT SNLHRTVPHSYPPPTQLSINLVMAIHL AGAWIISYPSMIAKNAWHLPOGSETPL IPILVIIETISLLIQ\PRPLAVRLTQNI TAGHLLMLHIGSATLAISTINLASTLII FTILILLT
10001	23902	A	10076	3	419	KKKKKMWCLQKMEYYS*KGKLLSHVT IWMDEEVMLS/EIS/SVTEQILFNST YV
10002	23903	A	10077	335	414	DKSPF/D*RFPLPNSNGFLVKMPDSVK RLPFFFFIFPFSFFFFFETESRSVT\RL SGTGLAHCNLRLPGRDS
10003	23904	A	10078	279	1	KDTQLPFIQFFFTGSCSVPEAGVQWCD HSSLQPPPP\GSSGSSPLS*VAGTIGM LIFKIFSRNPLNFFFLRWLSLSPDWS AVARSWFT
10004	23905	A	10079	397	3	KSSSLFQNLHWNSSYSHLIPTLGYIL NHGNQFDPDTL/RDKM*NFFCTIVCPHY ELPSLEQ/VSLGSLNYDTILPLDLFCK RQGWSEI PYAQDFMTLYQNL TICQT/P QNP PPPPKESSKVELDIDDPH
10005	23906	A	10080	281	1	IFLGEWGPFFPPQKSSFFPKIPQWVFT PPYRKKIFFFLPR*NNVA/HPKIFPKRPP PFFFFFFFFFFGKENCIFILLPKKEHI TQAPAWGFAG
10006	23907	A	10081	207	35	QENRRC*RGREGS/GTLHGWRECQTVQ PEWKTVMQLKRLNTEFFPYDLAILLGE FH
10007	23908	A	10082	2	408	IAPLHSLGDRARLRKKKKKKGKIRPL LALFPKKQVPSKKHSHFSGALMEP*P PPHIPFFFWKVOPLPFFFGTLEPPGP IGTKCLQTLGSPG*WDPCEPLPHQSPGR GGILIPGRKGEDDPSFRGLDPPHF
10008	23909	A	10083	195	2	ECKQRQGLMEVSRFRSSHEFFFTETGR SVAQAGMNH/DLSSLKPPAPG/SGDLR TSAS*VAGTI
10009	23910	A	10084	219	1	RLKIKLLKIITTTITDSGICSPKSKL* H/LKIQNMWLDKLAHAYNPSTSGGRGQ IT*GQEFKTSLGNNVKP
10010	23911	A	10085	364	413	KKKGGEGKPLKKER*KINGQFLVHTNF /RLPGLKYFF/CPPPPSKWLGRAPPPK GDFFFFFFLVFLVETGFHHVQAGLE L LTS*PIPLGFFKCDWYRRE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USNN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
10011	23912	A	10086	200	3	INFILLLEIFVLLIFETGPGCSIAQATVQWRDHGTLQPQPLGLKQAILP/ASAP*VP.RITDVHHHARLN
10012	23913	A	10087	154	329	FSLSDFKTYTKAAGHRGSL*YQHFGKP\RRTDPLRPVAVQDQPDQRGETPSLLKKKKK
10013	23914	A	10088	157	390	NSSEFFPPSCGAQ/KSEVKKSSGPHSSSSG*RG/CLPLLVSOGSHFLAYGSLTFVSACVFT*FFSMSCLVYQISVS
10014	23915	A	10089	305	1	KKRAQSLPFGKGRGFSQPVTAGDRSPRKIRKALGLQGLGLDLCTRTFPPTATG*TFSSAPPFG/YPPV*PTKKNTNLN*PTRIKIIRIFSGHEK
10015	23916	A	10090	329	2	RGFFPGLPFWDFGFIENLGGPKNLLKAEIMGYNFCVPPFPGLPLTHFFFPNPPF/CFPFTPSLGFSPNPDGFFFFF
10016	23917	A	10091	84	408	FFLSRVSLCHLGSAAVA*SWLSAASEKKGENKLPWGLLGLTFGGYRFKIIIFCLVGYFIYILFGEME/FSILLPGL*CNGTCSVHHNLPPLPAGSGSPASTSGEGGITGMRHRPLRY*YILGRWSFALVARAVMQWHVLGSPQSPSPAWCKRFSCNLRGRWYRHAPAPPSSLNIQKIILGFWLAPVY
10017	23918	A	10092	184	359	FQINSSVTRRSFVLAQAQGVQWRDLGSLLPFP/GSSDSPASAS*VAGITGLHVLGSHK
10018	23919	A	10093	298	386	KLCEK**ITPIRMAII*KKREGENS\KCW*GCGETIGTLVYCL*EYKMQVPLWKIVWQFLKILGIEL
10019	23920	A	10094	310	1	ICMNMELIKYQDFGRTIIRKIVYFWIFN*FGH*IRIY*NLRYKTCLM*RG*INLPQRSFKNLRKI*W/WPGTVAHAYNPNTSGRGGGRIT*DREFETS
10020	23921	A	10095	40	407	BHTHTTACEFGGI*IRPVD*MVLIISWL*HGTTTCMVTLGETGQKQPGISLIIFFFFG\TQSLFVPNGVHCRGPISAR*KLCLPGPPLSP*AS*VAETTGACYCTWFENFFGLRLPLHCY
10021	23922	A	10096	189	2	PPFFFFSN\FKKSYEQQLALSRLRCKRGIIA/HCS/L*TPG/YK*SSCLSLP\S SNNDRCAAPRV
10022	23923	A	10097	260	401	DHLRSGVD*LGQGHETSLLKQKLDG RGGLQLIP\RLRMHENHNLN
10023	23924	A	10098	187	464	WYMTKRCGLSPSSAAHSHHPPQQLMN P\PPSPSSAAHSHHPPQQLMNPTPL LSS*TPSPSSAAHSPRGVRPEPTGGAHGYLHLSFP
10024	23925	A	10099	397	1	FFGGACPPPPRRKCKTTPPPPKLFPFFF PKKPPPLPKNC*KNKPLLGPKKKNRPP PGRFFKGF*NPFKAPLTNFWKKKKK\SPFFKGVPFPPEKPPPPPPPPPP FFFFTDPRVRPRVRPRV
10025	23926	A	10100	253	3	NAINRNKMQ*TKTSEKVIYADHNATIKQ KQKRKCQVL/WRGCGETETLVACWECQ MEQAPAVEN/W*HFLNENIKQLPYDPAI HE
10026	23927	A	10101	121	404	VLASVVSIFPPFFFNKGLIFSPRLGEGG/LILG*LKPPLSGLGPPSCLTPEGWE

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						LKPPFPDPGFFFF*GKTGPRGGQEGLNFLTWEPPPLAL
10027	23928	A	10102	468	1829	IRDTYTONPDKAGYFCISFFIEETIMSRKQNKQDSSGPIFDLQSNVLAQGGAFENMKKEINAVRAIVPNKSNNEILVLQHFDCNVDKTVQAFMGESAEVLKENTVTGKKRNNKKKNKPKPAAEPSNGIPDSSKSVSIQEEQSAPESEKGMNGYHVGAINDTESVDLSLEGLTSLIDARELEDPEASAMLDMLDRTGSMQLQNGVSDPETKSLTMHSIHNSQQPRNAAKSLSRPTTETQPSNMGMEDV/RPRHQ*KS*VP/IFEKSVKDLQRCVTSLARYRVVVEENDASIKMKQAFALLETLINGSRKWALLLMDKVKYAEPLLSRQKKAELLKMYTHAVQMSQQQLVELRADIKHFVSEKRYDEDLGRVARFTCDVETLKKSIDSGQOVSHPKNSYSTRSRCSSTSVSLSRPSDASAASSSTCASPPSHSANKKNFAPGVY
10028	23929	A	10103	254	2	KKKDFPLTFLGFGGLKIQLEFFLQKKKNFYFPP*IFPKIFFFFFWGTQSCPVTLRLECSDRIPAHYNLHLQSSSHSRASVSH E
10029	23930	A	10104	256	419	KVIELHTGR/CAVGQHVGRPRRVDCLSSGIGDQPEQHGEPLHY*KNAQSSQAW
10030	23931	A	10105	153	439	TTVTSLCIYTYTYTYTYFRLLSHAYTHIYTHIYV*KLTIKQPAQGPSEG*KEF**RRW/VWGTVAHTCNPSTLRCGGWMT*GQEFETSLANMVKL
10031	23932	A	10106	424	157	SSHGRPRWVDHLSPGVDPQWQHGETPSL/LKLAGGACL*SQLIGRM/RLSSGGRGCSEP*SHHCIPVWETEQDPIISKNQITI FRMFKN
10032	23933	A	10107	213	3	NYKCPPTPNLNTLKALYFKKLLSPKA*AKEKID*/IIKIKHFYASNIINRMKRLTEWKKIFANHVSDBG
10033	23934	A	10108	300	1	TPKQRGKKGSPREKFPFVNLPQKTLF/YEV*FNNPLK*QKKKNQGFFFFLICGTVHQPTSK*ERGVPQTVHTCNPSTLGGRGQWTI*DQEFETSLG
10034	23935	A	10109	120	421	KYIKKKNNHMITSIDAE*AFQKQHRFMKTLNKLGPPEGHI/KIMKAIYGRGGQDQLHTAKK/EPLPRENKISGKP
10035	23936	A	10110	102	418	TLVCVCVCVCVCVCVSLSVFSLSLCLSQAGVQWCDHSSLQPRPSG/SGDSPTIASVVGITGVHCHINPTFYFLFLIRLKSMLL**TSSEMALTKMGVSHGLEFN
10036	23937	A	10111	382	2	VNNATMPSCRCTSKSHMSLTSNOKLEMIKLSEKMKLAKIGLKLGLLC/QVSQVNAKKKF*REI*NPTPVNIR/DMQKVLV/VKTEDQTSNHIPLNQILIQNKSLTLFNSIKAERSEAAA*EKCEDSRG
10037	23938	A	10112	61	427	ENTYVQVCSIKEEYLQRLTKYASLFQKHICGSLAFLLH*PKLYHSRNSAESDWIQLFVSQPNVKEISKHIGW*RGHACN/RQHFERPRHKDHLRLGVRDHPQCHGETPSLLSLLKTIH
10038	23939	A	10113	71	399	NVLGKEARSVGVEAVRGQISRSVIQMKW

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						KGLIKGEKLMKEKSQACICYPFFFFETE TNFIAQAGQGQHDLGFMPPSPG*SDS PA*APHEQNG/L/TGMHNPRVIFV
10039	23940	A	10114	362	1	SKKKSWGSHSGSKCHTSFLSYPTKEOKS YLSLFYKCNQLQSLTFKELLDFRFPVCLP TIY*KNWNP/RDLPLKFSFKTLM*NOT L/WPGVVAHACNPSILGGQGWITRGQE LKTIKANTVK
10040	23941	A	10115	314	3	WRERRCGAHLMRCSANMAHDKPSPRLNL *KPKMAT/RNTDHDNF*GHGETEILNH YWDYKIM*FLWKT*QPKMFNIKLPY VSYIQLLGITYPRNLKINIHTKT
10041	23942	A	10116	44	394	RSQQRVSGQGLDILTS*SAHLGLPKCWD YRHEPLRPAGIYVPAVLELSTVRASN IT*MLWTKPFTSG\VSPLLSFRFSFSY LRDISAYMSLSCLKNVFKSKPIIFLSP LWLLV
10042	23943	A	10117	398	3	MESCCFMGIEFLVKEEVLIGCRIM*TY LHY*SLHLRMVMKMTISLLCVPHN*TI FKSSVFLYAGNKQL*1*ILKNYIVMIP FTITSRNKRNNTKDGKDMSTETIKTQ LKEITD*NKWRDITFMHQN
10043	23944	A	10118	104	386	KVPVWATCGVMHRLAGHGGWRWLRLP WRLRRDNLRLSSGSRGA/AEILPLCHCT PTWTEHDSITYK*KKGAPCWRASS* C/TLSGHALFFFA
10044	23945	A	10119	258	401	VNYVFLTCVMKEKIGAGMAAHACNPSTP GGRGG*\TRGQHLETSPNTMV
10045	23946	A	10120	310	384	GVFPFLTFLYGGIKGGFPFPPFFLF*FA FLFFFF/ETGSHSVAQANCSGSVAHRS FHLPGPGDPPTSAS*VTGTGICHHS
10046	23947	A	10121	245	479	TSSLYRKIKRFLMYLALVILKTCNTYF MNTERFPLKLGQFS/FRIISI*FPFPL FPKIYHYFLRDRV*LCHPGWSAV
10047	23948	A	10122	268	469	NSVFWLGVVAHA/W*VNPSITLGGRGGW ITRGQLETTPANILPP
10048	23949	A	10123	221	423	GQAGAVAHACNPNALGRPPRDSLRPGV GDQPGQHSKTPSL/LKSDNF*KMGM LGP WAWLTPILPALW
10049	23950	A	10124	73	183	AGGGWALTNVINPT/APSTPTPTCLSY SCTISTASAFRPPG/SSTAVLTHVRIL KSTPDAPHPPLKTPRARNIQRDHTLSS NLFEYNHQLNVTETLYTDLT*INPTAT IHAHNTMPLLLHLNLCIS1
10050	23951	A	10125	342	2	PNLGPCCPPRGTKGGFPFSSHPSTIG PNPFSS*RP*FF*MLKSLGV/PTGP IPKPPFPFPGKNYSPPL/PKGPLKPP RALFFFPFGRNRHVL\CPGWSPTAGLK RSSC
10051	23952	A	10126	85	442	KKVINIKCW*RVWETGSLTHCSWG*KMM PHWRAVQSF/SLSMYLSYEPALPLG SYPRALRTTCVCHSRCSLLELPQA/W NH
10052	23953	A	10127	180	484	KSFFFFSQSAQPIKVIAPF*NFHFFGVK RSSCLSFLRKWGPWVPPPPFFFFFL IFVEMRSHYAAQAGLKLASS\VPSPG IPRTL*SYPD
10053	23954	A	10128	376	1	WSPGAQLLFISCLYLNLSLHTRGTPAK

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						PF*GWTLQKTTPLSCFAP*LPPPLFSPL QOIDLKELVFTAPACSL/PHSPNSSPW PQRRWFSVS/P/PVAHPAARLP PPPVC ARPLWLPEAPLLGIPPH
10054	23955	A	10129	140	454	CLIRSSINSVHNNIYIHSTPDRHLGCFQ FLVVTKNAAVSRLAYVF**I*IPYDHI HTHTPAGYIPRHGIAGSQLTNI NFSS* LSSNSF/QVGCTSYELFPSHI
10055	23956	A	10130	340	473	AGARHSVLRFPPPLAGSSCPSS/CGGHC VALGVS/CPGGGCRACVPGCCCLGCLP SDVCVC/SVCGGSGMSRLGGWAAPGF* GNSREGPGNCGSSGRKAGLAGGGLGPAWA EQAPDILCCGPGFHWLGAQVPLAPPL SPPPCLYOCLYSDRGDL
10056	23957	A	10131	280	2	DSLALLPRLEYGNVNAHCKLKSSWIR SSHLSPKHLDYRSMSH/LPGL EIF*YS YCK*CLTSPYFELMNSLEDISSCFPI TRVMPKCRMK
10057	23958	A	10132	244	3	IISTDLISHSWTLYLISLVVFLKQHS LAVLPRKDCSGMI IAHK/KLQTPGLKR/ FL/CLSLPST*DYRHTTPMRAHYFYIYF
10058	23959	A	10133	272	3	VGKPRVPFYRIAFNFGVTSILGPHIKK YHFQCRGGKHCFF*KAPPFFF\FNETG FCSVPRLECSGTI IALCSINLQSCNSP TSVSQV
10059	23960	A	10134	217	3	FPFRPLVPSFALTELQGF/HFLTRGL*K KKPFPLFFFFSETESCISIA/RLWGS ISAHCNCLCPGSSRTRG
10060	23961	A	10135	229	3	KNDYLKWCQCGRTETQMLGCWDIK/LI QP/LWKIIWQFLLLKLMHLLCNFTPLPL GIYP*EMNVVHTQTCTCDAW
10061	23962	A	10136	84	352	RREFKTGLATWQNLVSTKKYKTTVRYHL TSTRMDIIGKR*QVCW/RKC/GDKGL LDC/WMRMLVQPIINKIV*VWKFCKR*KL NLFFPPPPQ
10062	23963	A	10137	280	2	KCVVPEERILEKRSQHLGKIKQEGRLN AVVLIQPGQHGETLSLOKI/QLAGHGA PLRSQHLHRRMRREDHLSPGVRSRSEP** LSLHWVTEQ
10063	23964	A	10138	2	386	HICEKOLFNKDSLTNPYFLGISILRRKD EKIQPKSCXMKKRCSTSLVIREMGIKRS HFP*VGKILKSANIKRW*MCRRGVT ITC*TYKTLYLKF*RIILQHPLLK THOSYYPAPHLKETA
10064	23965	A	10139	229	1	TRSYHESLTILTHNHLNCSFFQATTF *SRFFYSNRA\WLOSVAHYTNFSTLGR GRNA*QGEFTSLGNLPK
10065	23966	A	10140	261	429	LSHLEHVALY*IGLVN/SFVFEVFTGS LPRLECSGVITAHCSLDLGLSLPTS A
10066	23967	A	10141	377	34	WVGSSGPPPPGFKFFSPPPPKNNR GPPPPPIFFFFCKKGVSLFLPGGGP /HFFLSPPPPGVKPENFFDPGGGFP* T KIFSRPPPPGQKQNFFFLKKKKKKEHO IKR
10067	23968	A	10142	208	424	FFSLFMQTFHIHIRFYFFLAGGGGAGVD RVS/LLSPRLECRDTISVHCYHLPGSK QFSCLSLLSN*NYRHAP

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10068	23969	A	10143	1	297	PTRSQVSNLNHKS FIFSYFLIDLLSVC LSVSVYPETSLTLLPRLECSGAITTHLS LLSS*GHRHAPPCV\FVETRPHNVSQ SGIELLSSSHLPTA
10069	23970	A	10144	185	488	SGFPRGTELIGAVCVCCVCAVCVCIK LGYI*NNHRYIY*LLYISTYYIFNLSL *LSV/SVVRNS*DRSQSI*IFILPK LKTCLENTHTLKNTHCCG
10070	23971	A	10145	283	3	LQWQKADGSGKLTIDYGRDLKLVSF/ I*SAISDMASTTKAVLQARDQVSVLDD AHAFESIR/NOSQSFIRDSPOYAFTLP SEEHLNSLDGQ
10071	23972	A	10146	146	380	CFLWDNPPFFIFTEKTGSCSIAQAGAGT Q/WVGIIISYCSCLKMGSRDPPTLSCV A GTGMPPHQAQVIYFFIFL*ROGL
10072	23973	A	10147	275	3	IKGMLKAKTG*KLGLLQ/TSQVENAKE EFLKEIKSATPVNT/RMIRKRNCLIAEM EKV*VTILDQGTGHNIPLSQSLPQSKCLT LFNSKKAER
10073	23974	A	10148	281	2	KIFLPQPPQEMVFGQFAPPGG*IFLVF* *KQPPPLGRFVFK/LPGGIPIFFFFF FFFFEFETESHAI/RLCSGTISAHCHL RLSGSDPTRP
10074	23975	A	10149	413	139	SLRWPIFGLLOANKKFFWILFSL/IR PLFFFSRERGTPLFPPFLRNGKKS F PPG*PPPPLKIQFPGKYFTSRPAFFFF LFCQPPGKNLNYWGLGPGPKIPPPPPL FFFFF*DRVSLCRSGMSKVARS*LTWKG AFPTWVS
10075	23976	A	10150	100	431	GPRLTDHLRSGVPHNPQOGETSFLLI/ HNYSGG*GRKIANRLNPRGGGCEPKSC HCTPSWGKKRNFVSKKKKKRE
10076	23977	A	10151	134	417	GLAAPLVG/WGRKNPPPP*PFG*GEXTGW GPHGKIFLKKKLLFFFF*KGGLSFPP GGRERAHFWLKKTPPSRKEILPPPPR RGCGGPPPPFL
10077	23978	A	10152	403	2	LAFFILQEVQCFPCNLLHSLRMYSSTGS KLFPLASQPM*LYMHTLAPNILEE LQSPNTALLKYL*EALKKKSR*HITS SL*KVDLSFLETKRPIA/RLCSGTI SAHCSLRLLPNSCATASQVAG
10078	23979	A	10153	382	297	GLN*ESWSGERGT/L/HWCNECFVQPL WKMV*RL
10079	23980	A	10154	209	15	SSPKF*FFFLSKKILPLFFF*PIFFFTK TP/HFFF/SFFFVCVSGSHSVPRLECS GAITAHCSSTS
10080	23981	A	10155	153	422	RTSGKNGNRGQILVMTVNTNLFSSFFFF PLKTGPHFVIOAGGQGRAHGLQA*IFG \SGDLLALVSLQAGTAGFHHAQLSFFF KKTGLF
10081	23982	A	10156	257	3	RRLQNSKDCCLFFPLEAPRGATARCOPE LSCMRCLSA/LLGVSQSGYMGVRDPHK EAV*PLAELKR*AGRSSAPFKAVRQGL S
10082	23983	A	10157	37	386	DATRFINSVGTAEGLDRIEPNDLO*Y INLVGTAVRRPDRIENFESSTVGKLS NNIVCYRSFFCERESLQTQTSMLYFK KLPOLPOPSAITTHL/SRODPPSARRLO

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10083	23984	A	10158	407	272	LGQ HKGGKRRERKKKKKKKKGGREKGGERRK ERE/REKKKKKKKKKKKKKKKKKKKKKK LLSN
10084	23985	A	10159	248	478	VKVVHRLLLDPSVEDPFWKSLKGLQFP* /RL*IFF*NSGLLCHPSWRAVAQSRFT GVSTSAQAALFSPSLPSSWDV
10085	23986	A	10160	458	129	GFSVLNLEDEDLRQENLLMF*VDPG QHSKTPISTKNMMPAGHGGVYP*SQLL RTVRPEDHLY/SNKPCSYLCAPAWATET LSLKNFSCCSNHYGLSFQTSFIRILMF
10086	23987	A	10161	82	291	YSKTKSLFFAGHGCTCIYSQLFRRQVOV RQEDHANPGV*GCS/DTMIMPMSHCTP AWAA*DPVSKKKK
10087	23988	A	10162	6	409	LRINILPEPISLSPLTAPAVFMPWNTYS SCDTFSLASMTLLPLHFLSTSLALPWSL FLAPSLFQISKHQLYLSFVLLTSSCYF LMPCFRNHLLNLRGRQANLRSQV*D QPGQGETSL/LNKTKTPWW
10088	23989	A	10163	249	415	APPECSLPLVLLVLLVLLVLLVLLVLLV GGPG*GCSEPKSYCHTSANWTR/GDPVS
10089	23990	A	10164	1	405	RSEWRLRQPERQSETVKKKKKKGFFFFR GGGGKKLFGLMESPSSGLGQFLFTPLPE NGGYRPPPLGGGFFFFFKKGGPPLCGPG GFEPALOTPLPLFPKGLNFRGGPTPPA RFFFFWGVPVSFVSPKN*NPVPFRGKNG KNRPKKKKKPGRG/WGPPRRFNPFGNKR GGVPRAGNSKPPGPQRGNPFLKKKKKG PPKGGGR*PPFSRGVNKNKCPKEGEGS INPKIFPPPPPREKKKKKPPFFFLTYSLC RSGWRNLHSL
10090	23991	A	10165	175	404	ATKMVVIQAVPSQCLHGVGFLPRSVCV KTP*NRHRQGVVAHGCNPSTLGGRGW I/RQGEFETSLTNMVKP
10091	23992	A	10166	317	2	PFKNSPLLNMETNIHFLTEPTCNVNVNS PFLK*HKFLFF*EMESCSVT/RLECSVT IIAHCCLLKLGTSNPPTSASWAPGMIIG MRHCPAPVKVCSHASAHASAHAS
10092	23993	A	10167	325	2	KMGKQGHTFKKEIRKANKHTERCSRL AIEEM*IKATVTI/RKHQTKC*QG*RES GSLVHG*KKHIVHPLNKLILSVSYKTHG SIIIGYSSVLLGTVLVHSGSDAW
10093	23994	A	10168	245	3	GEPLFCFPFKPKVFFCFPFNQAVFFL ETHRGFFEFFFL*KKKKK/LGLVAHT YNPTLSGRGGQIA*AGSFT/LGNMS
10094	23995	A	10169	164	1	NMKMSQYTFPVKN*QWGSVAHYNPS TLGQQAQIT*AKEFETSLNMAKPC
10095	23996	A	10170	214	419	LS*PPFFFGFKKFNRLVRFYGGSKPGP /FMFVALQKGGFFQNIIPPVKLEPFP PTILRVSEFFL*DGWVLCHPGNNAVA*S QLTASSTSRVH
10096	23997	A	10171	168	1	WTWMLFPFGSITNNYKSHFSSSLHLATW LGTVAHACNPSTLGG*GARGQEFETSLT
10097	23998	A	10172	139	3	PAH/CES*PPGLKRSYVSLPFG*DYR/ HTPPH/QLIFVFMVEMGFHQPA/SA/FP KC*DYRS/DHKKWPT*HLK/SFHFICK* N*LKRYLACSLRWLYFCLIRCMV*NL DLSILYLHLNKFQPLFYLFEMES

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10098	23999	A	10173	253	2	EPKIKCNFLPQISTORGLLSLPTTIFLLSLILLRPFFFF*TESHSVPECSGMI SAHCSLRLPGSSDCASAS\QVAGKTCAR
10099	24000	A	10174	300	3	GRAFFFKGLVKUWFLTPNPIPLKLNFLKRVFFLPADSEKFFVFKWNP*LSFLIPG EKNNFFFFFSEMECSVA\RLBCNGM ISAHCNICLPGSSDSP
10100	24001	A	10175	117	381	EILRYIVSIRIRRTNLKPOQELRVNIKNNLSLGNMVRPRL/ECSGVITAPTAVSAPGK*SSHPSLPSSWDHRRAPLHLGDF FLIETRSHHVAQAGQVIFNVYSKFLLLKFKISPDYPRNNISQDFLAIGPTNMVPL QPYIVLCACRTKNKIIDLSEQSSRT
10101	24002	A	10176	194	412	TLKNLLLSLHCLSPVPTDLYOPERLSKPPRAKKYKFLIL/WLGVVAHACNPSTLGRGGWIT*AHEFDNLTK
10102	24003	A	10177	100	339	VPVKSLLLCVCVCLL*RI SDHLP TLYANLG*CFSSYLVISYS\NSTYCI LQRHLAIQKOP/CSFLRQ/HLVGLWKKKHTHTHTHTHTKSNTHTHTKSKDLTGQTNTTEFLK
10103	24004	A	10178	229	2	KEKYIKSKLHFEARHNGSHL*SQHGRPR RIMDC/LVQDPGKCGENPYLQKNTKIS QAWLWVPVVPVYSHRASKTLS
10104	24005	A	10179	368	2	SGSSPSTSPGGRPPDLGLFSAKIVLGLQATIPLPCLCLLKI FHP LTP LPLLLGGE FNLSPOQODSISLWFLCRYGPTYKAF FVY*ASVPEKI\FFFFFF*DTVSLCHPG WTTVAQSRLTA
10105	24006	A	10180	398	1	QNIIMLYTINTYNFICQLKKKTIGWENF FENKWC*ENWIFTCKRKNLHPYLPYTK TNSKKWISLNL/KSLKVNRRGNLHDFQF GNGFLGDTKSKTK/AKISKLEFIKINVF CVLNDI IKKVKRQLEWKKYQ
10106	24007	A	10181	252	419	GARFKGSNFTSAGGQGITFFMGPFKLIS RPVF*HRGEGKTPGVTLNRLLEHPLFA FCWYINSWLYGLFFFPFTLNILAMCGG SCL*SQYFGRQADHLSPGVDRQDQGV GETPS/LTKISWANHVPVVPVATQEAEV GGSLEPREVK
10108	24009	A	10183	2	377	PGQVDCFSFGVDQDPQYGEILLFLKLQ KLGGHGG/IR*EDHLSLGGQCKEPRLY HCTPAWTEQYLVSOQKKKKKK
10109	24010	A	10184	140	3	DGVLLSLPRLECGATSAHRN\SPSCDS PASASQAGCCGTC*SQL
10110	24011	A	10185	364	3	SVCPPRLGGVSGSGDMVRDPFEAAV*P LAELERCAGRSTAFRAIR*AHLSLLK\ FTRNHPFPHVPCPRVMSR*FGLLPFFQR CPAQRGEIWRSLAAVALRSCGRLQVR TCWQLCLHR
10111	24012	A	10186	2	249	SVRLNNKNTQIRNNKGDITNLTEIKR IKEYSEQLFANKLH/SLDEMNKFLER* NPLRPGAEAQRLVS*RFWRATAIDHMRP
10112	24013	A	10187	270	2	FWAQRCGVFKTNQIFPFFFEIHLID*F CVFORPS*FVRLIFIGGGFKPFFFFF FEMKSCSVARLECSTSAHCNLRPLGSS DSPASA

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10113	24014	A	10188	428	28	PIFDKG/E*GN*WGKSKIPNKCWEKCI C/KKLDRSSLTSTY/TRINKWKIDLNVR TK/STKLEENIDIV/IYDLGLGIGFLD MTLKARATK/AKIEKLDKIKGNFYASK DPKKMKR*FIEPIQGGKIFTMHVSDSTS I
10114	24015	A	10189	85	243	DRVS/LLSPRLCESGMISAHCSDFLPG* SDPFTSPVKSSWNYRCPARKLSFT
10115	24016	A	10190	96	440	LQSNHINTLNVRNLSNKKRFRSLSEIF \KKGHPALCCL*ENYKDKGTCTLKIKG WKNIYHANANNKKT/GMVLLSGKIRLES N/TVIRVKEG*LVI/INGRLI/QEDLIL LFILNVYAP
10116	24017	A	10191	137	423	AKDLDQFSKEDIHMTNRYMKTC/SGRQ LIRETQIKTITMRYPLTDLRKSDDKKS ***YEQKGTFAHC*ECKLVQPLQKIT* TFPKLLKINL
10117	24018	A	10192	221	72	AKVK*VVVFCFLFF*DGVS/HVVVAQ ECSGAI SAHCNCLPGSSDSVRVG
10118	24019	A	10193	460	121	SDTKRY*RCRAKRTLTTHF*LKSKLVPL L*TTI*CYLAKLKHIVDSAIPL*DTY FR/E*FCICAPKTYSMNVIEALFVPANG TSKKGNWK*LSCPQIVNPNLHLMKYH LE
10119	24020	A	10194	393	2	ATMPSYQRLLLTAVHELESPE*MDGFLD TYNLPFRNQEIEINLMSFMSNEIQSVI KCLPFGNPGNPGNGFIEFYHTYKEE/LP ILL*LQFKIEG\ILNPSFHEVSIITLRK TDKDAT*ETHKPISLMNTDA
10120	24021	A	10195	3	353	EAAPMVKRFFOLLEPSGGPGLMSCLGD CNGYACFSVSLHQSANOSIDO/SIYQSA IHLLIY/VSIIY*SI\YLL*SLI*PMY VPIYPLSCLSIYLSFMPCLSLFNNLSI TRHGSMLC
10121	24022	A	10196	118	395	DFNAGLLPSYQVLSLYFCF*NGV\CHCT P/RLGDRPLRL/PPKKKKKTPPPPLGG SPPGGEPTTPRPGVGGPPPPFHEHPREN PGCFHPPPKAWP
10122	24023	A	10197	437	160	FGYPRVFPLPALLKRGPGILFWGNPKN YSSPARGSKICFFKRGPPFFFFFYFF* QTESCFVAPVGQVQWCDHSLQPPPG/S SGPPPPSTS
10123	24024	A	10198	259	3	ROGNHVTHVYSSRLQLLSPASLAVFI QKIYVNLCTYIHIVNLVYA*MCICVCICY GS\ICIYGLVAVAHYTNPTTLGAKLG GS
10124	24025	A	10199	1	416	IISAHCNLHFPSSWDYSRTPPYANFCI FSRDRVSFCWQGV*HHLEQHSKMLSKK* NKIDMFGWCL*S*LLK/RAE*DVLRGE NCLNPGGRCCEPGSRHCTPAWTRAKT LSKASYASSSSSPKKKKKKSPS
10125	24026	A	10200	369	3	TAPFFFFCRDGLRTSLTIFPSRATDYS LVTSQSFLPAGAGRGRLSLIEIRVLDLVO DGCPSCSOAWAAALGGPGWAPPLCFEFT ASCSVAQEGMQ*CNLGLQPPSPG\SSD SPASVVLNTSK
10126	24027	A	10201	314	2	LHMRPEV*PTPSKIGVTGYMWSINISY WRCAHAK*SQVLVSLRKHFLPPEMESG

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						SEVQL\DTNRCISANCFCLPGSSNSPT SAS*EAGTTDSRQPDADAWADAW
10127	24028	A	10202	68	413	KIGILLKTH*PSIC/VSTINF*YNDTGE LKVKG*KNIYYANINQK/KAGMVMFVLD ETDFRACK/DYQGH*IMIEVSVHKE/E/LVILNLAYSANRVRTKYM*KDIDIKGEI DKSTTIVGDL
10128	24029	A	10203	351	1	PKFPPLNPAWGTTIKIPFKKKNAHNWFS PRKEKALQIKHKG/RLLAKEISFLGGF *TDYKTNPDSSQSI RTLGEKKKIRPGTV AYAYNPSTFGG*GRWIT*QBELKTS LAN MGRV
10129	24030	A	10204	2	392	FLSGVLLLLPRLECNGAIPAHNNLHLP S PRFKRLSCLSLSPSWDRHAPTRPANPV FLVETGFHHVGGQGLDILL*SPCLGLP KCWDYRH/DHHAQSPF
10130	24031	A	10205	264	2	FLSLSNLEPIPLNSTLKTFFILK*L*TH GKHLKMYRKV/LV*TSPPSPQC*HLR*V *HNIQNKKLMGLGAVAHANPSTLGGRG GWIT
10131	24032	A	10206	281	2	ISPPPLFLFSPPKIFFFSQKHIFLGEPL FYPPPLFFSPPP\PHFLMGFRPVNPMF KIDPQTWAKNKDKGNFPDPFFFLPFPK KNIFPTKYTFGGPPPLPDPFFFSFPK KK/SYPPFLKNSPNPPPS*K*AAISLP PFFFFFFFFFFFSFLENTWMADAW
10132	24033	A	10207	340	1	STKKLVQKLGEHTQCWQCEATGTLHC RWECKLVQPLWK/SANQILLRL\NFMHL PYNPTIQLQGSYSRE\QHTCPYKDLVVA ALFTIAKNC*QAKFLSTGE*INKLWCIH ITE
10133	24034	A	10208	136	3	KNRGPPRSRGKFFFLPLPFFFFFF*DRV \YPSHPGWSAMVPSOLT
10134	24035	A	10209	327	2	INKRYEQLYA*KFDNLDEIYQFPGRYN LPKLTQEKANLNRPVSLRETKSTINNL PKRKVPDPDGTGELGYOTFKEITP\FS TEAKGILPNSFCEVTIIVRLFLRLQ
10135	24036	A	10210	89	485	EIVPLLRFPPLVFIASPTTFYTVGVSG EKSYQKKREKLCDKTLEQSRSLIGMHST CGIALHFKKEGGMCTLCACFY*FPLKES HBARAGQVMHNLSSIQLPDPSNS
10136	24037	A	10211	361	462	IQQIGSNTGNTAREIALKRNSTNRL AGWNGP*VFAC/PKNVLFYLHP*LGQ* I*YQLKITF*NYEGMVP/FVERLEPETR SLLSPRLECSGTITTHCSLELVGSINSS ISARAEFLQGANL
10137	24038	A	10212	62	469	SLLNKLSSGASTSLRLCSLA/LLGDOVSO SGYTVGRVDPLEEAVCLLSELERGARTT ALFRAVRQGRSLSEKL/LLPFVQICPAP GGGIYR/GQ*ALLSCGGLCPV*AS**/M CLPC/EA*TRLLKPPPGS
10138	24039	A	10213	197	1	VVTQPNNEWCVTKNDASFOQRCTKIKT/ WPGMVAYTCNPSTLGGRGWIT*GQGFK TSLANMVRPH
10139	24040	A	10214	31	213	HASLDEGFHHVGGDGLNLLTS*STCLGL PKCWDYRHP/PAPNWWKFLSSKAFKR *LGCV
10140	24041	A	10215	442	29	PTINPTMACCKLSKRKSHTSFTLNQKLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Value, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TIKLSEEGMLKAEAG*KLDHVH/QVSQI VNAKEKFLKEIKSATSLNI*MIRKQKRF IVNME/KKVLMEFWTEQTSNHIPLSQSL IRKRP*LNSLKAERSEEAPEKLEASSG G
10141	24042	A	10216	195	533	LWNFWLRVTVGVAAKMSSGTTIIGRLSW GWRLHF\KMAHL*GYWWEASVPLHMKLS SCHGTG\SLRVKDPRERLRQKLQCFYDL VLEVTVWHFYCILFIRSKSLSPAHIQSK RI
10142	24043	A	10217	274	494	CVLKGLPFALPWFFFFF*DKVSPSPRL CSVAI/SAHCSLNLGGSDPPASQOLA GPPGLRR
10143	24044	A	10218	142	480	VTKRIYLIHPDHTTTLPRQGGSRLEKILV SY*QOKVETRPSHVIFFTVISTQFKKTV TTRSGAVHTCNPNSTLGGREGQI/T/RG QEFETSMTPVK
10144	24045	A	10219	163	464	AVYFSFWRVCEHDLASLYFENSQGRDNK FVFLVLQAGQPAWRQGEVHKHLLPCVYH FAPVVLQOQSGFF*DG/QSHSLAR/LE CGVVISAHCNLYLPGSSNS
10145	24046	A	10220	379	469	V*KVQM/WEGKVAHTCHEPSTLGG*GGWI T*DEFFETSLADVAKPC
10146	24047	A	10221	211	473	VTWLLLFSTFRASSLSTDSVSVVIAFG FYFYLFIYFLFIPETESCSVA*AGAOW CDLCSPPPPRGS\SEEPSTLQWTSQSS NL
10147	24048	A	10222	142	394	GVCQSLGLSLCQLGGTVRDLSEAVCF LAELBPCAWRTLRLRICCSLQSQAGIF /RFC*SYIHICFPFQVLLSSEMGLSIR P
10148	24049	A	10224	77	396	KRKTKKSFWTFSGFGLRPPIPKKKKFFN SRGKQGGFGRGSGSRGGGGSTSGRGGGY MGKVFEGMGQ*NFTGQGLAKGGFVVFPL GRTTIGIKGALKRLFA/NNEHDLR
10149	24050	A	10225	155	443	GQAREGTLSQFFPFPSPGWFLILPGGV FSPKFFFFFFETRV/CAVAQAGVQNCI DSSNSCASS*IAKITGAHHH/TELIPIV F*ISPPSQ
10150	24051	A	10226	290	485	KRGEGPVQKKKFFFFFTESCTVAQAG VQWHNLSL*PPPPG/SSDSPAEPFR
10151	24052	A	10227	228	424	KLYQNLDHTLGFELSHYEVH*XMLKG SSWEFVNHSS/VSNKCILICSAKKKKK KKKKKKKKKKKK
10152	24053	A	10228	269	454	DLFAASQGHQALEELMATLTLSTHTHT HTHTHTHTPWSLF*SR/SALSLVC
10153	24054	A	10229	255	1	FYIFSKFLYVNLVSHLDSHICFCIQSV IISCQGFVYYYY*FF*HQSCSVHTGV QWCDRSSMQPLQGGNDPPTASQVAGS A
10154	24055	A	10230	18	472	GPEEFCTRRERDRERERTDRSRRVER VRERER*/RORERERERERER
10155	24056	A	10231	52	361	WKKNYVFOIKITVYLENTKDFQKLFK CW*G*KEIGRAIHCWCECK/VIOVPWK R/VWQFLRLKMLLPHNPAVELLDIYPN ELKTHVCTKALYEAGRGGSRL
10156	24057	A	10232	3	402	APRLFLGGWISFSSPWGAGLNRATGM GSFFFFLKRKSPGLGPQGEGRGNLQ*G

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						NFGPRG*THFG*TF*KAGNNGEGPPFR GNFGFLKKKGVPQKGGQSKP/RDPRGT PRLGPPKGLE*RGGPPPPAPQK
10157	24058	A	10233	48	470	FGRRFTTAGLQKQEPAAAGPRAPRAQT PLKREAAARPSLRHLPEGA*APRSSARSP LLIPAAASLRSPRRRTCKRRRLRHFGIITR PFQPGVRLPDSGPGLA/RWACAAPVPAAS RALPALRRPL*RRPGHGAFFSSKHGHSR SP
10158	24059	A	10234	169	446	CPFGPAPSHLLEDREDDPQAGROSSFYAG WDDRWREKTLFLFRQSLTSPPTTFFP \FEASHSVTHSGMPGVISAH*NLRLPFG SNNPPTAS
10159	24060	A	10235	264	2	KLKPIFKMVLKIMFMSYIMEVFFET GSRSVTOAGVRNHOLDLOP*PPGSSD PPTSVSQGVKWKWTAEALAVSRDHATP RAKL
10160	24061	A	10236	306	3	SQDMVSKPKKFF*LV*GLTEI*KIRAL VFNNKFFFFFFFPETGSTGSCSA\RL CSGTIIAHCNQLQLGSSNPASASRVIN SIKKLFANFIVSANPRPT
10161	24062	A	10237	20	469	QCGATPRRGDHRSGV*DDPGOHGETFS LLKIQKLSRHDGH/CRRLSHKNLNPFG RGCSLELRSCHCTPAWATR\GNSVSKKKK S
10162	24063	A	10238	313	3	TRPRFTOGPPHSGGRACLCIFSPHGPFO TRLSTPVSPSVRLPGQVLLSARHGFL CQHGMF\PSLFTMSNITLWPGVAHTCN PNTLGGRGGWIT*QGEFQTS
10163	24064	A	10239	274	49	KGNPFFVFETGSHSIAQDGVQWNCNHS LQ*PP\G\SSDPPTSASRVAGTTGVCPC EDKLSHLRRCYAQVFMLAG
10164	24065	A	10240	144	454	VCKIKITLYLVLEDYIN*FVKSSL*LK S*K/LIQMWAIISLPECLNSVCLGKV G*KRCSQGTVAHTCNPTLGGRGGMIP R
10165	24066	A	10241	289	178	FNYSSIKNNTDGWWNCLLFPVIFALWEV EAIIESF/CSRDEIPLSCPGWSPVKLKR FYCNLP*CWDIRQEAPEHFAISIFDA TVIELFS
10166	24067	A	10242	352	294	PBRTTKMVV*DDPGQHVEAVTLQKQKL VERGGKHQPSQLC/REDH*SMGGGCS PRP*PCTPAWVTERDHVSKIK*NIKIK VSLCRESSNSFIWQCPVVSHTLALCFQR EKKRLDLP/S*MGVK*EIPFLVLLFLP HWPLLLMK/YM*IFFGNNRSLCHPGWS AVAQSQLTAASVPRR
10167	24068	A	10243	293	1	LERHIPVRPIIDCYKWWRF/HFLRPL HN*FLSFFSFFSFFFTGYSYST\RL CSGTISAHCNLCVHLL
10169	24069	A	10245	185	1	KKQPOQTKNPLNNVKKKGQHQHFFFE L*TSRSVAQAGVQWCDLGLSLOPPPG\SS DPPFS
10170	24071	A	10246	2	265	AHKKKPAKIIAPSTFLYGETEARRSMFK AAQLKCGRAGIILFVFKTESCSVAQDAV LWNCNGLSLOP*PPG\SSDPADSACRVAR TTSI
10171	24072	A	10247	2	430	EAGGREALDGGCLTGRESGVQRRRDSMG

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						CQGTAGRGTRAGKGGPWRPEHLSSRRPPA SSVLLSWAHLAWVEGS*TGSLCDLEAP GPTLSFWCSWSPELLQLHV/HHHTHTHT HTHS/HPNTHTDQTSLCHQPSFSVSPRA RTVL
10172	24073	A	10248	201	16	TPFGGVFFLGGFFLFFFFFETSCVQAQ GVQWCDLGSPPFPASRRPGRNSSI/AAA *GYHFK
10173	24074	A	10249	167	2	GFDFFPEGMLSYLEKEET/WPGTRAHTCN PSSLEG*GGWIT*GREFKTSLTMEKP
10174	24075	A	10250	92	389	FQPGQHGTELSLYEIKKI*/ELAGCTDM CLWSY/LLRLLKQDDCSST*VQGCSEP* CLSCIPSWVTEQDDPSGRQI*KKKLSL GRRGGIFLFLKIWHVFFL
10175	24076	A	10251	221	415	KKKKRGGRFKGSNFTSPGWRGNIFFMGF PKLNSRAGV*QRRD/WEKPGGPQFNCFG SNPPFPFGGK
10176	24077	A	10252	94	383	GKLNRCGIWLLGRQCRSPAVSNALWLHR VAPEEEAGEAWAGTSLQLSCKSKITPN KIVY*KNKT/WLGTVAHVCPNPTLGR GGWII*GREFETSL
10177	24078	A	10253	249	2	YFTMIFKCSKKRSPSTSLTNQKLEMMK LSEEGMSKAELS*KLGLLH/QVSQVUNA KEFLKEIKSTPATNGWIKRNGLIA
10178	24079	A	10254	132	414	NNTYVQCKFFLLNSQVKGMLTCSWCEK *VEPLWKAHVWFLK/LEONSKEYKL* WNQPRYPADVVDWIKWYIYMEYHA/A IKKNEIMFFAA
10179	24080	A	10255	359	3	YSLRHNIEMRVSNPSTRASKCHERRSV ISLTLNGKREIIQEAESKGTLANKPKA KLFPVPRQVNAKEKFLKEAKSAAPLN/ RMIRKQNSLTADTEQV*VIWIEY*TSHS IPLSQSL
10180	24081	A	10256	283	2	SLQPWKLYVHVFLPKYATYPPFGTLPT HFFHKILPSKAGSDLNSIYAMTYSHRIH TIFPETESHSVTRLECSGAI/SAH*NLH LPGSSNSPATK
10181	24082	A	10257	216	386	PSKNPPFLINPFFFFETDSCSFA*AGVO WRNLSLQTPPP/GSNNSCASAS/RIAG I
10182	24083	A	10258	263	1	FSQWLTLPSPLSYSLFLRQGFALLPRL ECSGEITA/PSSAS*VAETGACHIAEF LNFFVMEFHHVVQAALKPLGSSEPPPT ATK
10183	24084	A	10259	248	47	IPKSRVKRENRLNPGGKGCN*PRSPPCS PPWAKQNSLSK/NKVKIYNLHTETQ TVHGDIRGOEK
10184	24085	A	10260	159	2	KRDMSLLKLEY*KKE/RIWPGAVAHYTS LSTLGGREWIT*GQEFISLTNMVK
10185	24086	A	10261	190	405	ASLHHMFYFFFFFPKQIFFFPVQAENQ WGNLCKRNPFPGLRDFPASPPKEAGF RGDPH*PGLFLV*GE
10186	24087	A	10262	39	293	PSSSTSRITYPDETLTKQVICKILFTV ALFIPKHWKLCCKPHIG/E*IKLCQY TWRYVAVQKNEENLYQLMNDYQEILV SD
10187	24088	A	10263	282	3	AFYNRFLLKIFFKRGPRGKKGKGGKEK KKWKKKKKKFFFSPPGQIFPLGVVFFF

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						FLFFFEAESRVT*AGVQWCQD\SSSQP RPRRLKPPFQ
10188	24089		10264	196	376	KKGGGHIIINFPEHKGYKPGPKKKKFFFF FFEMESCSVA\RL*CSGMI/QAHCNLC LPQSSN
10189	24090	A	10265	514	157	GLTLSEFRLEVSGMMSL*P*LPG/FR*FS RLSLPSSWVFPLMVVHYAQQSCIFFFV ETGFHRVVOAGLKVLGLRQSAHLGLPFC W\DYRCEPL*LTKLICFTYGLR*RSKPF FFVDGIQLF
10190	24091	A	10266	57	378	RSKTN*DSVILCS*LVSV/VDQSYFF*V TEILEQIKLLGSKIMCPCILQHLFCFL CGSFVGST\IFIFSRNIWLGTVAHACNP STLGGGRWIT*DOEFETCLASVMK
10191	24092	A	10267	1	212	LIQKDTNIYYIKAL*IPNKHI/KRIS IVSHYKMQIKIMR/YHTRMAIKRKTDC LYECRETRTLMHCW*GC
10192	24093	A	10268	3	399	MANKHIKIPASLIRMEI*IRATMRE/H *FIPIKWLVLKSKRESNKCQGGCGRTGI VIHFQRECKIVLL*KTV*QFLKKNLR LGAVAHSCNPSLTGLCLRPRVODOPGGHG KTLSLLEIKQLAMHGLHLSFS
10193	24094	A	10269	190	386	FSPFPLVLPTLITCECKAICRRKGSFDFFL LGPSFYFFKLL\FIYF*ERVLLCGPG WSTVAQSWLTA
10194	24095	A	10270	166	327	KINSKTAECVCLPSVITLNLINGLNSPIKR QR*IDF*NPI\ICCLQETHFRFKGTN
10195	24096	A	10271	180	1	IFFLEFEVETCSVA*AGVQWMDLGSQCP PP\GSSDFQLIFAPLVETGY*IMVPSS CRT
10196	24097	A	10272	273	3	FLGLFSGNPLKANKPVCHLTLPILQRIF FFFESEFHS\VAQAGVQWCDLGLSLKPPP PG\SSDFPGRRR*Q*AMITPLHSSRGDR VRLRLKKK
10197	24098	A	10273	399	27	IYHFVTRMAIRRRKN*CW*TCGEIGNL VYCWECK/LV*LLRKIVQFLK/DVKQ NWHFVILLISYRT*EDCLFLCSHVM *LISGVRVGAMWVIGSREWFMSGFTI SSCHODCEFSQDLIV
10198	24099	A	10274	275	462	KINVLQLODFFFVEMESHVSIVQAGVQW HLSSPOPPPP/GSSGDSRASDS*VAGIT SVHQHAGL
10199	24100	A	10275	2	379	RGPGGRGLSGSGTCHPGRGGEPVVOHL F*FFGP\PENYILILPGFGIISH/IVTV YSQKKPEFGYIGMA*AMISIGLGFIV* AHHIFTVGIDVDTRAYFTPPYHTFEEPG YILSRRRRTKGLF
10200	24101	A	10276	2	407	FPSPSPSPFASVLSLSFHLPLPHTW FIDGSP7XPNRHSQAAGYAIVPSISII EATA/PAPFTTC*QAEIALTRALTIK GLCINIYTD/SHILHHAVMG*K/GFLT TQGSIIIDVSLIETLLKAFLLPKEAGA
10201	24102	A	10277	203	545	FLWRGGSALLLLRECSGSL/ALCNL GPHRFKRFSLPQPP*LSNW\DYRRLPP CPANFCTFSRSGFTTLGQAGLQLTSSD LPTLASPKCW\DYRHEPLVHGLTFNRSF NFFF
10202	24103	A	10278	250	3	AKWFLMKSTPGEDAANIEM/TKLDLY

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						DINLVDEAVAGPGRIDSNFERSCTVVKN VSNSTCYRELPHERKSRLMCQM*LSYF
10203	24104	A	10279	333	3	SLILLFQSMNHTHVVRVTFIDQFCVCSN YSTDWLPPLHSFISLRTYPSLRYNIKIR PINHPTMAMASKCSERESRISITLNLQK /LETLIL/SEEGMSKAQIG*KLGLLCH
10204	24105	A	10280	251	3	ITSKVIDSNPTTSTITLNLNLGMLTSF*R QRLL/DWASSPK*DSII CYLQEMNPKYK IFKKIGRRIYYANISQKRVGVAVLTPDK V
10205	24106	A	10281	22	226	TRINSGKNKELNVRARTIKLLEENIDRN LCDGLGNCFLD*YCIL*TKINSGKNKE LNVRARTIKLLEENIDRNLCDLGLGNCFL LDMTFNAQITTKGR\IDKLDIFIKI*NFWL DT
10206	24107	A	10282	238	383	DAKRKVSSTEGDSEGVHAHERRSASLSAK PCPRAVE/AKPQKAAEKG*SS
10207	24108	A	10283	127	377	RHPGGSALGKELRQCFGVKGQAEIGKIE MSQPTQREVVVEGIGSQKAAQVDHLRSQ VQDQPGYGETPTLLKIH*LAGHG/GRCL
10208	24109	A	10284	328	370	VGPFGGF*SSGRVSSCCPGWS\PSSEL* SAHISLSPKCMWYRCQPLRPATFFFKTAS HYVAAQKQVQCNYSILQPGTLRLKCCIF KKIQVVQV
10209	24110	A	10285	341	1	KVVCULTAPLSGRFSVCLPFLGPPYFLQ HSDIEIKPINYPTVASKCSNERRSHSLT TLN*KLETIKLIEGGMSKAETGRKLSL L/QSVSQVNAKEKFLKIRSIPTVNT* MI
10210	24111	A	10286	199	329	LFFSFLNCLSPHRIEESY*KEIKSAPFI TPGIPRK*TSLAGKNVFMWDKQDQTNH NIP/LSQSKTITLNSMRAETVEEAEEK L/ERGCFMRFKERTHLHNKMGPGVVA HTCNPTLGGQGRQIT
10211	24112	A	10287	358	387	YTNALLLYV*DPQGHLMGKDSLFWKNC* KNEYSHAKKQNH/P*FSLYTKTNSKWS KDLNVRAPKIPKILEKK
10212	24113	A	10288	111	373	SAQQCPDQHGKTPTLRLRIQKLAPDGAC L*SQLR*GCGEPRSRHCTPAWAT/EG KTPSQKKKKK
10213	24114	A	10289	197	375	IRIGLCFTII*FLETKLHTVAKVECSA ISAYGTLSLVSDGSDPASAS/RVGTGTG
10214	24115	A	10290	118	371	QCILLMSPGLRT*MTGRLRQENKRLNPGG GCGGPRSCNCTPAWATK/GNSASKNQ TKNNKQQQQQN
10215	24116	A	10291	214	368	CGYHQRKKKTNPKNSKMGCGEIGTLM HWKDKHQ/Q/EL*TIYQSLKTKZI
10216	24117	A	10292	2	376	PFFLMAQRQTHLVPLASSGTSLLMPTST LLWLPLWLYKAHAVTPTLSKLFDPHTKPY AVSKNNLGAISI*SY*VIFVPPRSRF/S FIRDKPTS
10217	24118	A	10293	1	379	NILHNLDFFKNTLLEPQSSRLQRAVIAF LHFLSGNIIVRCFFKKSQWQAQWLTPVIS ALWEADVAGSLFPESETTLNMMMRPCLN FKKKKKKAFLPAGPQFFFMGGKILFGI AAPF*SSGRVSSCCPGWS\PFEL*SGH ISLPK*DYRCQPLRPATFFFKTASHYV

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						AQARVQW\NYSSLLQPGTLRLKCCIFKKI GVQDI
10218	24119	A	10294	201	384	GEERLSVQCSAFK*LR*HINISLQTFFF LRRESHSA\RELECSGVISAHCNCLP SSDSPA
10219	24120	A	10295	161	400	VCVTESVKANHLVDEHAKLSLPHLSLL FGV*GVVCVCVCVCVMCF/CVCIVVC
10220	24121	A	10296	1	433	GEGGGGCSGWSGVETAGSRFAPGAQDL LPAPALGRWQGLMSVCYPWAPQPNRKP LAILCAAGLPGQORLECSGMIHAHSLD LPGSGDPPMSAG\SIAGTTGTCHHAW/E FHHVAGGLELLGPGSDWPTVLGLQMA TTPGH
10221	24122	A	10297	209	1	LTPELLYHHYTYLFF*ESGSCSVAQARM QWCDLGLLQPKALG\SGDFPASAS*DA* STGVVDYVSWHTCI
10222	24123	A	10298	225	1	RFGMPLSALPCTGHAPARQPHSAACSGF KCPWQCSQPAPVAGTIV*VCPLESLFCLC /FCVPQPMHGGLEPLCPFV
10223	24124	A	10299	212	367	VTAGSGHMCYTWWECRLBQSL*KIVWR LK*LKVELRFDPAVLL/SIYED
10224	24125	A	10300	97	406	LHRCPTAWVTERGCKLTNNQNGHNV GEACSRPFTTIC/EEKIHLVCLTEED *RLAAETTANTTDIPGSAYRILIKLK PSKLSCT/YVAKQLSPQQLTK
10225	24126	A	10301	3	422	YRSSSKTFLIIRRGFISSSTPLLAHLST TLSTLSHFQKGWVLF\FFFFFKGFFFW PPGGGGRAKP*F/HGNPPPPG*KNFPAL PRQGGGKKG\GPPPPGQFWFFKKKGVS WGGGAKTPELGNPPPPGPPKGGITGGPP FF
10226	24127	A	10302	330	1421	RTKGRPLLLALPVLLLLFHLAFSPAP QPSLSSTEDLKWTLSPQSRKLQPS LHRAQVRDLOWCRAGRELTAC/WRAP PRPRTAVLLQGLPC/QEGRILLLESINGP ALVVAEAGTIFYASATIVDYLGPHQTDV MHQNIYDYIHVDRQDPQRLHWAMDPP QVVFQGPPELGTGDDAILGRLLRAQEWG TGTPTFESAFLTRCFICRVCLLDSTSG FLTMQFQSKLKLFLPGQKKKAPSGAMLP RLSLFCTIAAPVLLPSAAEMKMSALLRA KPRADTAATD/SKMS*LTLSERLPLN *FEIWDSAPGTLPSLFFGAFDGHIF CIHTRALRGSTRTRQCTAAALEGASFRN HVEL
10227	24128	A	10303	172	383	KIENKRVQGYBEIETLVYCWECKMVOL LWKTWVVLKILKGP*\DSIIFPLGI NQGTIEIRFCRYSNT
10228	24129	A	10304	205	2	NFYPA*RTDFVLVGSLEIFYE*ASHFIT /RECSGTIVTHCSLDLQSCNPPAS HVSGTAGAHHCII
10229	24130	A	10305	423	30	LLEGKLTNRKDIRTKTFSVRRLLHQSPKV DRITAKMGKQSRKSGNSKNQSAYPKPK HSSSPAMEQSWMENDELREGEFRQSS/M SKLKEEVVNGK*VKTREKRLAKSLTRI TNABEYVKDLMELKTSVLRPL
10230	24131	A	10306	211	387	LEFFF*IKACSVAGAGGQRRLGSLQFP PPLKQDSC/SPSRGVGTGTMTTHAQFI

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10231	24132	A	10307	229	382	FFGF ERAVVQPG*HGET/PSLKKL*KLSRCGG MCLYSKLLRRRLR*EDHLNPRSWG
10232	24133	A	10308	168	417	GSYCFVRRNLLIVKYMRSVHLLFMILL YRGD*WYVTTQYNFCILQKQEKLIYRIA /HVRNPSLRGGG*IT*GREFKTSLAN
10233	24134	A	10309	253	402	KGGGGGVKTFARGNPPFGPKGGEKKGG PPPTQKGF/CFPPKGTTRPPGKGTGR RAKPNIEIPADGKKEFFLPKPEKGKIGK /PRPPGQINF*FLKKTGPKGGGGGSKP RPGGTTPPPGQKGGKNGGGPPPPKGGF FGKKKKKINPPR
10234	24135	A	10310	182	400	LHVTHIIFWLYLYKNMMLNTFY/CYIF SVATSTFKIVCV/WLGAVAHICPHLIG G*DGWIT*GQEPKTRLANM
10235	24136	A	10311	371	400	FIWGNIT*ASNKHKKT/STSLAFRKIQV K/ITMRYLSPPPTPRMT/1/1*KSYSK K*GCBEIRSLHCHMLQPT*KT/WQPF KIINIOQLYNPAIALKCNTRG
10236	24137	A	10312	113	404	QRGKIGTETHCWNEKRVQPLMKTDWN LQRLNIELPCDLAIPLNLPREMKTE IYICT*MFIALPFI/AKWRQP/KCSSA DE/IGKMHICIMK
10237	24138	A	10313	146	1	FLTKQFFFFFETESRS*AVQWMLDGLSL QPPSP/GSSDSPASAF*VAG
10238	24139	A	10314	157	434	FFFFSIFFGPGQVSPPPFFFGGPGIFF FCPLKKKILPPPRGKKFFFKKG/HPF FFFFFF*EGVSLLLPRLECGAILAYCK IHLPGSSDLF
10239	24140	A	10315	277	2	FFFTAFFLGVGVFPFPPRFFKPGPGFFF LGP*KKNFFPPPRGK/IKFFFLKGPPSF FFFFFF*EGVSLLLPRLECGAILAYCN LHLPGSSF
10240	24141	A	10316	1	388	KTITHEVITECIWLKVLVLLFPNMCNII VRMHCVCVCVHISI*MDHIVSYKCIHI /LCIY
10241	24142	A	10317	134	399	LGLPGGDTGGGTIENPPFFERALNSQNG GK/NPLLGPKTRPLGNGLCSTPKPWEKP RVRVDLN*TTPCLEKRAPWLKAKKTPA FEIRI
10242	24143	A	10318	233	3	EFLFSLICAICL*CALQKQSSCFCLAL IELLGSMLLFH/SSLETPQPPFFLQIFF /SFFPLFFGANYTYNKPFEYSLI
10243	24144	A	10319	221	8	CDQPKSPPLSGVQMGDILVVLVFLFLF AP*R*GSHCVQAQGLEPGSSDP/PQAT SQVAGTIGMHCTWLVF*
10244	24145	A	10320	1	407	RESTDPVYLGTSGGCKTEKAGCFFLW KLHTKGAAPARCPELSGMRCA*P*PLLG V/SQSRYNAPQKLSBACPLSELRCRA GRYTGFLKGRLDHLRLCPTTLCP GALSQDGSFTYKPLTGAALFLSYM
10245	24146	A	10321	115	398	ADEELLNMQIYKLYLLEMESTPGKDDVN TVEMTKSEYSI/NLKAVAGFERIDNSF ERLSAVGKML*NSITCYKEIFR/RKSQL MSQTSLLSYFKLP
10246	24147	A	10322	137	454	FFSLYFQGGFFFFFLGKGFSPGKGI CPKPPGPPPPPGKGFSPPPPGKAKKK GPPPPPP/GLFF*KKGGGFLGGFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
10247	24148	A	10323	246	372	LGKKIFFSPAGGKGGPOKPPFF ISKSYQLW/LGGVAYACNSSTLGGRGK WIT*GQKFKTSMANN
10248	24149	A	10324	415	1	IWGA PRVFPFPPF*NPFPKFNWGPKKK KKFPFPPG*KIFFFKGPPPLFFFFF SETESCSVT/RLGCSGGISAHCNLRLEA SSNPSPSSSLRMPSTPVLPRPHGDLSPQ LSAWVLSPWFLPSLLPDLDFIVQ
10249	24150	A	10325	3	559	GGGITGLSPTISKFLFFVFESISLSPL GSSGAIMAHCSLTSRREPPCRSINFVS VILANVNTNKGIRGMDFF*MM*YTIQ ICMLQNTHCAP/KDNCMKRRKEIHH ANGNQKAGVALLIPDKDFKPNVTER HRMLVRES/ISQEDVTILINTY
10250	24151	A	10326	24	387	NGGLGARNQSRQVFLAGFFFFFESSCS VAQAGVHW*DHSSV/PGSSAPPASATVV VGTGVHNPWLIF/VFPVETGSH
10251	24152	A	10327	145	396	CDYFGEMFSYLLNLIYLCDDPAFLPEY VPYENENTSLDKMDTDAHSSFIHNSPKL ETKCPGTDEWI*MTKKSDYCKH*GYRV TGTLLEYGECKIV*LLWGNV*LF/LLN IYLCDDPAFLPEYVPEYMKTRIHSKT *PMPIAALFIIAPNWK/PKCRGTDEWIN TL*HTHAVQYHVAVER
10252	24153	A	10328	94	639	ASISSIKWDNISFLVGLLGELNEIRNI CKAVNMQALNKWLILLFVIEENNVSA SSNNFKIFYAYIAKAVLLIITEHITLS IVLILKKQNNTRAVTKCW/RGGREKTL IWLVG*ECKLVQPLWRRVRLIKVKIE LPYDPT/ILGLIYSKERKSVYRK/NICT PMF/VAALFTTARTWKH
10253	24154	A	10329	143	3	SAWFFFDORVLL*/SPRLCTVSISNHC NLRVPGSSKNYCLSLISIDWR
10254	24155	A	10330	153	389	RQSLTLFFGLVSNFWLPVLSHGLPKH WGQCYCHAMPS*CF*NRSI/WSGTVTHA FYPSTLGGQKFI*GQEPFETSLA
10255	24156	A	10331	382	422	RYKDL*KLNTLEYPDTPVLLGNYPKY *TAP*\SKCT*MEIAYSQPPKGRSK SSPNE*INKMWTYIMR/YSAIK
10256	24157	A	10332	194	1	CKGQCNKEDRNT/CSK*NPFTLFT*TK RKQ/WLVAHAHACMLSTLGG*GGRAS*A QEFKTSRANM
10257	24158	A	10333	348	1	NSGQSWIYFLLKXGVGRVSPDPDIYN SISMVWCGRLFSNERFASLLTKKLLA GHGGTCQLSLPLGLRRDRSLSGGQGG/ C*GYSE*LCRCIPAWAEGDLKSSSPN SVAY
10258	24159	A	10334	388	2	IPGSPKRGPGGKKKTFPHYLFIRAAPP LPRFIFPPKPNPPLKGGGGFFPPPPKL KTPRLRKKKKKENFCWKKGFFKKKQTPQ RGRFFFFFLRQSFVAQAGVQWCDLGS LQSPDP/G*SYHPARTRG
10259	24160	A	10335	3	396	LLRPFCSLRHNDIEIMPHDNPMIASKSC SKKSCISLTLSQLDLVILSGKMLKA KTGQNL/GLGHLYRTVRHAVNVKCKLCK EIKNAALLNTQWTRK*NSLIADTERK*V V*ICE*AS/HSMFLRNLQNK
10260	24161	A	10336	165	442	GQMLLLIARNFGLIHLNLSIYYRRLF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FSIPRYLFIFTYLYLFYLFYFESVAHSD AQVECSGTIMALT*KKNASLP/ASAPRA AGATG
10261	24162	A	10337	33	430	TGSTHASANFCUSLVWLTQLISRSSGQGL ARLQLRCLPCCILFFSFSLVIYRLHSY LRLPWRRICLQVPSGC*QNSFPNFRIO GSLLL*/MQW
10262	24163	A	10338	284	3	SQHFGPRWHDHLSRGVRDQPGHQGETL SRBTP\SLKKIQKLSGHGSACL*SQLFG RLRQENCLNPRGGGCEWRHQCTFP*V TEQDSVPKKK
10263	24164	A	10339	414	2	ERAGPFSRKIFFSPPLAKKVKYFPFPT RAAHKRPIFSRYVKERGNPSPLWFPP FFSLW*KQ*GSLGRFLFPV/SWGIFLP SKP*GPGPRKIVCFELG/LPPGPFGGP FFPFFFGDRVSLCHSRWSAVAQSLTAR
10264	24165	A	10340	211	422	ASLNGGGRFSPSLAAALQ*PDL*LRGIT PALFKAARQCDLSL*RLLSF\VLGIL PRGAYRGRQAFLSWGLHPDRASLFC LPQAWAMAGAPPALLLPCLSLISYCRA SNQDSGGIGPSESPSAGYLLVPGFLLP AEK\RTIYGGVTRFFRGP
10265	24166	A	10341	116	432	SRQRMPTVYHVGSGDITKGEKPCANGN KGGSSILRSLCHLRKRFSP*SLKALVWC GGACLEAQLRLRLRQEAHL SQGVPGCNE L*PGYCTPAWATEP\DSVSKKK
10266	24167	A	10342	103	458	SLNVCVLTTLPSSCSPISLPLRGFPFYS L RHRNIEIRPINNPTMASKCSSKRKS*MS LTLNQKLE\MINLHEECMLKAKTG*NLG LLHQIVDQVNAKKKFLKKIKSAIPVNT QMVRKQN
10267	24168	A	10343	53	408	SFQFCFSVFSPLWLYLLLVFDDGDVQM GFWCGYFCLLVLLIDTKLS CRSVGVF CRVRQCA\LLGGASQLG\SRGSGVRDP LEEAVCLLSDQLRAGRITTLF*AVRQG HLSLQRL
10268	24169	A	10344	265	421	NNPFPSPRGGNGNPGPPPPRFFFFFLK NPGLFPF*VIYLL/YFTLTPSCMLCWT ISVYGCQFVFFFSFFFFFEKKIFFFP RVEPKRIIVPKLLFPG*NNPFPSPPR GGNGPGPPPRFPFLKNGPL/HPF* KKGAKFPDLINPPWP
10269	24170	A	10345	207	420	WQKGCPTVMELGVGSPYPCFLHLWIQ PTSHRKYIHL/WLGMVVHTCNPTLGGQ GGWIN*QGEIETSLTD
10270	24171	A	10346	115	3	APRGAVKR/RPWNMGAAATHVCKPSTLGS RGG*IT*QGEY
10271	24172	A	10347	41	421	FTFVSVCVHFKGIFLSPLSFPPFETVPG SPLGPKRGGGNGSGWPNPPPLGRSGP PPPPORTGKGYPYPPPGNFFFKFFFRK RGV/PPL*HPGGQSVT*GTPPPGPKF WGAQSGPVWGNPLF
10272	24173	A	10348	228	1	SKQVKEKYSFLHKIQKQAT*NRTFFRV TKKHVEITKK/WAGHMAHAYNASTLGGQ GGWITLQGEFETSLANMVKP
10273	24174	A	10349	405	1	GGFLKRGPPFFFFFLRGQLSLPLRLECSG MTVAHCSPNILDSNLSRRSDYSHQA QLIFLVSF*VLGSHSVAQAGVLLAS/P

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KCNDYRHEPL/WPSSQSNLNSFFLDGFS LLSLRECNATISAHCNLLLGSS
10274	24175	A	10350	301	546	RELPFPHLPFPHNVLKTI ^{PHCRGKTLFLDY} SNPYLKQVSSSKPNCK\HLKE ^T LFLE AKDYWLGVVPHAYNPSTLGGQGRSITG
10275	24176	A	10351	873	1258	FCVQCYPHLLHHLHHHRRFSRL ^{EPFPFPFG} AALFPVPEGR ^I ILPLCPSSGPRQTITGPG KGRRHPAPHRT ^{TPASASASL} PARRTLPAAP PW*PLSFQNTT ^{PGSA} \PGGNGQASGAG GNSRT
10276	24177	A	10352	184	576	GLSPFLSHLMAASSEI ^{SEMKGVEESP} K VFGEGPGHSGAETGPPQVLGAVDPQPEA PQPGPNTTAA ^{PVDSPGPKAGLAPETTETP} AG\PGKQPRPQ ^{TSA} *AQEGNQRP ^{TAA} PK THAQETVSKPEVSK ^{EA} TAD
10277	24178	A	10353	110	384	VPGSPRKT ^{SPQME} RVLAPKTAKKGCP RPGDHRSLQNC ^{RDT} RARIKWADSV ^{ERP} PWAG\PVAHACNPNTLGG ^{RG} GWIT*GQK FKTSLVNM
10278	24179	A	10354	123	422	RKQIANDKSKLFI ^{INKYLVNVLNSPIK} /RERLAGWIRKEKH ^{DP} PSICHL* ^{KTHLT} \ KDTNSLKMEG*KKIYHANNY/QKAGVA ILISDKIDKF ^{KKKVV} REK
10279	24180	A	10355	36	426	PPERQYASRV ^{CCV} FYTECRGLAPKPE CRGATIAHCLLNVLGSQ*SSNL ^{RV} SS* DYTQLIFKL ^{FVQ} TGSHCIAQAGFELL/S SKDPPTLA/FPKHNDYRH ^{DH} SW
10280	24181	A	10356	193	3	FQTRIFKISFF ^{FE} KFLFK ^{FFFF} FLI* EPRSIAQAGVQ ^{WRDL} GLSQPPPP\GSSS PPASASLY
10281	24182	A	10357	205	377	SPVVPQPYRL ^{TI} FPYQK*LATYCI* ^{VV} *FFKLILYPAILLSII ^{IM} NTSD ^{EL} * FSSHITG*LSL ^{IK} YVNWVQGM ^L AHA* ^N PSTLGG/RGGWIT*GOEF ^{ET} SLAN ^W KP
10282	24183	A	10358	51	376	LCRPFQLCN ^{DR} TOWN ^{CP} PFEEQDRCS CRSTSMRVAG ^{TTP} CFKLKVLQNTY ^{TV} * ^M FCRTFRHGVV ^{PL} ATRLM ^L \IYNQSPV TLQGR ^{OT} TYLSCH ^{RG} KAG ^{RV} CRATQHAA GVVVTQGRACI
10283	24184	A	10359	295	376	ASELTSSQSGSL ^{FN} QKGR ^{CI} APL ^{FC} * KCNSEILVHCW ^{GCKM} \WKI ^{VW} *FLKTL \RLELVDPASP ^{LL} AIYPRCI
10284	24185	A	10360	451	1	CQDIKTI ^{LR} NEQ ^{VL} VI ^{PS} VTYKQVGR SFVSRRYLW ^{SG} CVLCYAF ^{VT} EASKTWHH FPYRSPGF ^{WGR} SGGRQ ^{FDS} *PKSQADFR APQGPPTPE ^{PGA} RRPEI ^{AP} PTPAD SPKPT/HSP ^{PR} SGAP ^{PS} APF ^{LL} GRAER GVG\PGQGRPRP
10285	24186	A	10361	2	776	FFFLRWSLAL ^{SP} RL ^{EC} SGATSAHCKL ^{RL} AGSRHSPASASRVAG ^{TT} GARYHARLI/L /YLFVETG ^{FHHVS} QDGLN ^L LTS* ^{SAC} L GLPK\C\WIYRREP ^{RP} PAYFI ^{FL} RRSL ALS ^{PR} LEC ^{VQ} WCD ^{RLS} LQAV ^{PP} G\LHHS PASASLVAG ^{TT} G ^{AHH} TRLVL ^L ILL\FYY FLRWSVTL ^{SCR} LEAGVQ ^{WN} HLGSLQAP PFGT ^{TF} PSCLSL ^{PS} SDY ^{RC} PCPPCLANF L ^{LF} *RROFTLMAR ^W YSIS* ^{PR} DP ^{PP} SSA SQSAHDLFIVGQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
10286	24187	A	10362	188	365	CPQLHTQSNLNNIMASQRYQFELKIQAL /WAGTVAHACNPSTLGSRGWIT*GLEY ATSL
10287	24188	A	10363	146	1036	GWAVYQTLQAANLGFRTESGVSPHGRFS LPHHPQPTLHAWPAPLQPEPCVPLRE DPFMPESW*LPPSIPAEGVSF*ECDFSR RMMGKSPVPVTAPPLGPAPEPFCVTAG CAFMHT\PTHQT\PPHCSIFLPKISFKSK HFY*LLFCCKLSSSVFSLPESILLFLIV ESVCQPGERCLALNMGWDGKSGRRWAT KSGGVMDIAATQTPA/VFSPV/PATSCP AGVSGGK
10288	24189	A	10364	229	1	PLENAKSIYWGKGRLLNNARLFTVA*S WNGQFSLMVDWIKKKWMRRMYTTSCA AI/R/DEIVSCAGTWELNEMY
10289	24190	A	10365	186	449	RFFEFFPKFFFWGLKSPFFFFG/RLGI *EKDGQFFFFFFPEPMASGSVA/RLECSGAVSAHCNQLQFPFGSGLPASA\PRVA
10290	24191	A	10366	445	3	RVNDGVRGRVYRGRGERGR*TRNGWHP QRMWDQDRSRERPRTRGRRAAGRRRETE AETGRRRRRERGRSDNRNR/RGRPRERM IEAGRDAGRERR*ARQESWTEKKTARQE EGRD/RQGHQETRAHKGWGN*D*GRQ AERSENRRMY
10291	24192	A	10367	1	491	NTAFPPTSLESAPVVAVQDVRV/LLSP GPECRGAI/LTHCC/LRTPG/FKPISHL S/LPS/SWDYRHVPPLDNLILCRDNVS QSGLLKLLASNPLTSAFFPT/YDYRRET PGPRASP*TMQPCFMP/RS*SQP*TDI A/R*QSNWGSQ*VLNNRELAFGTMFFGQ RPKAFF
10292	24193	A	10368	572	40	LHSFRQHFSTNYPQCTPGTF*VTQSLAA RPAGLPEPTSAAGAGAVTPPRTD\PP SVRWSGKGLDPLVLRGGAPRPS PANPAP APOGFAPRKGTECVPTASKTRPGGRWE PAAPFHAHPGKDLQPPSTLVKCEPCAR FRALTGDLPSGEMNRGLSAPQQRRA QKSGWNCEN
10293	24194	A	10370	36	517	PLFSDIDLFSEYFFLSPFFFF*KRGLIL PP/GPEQSGKNG*WPLAPRC*REPPNL TPOTRGKNKRGOTGPVIGILLRWGFPP FGQGGFKPPGLREPPGLALQRGNWGNP PYP/P/PKGFF*RTKRGEKSPQPPYNKP NKKFNAPMEEFSSFKEGRGPSLN
10294	24195	A	10371	60	403	DVEQPKLRISYPTLCKKPRSAITLCPWA LQYRSHGLIFGFSWGLSFETESCSVSQ AGMCWCNCHGSLQT/PTDSTSOAQADIPP ASAP\QAAGTTGACHHTCLIFVFL*RWG LAKP
10295	24196	A	10372	358	33	DSLGVFGAPLLSPGVTPHKGWFFRPTQ IKKLGFFPQIFFGFKV*KAPFFFWGFGN LKKKGFFFFFFSEMASGSVA/RLECS GAISAHCNQLQFGSSSLPSAPRVA
10296	24197	A	10373	264	3	RTSVSGSNDGKSWPADIITLKVIG NRLITQO*LIKLTSKQMITIHNTKGR T*SLILVSLIIFIAITNLLGLLPHSPPTT THCI
10297	24198	A	10374	298	384	TLVI*KDGVHITPHRQGHAYPGKEYML

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						HKAFLHLSVSRDPSFFAQSSNCYNRSIK QEPVDPLTQAEFVPRDAGMGKPTLSEV SQNGGPS/HK*GQYSGDV
10298	24199	A	10375	84	518	IMKLQKRSRSSLKIMRSKLQHTRAS/GT QLR/PHLGGNFIALN/AHIKKLGRTQIN NLTSQLKELEKQD/RNPKARGRQBIT/K I*AEKKTET* KKEIQKIYEFV/WFLE NINKP\VASRLIQRMIERNTIRNDKGNV TSADPDV
10299	24200	A	10376	70	363	FHQKNLVLGVLQQLGRITLQSHQPEAP PPSSPEVNVPSEVOAD*LCCI FYDVK VRKCTSPQKKTRKKRKGCLP/CAPGQTR /CLC*KRGEKNLVGKT
10300	24201	A	10377	299	2	YFVAGRGNR*GCGAHALGVGGAAMP/LGA TISVSULTISSLCAPFRRGGLPSLPAP HTFPFPPPE/P*ASSPSRGHVLVPFCMQ PGLPPLPPRLSPLV
10301	24202	A	10378	302	3	WPTVATTCSCERKSHSTSLT*NOKLEGTQ LSEEGMSKAEIGQKPGLCQHT/QQVNA KKLLKEIKNATPVNTQITRK\QNSLIA DT\EKV*VIQIBDQTSV
10302	24203	A	10379	125	375	NEYVFEKSLKLGRVSGCLLGRPRQVD HLSSGAQD*PGQRGKTPSLQNI\QKLSRH GGMCP/RRLRWEDHLS/SRGG*GCSETR ST
10303	24204	A	10380	458	3	ITISTISCKATSFERAPRASRPPEDEWV SQAGPAPLRGWN*GTRRRDDWPEASLK DPRRSGEPEAPL/PLRLML*SRLPPLPLR WRRRPFPDSTHTSPGNGKSPRVPRTGS KDKRPEALPP*FAAGEPLEANVPVQHG GGSVRSRGSYLTAT
10304	24205	A	10381	327	2	LSAPKFFFKQSLFLGANFRSPFPFGRFP FTNRSDLNVNPLTKKIYFSHKSSNPPT FFFFFTGSSNV*SCVSWRNMSLRP ESPGVSGDRP*Y*HTGAPYHTLV
10305	24206	A	10382	754	1	NTALETDTTTSFGSGGQHLCYRSRVSGG G*LIMPDLHNPLOQTSGRNQRLQGEVT DPSPGMSGGAQTGPKAPRPPPSALRHSG SLQGQP*FAHLYCGTIPYPCYQTAPLPR APPTPTGH*CPGEA\PDDELVCGCSP WPRPPGQAQAGRKH*FSGORSSRDITTA CSPCSQSQSPSRPPCVNDS/PQGGPGP KAPAGPPPALPEASLGSVHCS*VGVMT PTRPGHFLVPGKVTLEQAFGGGASGGPV P
10306	24207	A	10383	39	433	SHDQITYTEEBLLFMDEQRKWFLLMESTP GEDAVNVVEITTKNLEYCINIVDSTVA/ GVSNFERRSTVGQMLNSIVCYGKIF/R *KR/SQSMWQTSLLF\NKLQPP*PSTP TILISQQPSMMWRQDPPSEERL
10307	24208	A	10384	283	1	NVFSCKPTSSCLISPDSPTPDRFRFSKD TYRNFMPFLRRHTHMHTHYMHTHVHC TQLCLHLRPH/ITHGLSL/TCAPPVL*R PSFKPLHPTPV
10308	24209	A	10385	12	471	SPPWHTHGFYWEPTPPRFSVPHDALGQ FHTALFRLTRRPQLQLSSCINISPTCLP PCLGLCVGGPLEPAVCWAR/CP*RGMV SGWKASPLG/CPFTLLPFC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
10309	24210	A	10386	287	1	SFCVRSRPAPTSGRTPFPAAPFPFAAPP FPAATTPSTAEDGVPG/G/PAPAANCSP HSSQRGSAAMGIPLPQAS/PPAPTAPP SP*SLPFPFAPMY
10310	24211	A	10387	336	3	LIEGKLTNRKDIRKSTASVRRHHQSPKV DKPTKMGRRNQSRKAENS/KIKSASSPPK ECSSSPATEESWMENDELREEGFR*LVI TNFSELKEKTGRKLNPAALVCGRSEDOTT
10311	24212	A	10388	15	470	APSPDAMGR/VTEEDKATITSLRCKVNV EDAGGETLVRLQVVYPWTQRYFDSFGNL SSASAIMGNPKVHVHGKELTSLVDAIK HLDDLKGTFAQLSELHCDKLHVDPENFK LLVNVLVTVLAIHFGKEFTPBEVQAYLHK MVTVVANSLERYK
10312	24213	A	10389	3	438	QTGRPTMVLSPADKTNVKAAGKVGVAH AGBYGAALERMFALFPTTKYFPHEDL SHGSAQVKHGKVKADALANVAHVDDM PNT*LSDLNDLHAHKLVDVNVFKLNLHC LLETLDGHL*SAEFTP\AVNASLEQPTAF EITWLT
10313	24214	A	10390	2	444	TMSFNTLAICLDCCLSTLQPTRSTPGYP SSPLPGNPTPMPPTSSSSVPMSPNQEVX SPFLPDLKFNLSLHSSPSGSGPCDEL LTFPFVRGVV/SGALPPAAQPGC
10314	24215	A	10391	405	3	KMLTFLALPAHQCFPSACFPTMAQFPL PLSIKGAASMSDKLPYKADIGLATWGH KALDIVEN/BMPGLMGMQELYSASRPLK GACIADCLQITVETAILIETLSLGVQE QWSSCSIFSTQEHAVVFAEAGMP
10315	24216	A	10392	248	5	RLNKVGGHGGNYEHLVNVKLETLQEMY FLDIYNLPNLSLEEIE\NLNRPITSNKF ESVIKHFP*TKKISGLDGF*AEFLTN
10316	24217	A	10393	262	3	LPRDRQAGRSQGVVPAQVGRARKMPPF ISYQVYSKNFFEIESCSVTQAGVQWRNI SSMHPPFP\GSSDSPASASQAGPIPGAH HHA
10317	24218	A	10394	287	410	ALKGSSRILIMLGAWLTVPVPA/LWEAK AGRSSEVRS
10318	24219	A	10395	175	1	GGREVDDEIPLVRESTITPHIFFFFFETE SHSVAQAGGQMRDLGSLPSS\PPG\SCH SPA
10319	24220	A	10396	661	963	STLIAFIVISTLFBLLDMTEIYFSLLDE IVDTLGEAGAFKVVCELDHKAGORHVA KIVKNVDRC*EAARSEIQVLEHINTDTP NSTPRCVQ\MLEWFEIHH
10320	24221	A	10397	1	268	PQTHREAT*GLSTADWNTVKNAGWKGGA HAGEDGAELERMF*SFPTTKTYFPHFD LSHGSQAQDGHGKVDALTN\VAHVVD DMRNAL
10321	24222	A	10398	33	302	SRGATLIYVDNENGEGFTRVVA*DGALK ESGPSIKALDGRSQVSTFRPGQTFDAPP ALPKATKASGTVNRATEESV\KTHGHL VQEHF
10322	24223	A	10399	16	233	PTDYEFNTITYRECGFRREFSTSLDLL SQPCRAVYM\VGKENDIPFELRIVDLIT GKSLGFGEPKSEQGR
10323	24224	A	10400	177	1	KLLDLQPGQSPALAA*CLEYSGATAAM\C NLCLLGGSSNPPTSASRIARTVGVH*EAP

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10324	24225	A	10401	185	419	YA HVNKDTLESHLVWKLKRSALGRKSESVT GPSCHPEPSDKTVEL/WQGAVAHACHLS TLGGQGGWITLAQEFETSLDNIV
10325	24226	A	10402	104	3	GILILPKPRGDTTKENF/RPLIPIDAK ILNKILAN
10326	24227	A	10403	3	344	SQVMAVAGEPAGAGARPRLDLQFLQFL QILKVLFPSSWSSQNALMPLTLIC/LTLL EQFGNYQVGLIPNQYGVLGKNDLEGFK TLTFLAVMLVLNLSVRSFPLSVSLVLS SPV
10327	24228	A	10404	3	404	ARARQRGDLSATGRNWSPLPPAGLEPATV VLRHSGSLMAATCEISNIFSNYSFAMYS S\EDYTLASVPPAAFTGADDLVLTLSNP QTSLEBCTEKNWMOXGOSFWKTEQGLD WISFQAEKNKYEASAIQPPRWK
10328	24229	A	10405	254	443	NOLSSIMVMEFKTRFEEDFNDPEKVVY SGDKVAG/VRLIVEVCEDTRVKAIRILAC GVAKELRM
10329	24230	A	10406	26	461	GEVARRKSCCGAMAGTALKRLMAEYKQIT LNPPEGI VAGPNNENFFWEALIMGPE DTCFEGFVFPAILSPFLDYPLSPPKMRF TCMFPHNIYPDGRVCISILHAGPD/DP HGLREQ\PERNSPVQSGVEKILLSVVSML AEPNDES
10330	24231	A	10407	1	463	QQAARMAENSGRAGKSSG/T/PARGRGR C/PAEQVIAGFNRLRQEQGLASKAAEL EMELNEHSLVIDTLKEVDTRKCYRMVG GVLVERTVKEVLPALENNKEQIQKIIET LTQQLQAKGKELNEFREKENIRLMGEDE KPAAKENSEGAGAKASSP
10331	24232	A	10408	180	446	KKAASVSAASSGHLNSPFAEPESRNSGS MVRHSSSPYVRYPSDKPFLNSDLRRSPS KPTLGPESNSRAIFSA/LKNLQD/KIR RLNL
10332	24233	A	10409	1	417	EAGLVTMEIEGILGEKAQDEIPALSVSR PQTGLSFLGPEPEPDLLEYSRF/KKLQ ELEFLFVQEEYIKDBQKNLKEFLHAQE EVKRIQSIPLVIGQFLEAVDQNTAIVGS TTGSMYVRIILSTIDRELLKPNASVALY
10333	24234	A	10410	305	53	LEAQPHAPFLGHHLFCWRIFSHLGTGR RPRAMRVQSSSEGV/A/GQAPLFWVHR GSLPLVRRPACKPTGONAREEKGKVEG
10334	24235	A	10411	419	2	NNSRKFGNGTLKLVVEVEIYPLISESTPD KSEILLTTPQDKKHAPLPSAVNPESA/CP DLRPHHTTASFPV/PKTVTETRPAPQG PLGPGVRRRPRGRFSVRAASPTSGRRPA PRPPGPALEATDAPRAATPPIAALAGH S
10335	24236	A	10412	74	322	MDMATTQISKDELDELLEAFKAVOLSS NGFICDYELHELFFMEANMPLPGYKARET IQKMLDGRDNTDGKIS\YDEFAYVSM
10336	24237	A	10415	1	415	PQTHREPTMVASADKTNVMAAGKVGGA HAGEYGAEALERMLTFTPTTKTYFPHLD LSHGSAQVKGHGKMTADALNAVAHVDD MPNALVALSDLNAKHLWDF/VNFMLLS HCLLVTLVAHLPDFETPAVHACLDKLL
10337	24238	A	10416	19	454	AFSPNMGHCTEEDKATTTSLWGMVNVZ

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						DAGRETLGRLLVVVPWTORFFDSFGN/LSSDSAIMGPNPKVKAHGKVLTSGLYAIMHLDDLKGTFAQLSELLCDKLHVDPENFKLLGNVLVTGLAHFGIEFTPEVQASPKKMNNAVA
10338	24239	A	10417	2	395	ALSSSQSPAPMHPFYTRAATMIGETAAA VSFISKFLRTKGLTSERQLQTFSSQLQE LLAHHYKHHWPFEPKCKSGYSMIGVNP \KMISLILQACTEGGI
10339	24240	A	10418	2	374	LSTPHAFGTGKNGTFTISLLFLFSAYS GVFRDRAHSEAAHRIKDLGEEDFTALV VIAFAQHLQOWPFEDH\VOLANDVTEFA TTCAADESSENCQSLHTLFGDLLCSRA TLDESHCVQDGRP
10340	24241	A	10419	48	347	DPKAQLPEPLRVNLQTYAMAAGSR/TS LL/LAFALLCLPCFKAGPPNRLPLFD HAMLQAHRTTAIDTYQEFENLYPKD/Q QYS/FLMTPTSSALDSIPTPS
10341	24242	A	10420	166	1	NFLKKPKPQKPFQGRGLPLILITFFFFF FETKPHSVSL/LECGGTVSARCNCLLPV
10342	24243	A	10421	2	251	LGCTQHRSELVAARSTHQTCTQASEVD KEI/FARARNGKYRPLKISLENGQLMIG SV/SSQPSDSWNDYDSFVFLPLEDKQL CY
10343	24244	A	10422	251	1271	KEDLSPRAPMSGTQSTITDRFPLKPKIR HGSILNRESPTDKKQVERIASHDFDPT DSSSKTKSSSEESREIYGLVQRCV IQKDDNGFGLTVSGDNP/VFVQSVKEDG AAMRA\GVQTDGRIKVNGLTVTHSNHL EVVKLIKSGSYVALTVQGRPPGSPQIPL ADSEVEPSVIGHMSPIMTSPHSPGASGN MERITSPVLMEENNVDHVKVEILRKM LQKEQERLQLQEDYNRTPAQRLLKEIQ EAKGHIPLQEQQLSKATGSAQDGAUVTP SRPLGDTLTVSEATDPDGLVGRDTCSS GDASRPSDNADSPKSGPKERYILEENP EEQKKG
10344	24245	A	10423	198	569	QRNMVQGRLEPRRLKPGFINVKSYN NEWHQGFVLCVFPFLRWSLALS GAISTHCNLCPLPGFKQFCSLSPSSWDY RHAHHTQLIFVFLVEMG\FHVQGAQ GFFSLEKSLTII
10345	24246	A	10424	2	343	PQTQREPTMVLSPADGTNVYAAWGVGA HAGEYGAEALERMFLSPFTTKTYFFPHFD LSHGSAGVKHGHNKVS\DALTNVAHVHD DMPNALSALDLHAHKLVDPVNFLLS HC
10346	24247	A	10425	31	342	RAAVMPREDRATKNYSYFLKIIQLDDY PKCFIVGADNBSGKQMQQIRMSLRKAV VLMGKNTMMRKAI\RGHLENNPALEKLL PHIRNGVFEITKEDLTEIR
10347	24248	A	10426	196	2	KNLIYSOTKKVICNTPLVLPVFKRVFFF FFFFFETSR/SVSPRLCSA\SI SAHYN LCLPLSDSS
10348	24249	A	10427	1	405	RLECNLEPFGHAGLQGLGWVWSCSVSTG PTMQALV\LLLCIGALLGHMSCONFASP PEEGYPDPDSTRALDEDEPIFIDPNK LPEAGSNFGYDLVRLRIMSPTSNVLLP

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10349	24250	A	10428	223	361	PLMVATDLWDLSLEAQQLTESTII EGPTEENMAAKVFES/IGKFGALAVAG /GPVNSALYNVDVGHRAVIFE
10350	24251	A	10430	3	359	LTQREPTMALSPGDMTNVKAANGKVCAR AGDYGAELERMPLYFPPT/KTYFPHF L.SHGFAQVKGHGKVVDDALTNVAHVDD MPNALAALSDIHAHLRVDVVPNFKLLSH CLLVTLA
10351	24252	A	10431	273	1	NHKDGKQKSGKTEKSNQASPPPKERS SSPATEQSWTENDFDFREEGFI/RQSN YSLKKEIRTHGKEVKNEKKLDDRLTR ITNAOK
10352	24253	A	10432	211	3	SFLWKFCLRGIPSHVSCQSA/LLLGAS QLGYSQVRDPLEAVCLFSDLKHAGRT TTLNNAVRCQHLSLQ
10353	24254	A	10433	281	2	TNQBKKGDPNKIRSGKGDITTDNTYI IRDYVG/HTYTNKLKN/LEEVDFLDITY YLPFRNQREIENNMQPTISNEISVIKS LQTKKSGPMPAS
10354	24255	A	10434	219	1	SFLWKLRLRGAPGCMRCQSA/LLGAVSH LGYSQVRDPLEAVCPVSDLNLCERT TLFKAVERGCLSLQKF
10355	24256	A	10435	133	2	FPKPPGNFFFFFTESHFPT/LRECSGA ISAHCNHLPLGSSDSPA
10356	24257	A	10436	248	376	KGGVFFFFFFFTESCSTITOTAQWHT YGSLOPRPP
10357	24258	A	10437	250	1	KGTRKELTFIEQLLSAKYWAAGCMHYFR GSKYKSNQYVVFVVFIFSETESCS/VA QAGGQWCDLVSLQPPPP/GSSDS PGASF
10358	24259	A	10438	354	2	KRGLKKNPPFNPRNMGFLKLWGPENPK IPKCKIFKMGGLKKVLGYKNSKNLKR GKLNPFVIFFFFFFFFFLETSYSYIA /RLKCSNSGTNTAHCSPELGSRDLPDS TTQVAG
10359	24260	A	10439	126	1	GMVDCVCLFCFAIKEGREREREREKER RERQREKER/ERERDKEREREERK
10360	24261	A	10440	29	347	IQKPTADTKKFKKKLKYTTRENLHKN EDRKEGKKEKTKQHGGSKSLLINKTL NINGLKSPIKTRVAV/WNKNDPMLYC IQETPFTYKTHRL/RIQGWKKIFH
10361	24262	A	10442	405	1	IFFPHPPFFKGSFKLSPQVEIQGIFLPG WKLFPFGFNFS/CPNLPNNLGFKGLP RPSYFFRLCKKGF/H/RVYIPGFFPL ALCFPLFFPKSWGQDPPGWFPPFF PPVLVABGTLBECRLIRGWGVP
10362	24263	A	10443	122	372	LYNDISTYQVTLVRRVFFWLYSANNS LRWKNFLFSSFFKMASDPVAQAGVQC DLDSLQPPPP/GL/SDTPTLASQVSEIT G
10363	24264	A	10444	171	3	RHPTWAGSSEMPLSGFGCRITVPVLF TESCSVT/RECSGAISAHCYLSLPGSSN LP
10364	24265	A	10445	173	3	CMNVVCSIFIFLKNIFILETSHSVSQ AGVQW/LITVHCSKLKMGSSDPSSASQ V
10365	24266	A	10446	187	329	SFLWKFCLRGVPGHVRQSA/LLGVASQ LOYSRVNPLEEAVCFPSDL
10366	24267	A	10447	27	226	YSYPVYLLHLIFLWCCKSLYFIYFVEM

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						ESCSFAQAGMKWCDLQPLPFG\SSDSLAPASQVAGVDA
10367	24268	A	10448	119	296	SPIHYILVITICFIHVILLITIFSEVGS HSVAPAGV\SGAI\AHCNHKLGSSSPP VSVS
10368	24269	A	10449	111	363	SLKKLVFFFSITTHNFFPFDPLKNS RHSLYLSSLSLFSLSHSV\SRLECGGTI IAHCSLNLPGSSDPHTSMQV\AGPTGS C
10369	24270	A	10450	218	1	QRFWGPGENKVFKNLGSFAFFLGRGKLF LEIWGGFFFFLVFFLRQSHSLAQAGVQ WCD\LNSLQPLPPRFK
10370	24271	A	10451	179	3	GPFKTLFFFMGKFGALGRBKCHFFFFETE SCTVAPAGLQWRDLGSLQPPPP\GSSDS PAS
10371	24272	A	10452	71	232	SSPLSLLFNIVLVLAKIDMGEVE\IK LILIGKDEVKWSLVDRIILVKNKSH
10372	24273	A	10453	153	3	ARGELYELETGGGFFFPFLVFFLRQSHS LAQAGVQWCD\LNSLQPLPPRFK
10373	24274	A	10454	338	221	MGFLHVQASLKLITSTICP\LGLPKCWD YRHEPPRPVIPS
10374	24275	A	10455	214	366	YNYKYLHYVSVLEFFPIPIF\NTHYIF FILFFYLTSPIFLSYFFFFFTILE
10375	24276	A	10456	155	2	DRVSLLLPRLECNALAHCNLLGLGR HS\PRVAGITVAHHARLLFCIF
10376	24277	A	10457	870	1249	EGPRNADHLRPGVDHLG\QHGFTPSL QKIQKLARRGGTC\LCQSLLGLRSLQEN CLNLGDGCGCSEPRLHMCITWGE\GDS PKKKKE
10377	24278	A	10458	222	404	KORPGRAQWLTPVPIKLWEAELGR\MLE ARTLRPAWAT
10378	24279	A	10459	122	362	LSEDLNLCYFQRLHHFIFLPIVTRVQMS HYLCQCSCLPHFF\SFPLYFMESSSV T\RLCTGMI\SAHNSLYLPGSSSGG
10379	24280	A	10460	3	102	AASTLALSPRLCNSAILAHCKLH\LPA FTFPCSCL
10380	24281	A	10461	133	339	KLKSFQSGKKPEIKANSDDLALFYHNYI TRQCTFSYNSFFGDRVLSLPRLECNV ILAHCNL\RTPGFK
10381	24282	A	10462	3	193	ASNMMTELKSIPIILTLNVNGLNAPLKR HRVAGWINDPTICYLQETTYT\CRNNHR LTAK
10382	24283	A	10463	126	314	RLGGSTIKVQDLSLSDRSKPGRFLYTSN SYVRKGGKRNKACFTERVE\PVNDII
10383	24284	A	10464	1	332	KKNLFLSKDCSLFLFRFSKSPPAITGPP RGWTPKTRFIGKAPFFKKGSLSLGRKY HGGLKVPV\CPFFLSKTRFLPGVPVFFFF FFFTESHVA\RLCSCG\AISAHCKLR L
10384	24285	A	10465	173	365	RFVCSYKVLRLDLSLSDRNPGRFLSLQI PP\LRDKKNKAYTK\RPSPVNDIGT
10385	24286	A	10466	335	3	FFKKFYFKISTRALLEFVFGKKIRVFP QRLSPWAPLEKRGPPNSFQVNGVPLFF FFFFVRHGLALSSGVECSGTRLECSGAI /STAHCHLCHLDASHPTTSASWVARPTG T
10386	24287	A	10467	818	1008	VHTDVLADILKSNNAEROT\RCFLS \WLQGHCPFLTVMMQHLGCVLGGGLPG

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10387	24288	A	10468	111	1	PGDFCKRPR MVSFGRPRQADHKV\GVDRQPGQHGTEP SLLNIRI
10388	24289	A	10469	204	1	LWGPILKIFCQILKKTICENFRGPTFFI PFEMESQSVTQARMQNCOLSSLQPLPP GS\SNRSAS
10389	24290	A	10470	190	330	ERIKKQDLSTCCLQVTHFTFKDSQRLKV KGWKK\IFHTNKNQKRIWT
10390	24291	A	10471	162	2	IKGPKRAPANKGRAFFFFFFFFFFETESC SCLQAQVQWHDLSPPQPPPT\GSSDS
10391	24292	A	10472	120	3	SWGFFFFF\VEVSYVAQVGVCNCDLG SLQAPHVMILVK
10392	24293	A	10473	298	1	KRALFCFANFLIFYFLSLLFFETEFHS \VAQGVQWHELGSLQTTPPG\SSDSPA SGEYANVTGEYSANTYGEYSANTYGEY SVNTYGEYSVNTYGEY
10393	24294	A	10474	1	380	AVTGRAGSMVAPR\FLRLVLFYQCKLR SMAGNFQWSSH\YLQRLDKDLNEROK DLKVLSEEEYWKLRFFRTKVQALCEHL KLRQPGIATATAYFRFYARHSLKSIDP VLMAPTVCVLASTAN
10394	24295	A	10475	289	2	TQGFPPNNNSFYALYPKQKIPFSPDKLF RVKGFKGPVHYGVKDKPKMKGVFFIF FEMASGSVAQAGVQWRNLGSLQPP\PG SSSLTTSAPRVAS
10395	24296	A	10476	138	402	ITGRAPPKPFFLLKRGYLSGLTNIGFSF SFSFFETESRSVTQAGVQWRNLGSRSL EST/SPDSSNS/PAPASRVAAIT
10396	24297	A	10477	2	336	ARETNDTQTLLPANNNTTSDPYISI LTLNVGLNTPIK\KRVASWINKQGLM GCCLQETHLSSHETHNDTHLKIKTWRK IYQANGKQKARV\ILISDKTFPK
10397	24298	A	10478	51	250	RKVSFLKKWCNTLFIICK\LSLDYRF AKINFENITDLNVREKT/IKLLKGNKE NICDLGLGKDF
10398	24299	A	10479	216	2	GETRKALSGFFKTGWFWPPNFKLFFK KNFSERFFFFFEMESHV\RLCSG PISAHCNLHLPSSSV
10399	24300	A	10480	191	3	PSTDGNVNCLVKYSIYIYIYFFFLIFF FEMKCS/VSPRLCNGALSAHCKLCLP GSCHPARA
10400	24301	A	10481	135	768	LGQVLSGASQFVSLPFLPFLISFLGC LLAFLSACFASTFVCLGSPETSFPCL HPPPKVLSSH\PPCSRP/CPQPPKG/P PLPKHACPP
10401	24302	A	10482	126	333	MVVGRCYCMCPV\VLCLFLV/VWVW FLW/CSVYIVVWYGVAVLFIFFFFFS LLCPAVCLEVWLLDRF
10402	24303	A	10483	240	2	ATEKNMGLTSGVGLSGSNPSYGRVRER IGGGVCLWSQILLRG\LRWEDHLGLG GGCSEPRSSHCTPTWTEQDPVLV
10403	24304	A	10484	136	2	NRPSYIFSFETESHVAQAGVLWHDL SSLQPLP\GSSDSPARA
10404	24305	A	10485	161	328	EKNFKPYGSCRHFLYFIYFETESRVA RLCSGTISAHCNLRLPGSN/SPAS
10405	24306	A	10486	193	347	ILFSFLLPIYFFETESCSVAQAGVQWHD HGSLRSRAPG\SYNAPALDSQGT
10406	24307	A	10487	114	2	GAVVQSEVQWRDSSGLQAPFP\SRHSF

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10407	24308	A	10488	314	49	ASASQVAGLV IRRSTERSEPRYSVMVCKRQPRQGGPCL\RSQLLGRRLQEDHLSPIAGDCSEPRHL\LACTPAWATEQEPVLKQMSPTLFLCLFLWFLPCQ
10408	24309	A	10489	291	1	KSPFFPNRRGLTLRSRQQLNGVSFYFEAPVTDIFFFQSLVLSTQAGLQWQNLSSQLQLPPPG\SSDSPASASRVAPVSQGHATAPQFGRQTLSSC
10409	24310	A	10490	226	3	GSRCTMPRRLLAHAPFAARMFKRKVSSTEWATEEPPKRRSARLSAEPAKAVETK/PEKAAGKSSDKKVTQLV
10410	24311	A	10491	2	153	ARGLVFFVYLVENTLCHVAQAQAVKPLTSEPP\LGLPKCWDYRREPPRT
10411	24312	A	10492	123	342	THVLCCLRFFFFLDRGFLLLPRLDC/NAPISPNLNLRLPASDSSPASASRVGTITVNHVYRLTLFLIFQNETLF
10412	24313	A	10493	194	2	IPGWPFKNFSLPFLFFFFFEMESCSVAHAGV/GSSDPASASQVAGTSMRINAWLIFVFFSRN
10413	24314	A	10494	373	1156	KVQLKVYLFFFLRLSLALLPRLECSGTILAHCNLPSPSRFEQFSCLSLPSNNYRRFPFHHRLILFVL/SVETGFHHVQAGLELTSQDPDPA/FPKQNDYRE
10414	24315	A	10495	181	3	SPLKFLSLRGVFGVRQSA/LLGASQLGYSGQLRDPLQEAVCPPSDLLCAGRTTFLFK
10415	24316	A	10496	156	2	AASTTRLGDRDQPGQHSSETPSLLKIQKLG\SGGGHLRLRQECNLNPGRGCC
10416	24317	A	10497	157	300	IQSWNTLKSITHVTHSNRLK/EVNHIVSTDAEKAADKIQHPFLIKKQ
10417	24318	A	10498	3	289	LVKMLTGSTGLKSYRHSFPFINSQGHNA LRKAG\PLPRKAGY\LGQFSLRYGL\WDGDKDLTIHQPDTRGSLVSRISKRGRL/CSCSLPLGTECLSI
10418	24319	A	10499	138	1	WYGLIYLLLEMESCYVAQAGVQWHDLPFLQPPPP\NSSNSPASSC
10419	24320	A	10500	138	1	WEGLIYLLLEMESCSVAQAGVQWHDLSGLQPPPP\NSSNSPASSC
10420	24321	A	10501	200	343	LEAHSFLSFFFIITIFFDTKSHSVT\RL ECSAAISAHCSLLLPSSNS
10421	24322	A	10502	84	339	PRDGKRRDKQKQETGGEHYKSLRGLRLQEDHVSPPGRCCEPSRSHCTPAWAT\BSNSVSKKS
10422	24323	A	10503	141	362	EWNCVCVC/CCCCCRRCF
10423	24324	A	10504	198	320	TIKKQKNTGGLTFNSYIPLPLLEPGDL\RLFDVQNRVKLV
10424	24325	A	10505	30	356	GYPCNPLIYMTSTVGFTSLDLFDIPLFHPILKVCPTHRLALDLSSDRNPGRILSTSNSSLY/EKDPNRKAYFTK/RSPVNDIIST
10425	24326	A	10506	16	375	KKFPFKKKKKIFPPFPLKLNFFPKRVNFPFGRWPKKSPKKVFFKFGPGFKPKPLKKKKIFFPFVKMGPPKGFPGKGGPPFFFFFFFFFFFVFFFL/LCLIPR
10426	24327	A	10507	156	2	AASTRLGDRDQPGQHSSETPSLLKIQKLG\SGGGHLRLRQECNLNPGRGCC
10427	24328	A	10508	313	2	QSKWLLKEESTLGEDAVNIVENTTKDLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YYRNLDKAAAGFERIDSNFESSSTVAK ILSNVICV/Y/REILHEGKSRPMQWTS SYFKLPQTQTQHSAILTILSPRA
10428	24329	A	10509	325	1	ECAKEMNAETKRNIADATETQRIIRDC YEHYNKMNLEAMDKFLDTHNLPRLNHE EINLENEPTMSNETETV/I/NSLPSKKK SSGEGFTAEFYQRKXTPLLKLPKK
10429	24330	A	10510	126	14	DSSGGVQLWLFPIIV/LWEPEAGRSPEV RSSRPACPW
10430	24331	A	10511	435	769	PFKFFPLSHACGGSLFCRLALECSGVI T\AHCKPOLPG/SQSDPPASTSQELCP/ TGACHYTRLCCREVL\HVAQAGLELL CPKDPPTSASQHARDYRH\GHPAQL
10431	24332	A	10512	147	412	RFVCSSTIKVLRLDLSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSVNYE
10432	24333	A	10513	251	466	QTCPTGSPASLELEFNSIATQWELVRL IAGNALKDEND\SAVKMLASLIMS YKAA AAEDYKADCPPNPGP
10433	24334	A	10514	286	1	SFLRKFLRGVPSRVKQCSA\LLGGSQ LGYSGVRYPLEAECFPFSLHLHAGRTT TLFKAVRQEHLSLQRIILLPLVGRVGRPN DSRCDRVIGH
10434	24335	A	10515	28	428	RFVCSSTIKVLRLDLSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSVNYDIIS T
10435	24336	A	10516	263	2	IKKPADSESAGAILDPPASQTURNSPL LLTSHSVCFYCYSSPNGLRQQLKIIIF FPLRQSCSV\SRLECSGMILAHNCLCLP GSNN
10436	24337	A	10517	62	292	PATLFSGVILPPTNSINAFSGSDSKSAH K/CEMLGTRNFNFCTCHTHIAEHSNST HTHTHTTQTHTHTHTPLLFYE
10437	24338	A	10518	172	2	RGKKIIFPLEKGNLWVMTALFFFFFE TDSHSV\TRLKCSGTILYHCSLCLPGSS DF
10438	24339	A	10519	42	194	ILVETP\CLRFVSLLENLVMKRLFLKLLK KKKKKKKKKKKKKKKKKKKKKKKK
10439	24340	A	10520	120	1	IFAKKRWIKFFFFFFFFFFVTFHS\VAQ AGVQCWCDLGSP
10440	24341	A	10521	202	375	SFLNKLHLSGVPGHVRQCASLTQ\ASQ LSYSGVTDLEEAFCPSFDLKLRAGRIT TL
10441	24342	A	10522	272	402	PKIFVYTKKANNYPPTTTEYTCSE/IR KFFIHIEYKVEDNKG
10442	24343	A	10523	147	439	LILVYNYISRKSTVYDSRHPCYVILPE KNCKYKHCNFLT/SSSIPPTPTSPSR ASPKKKKKKKKKKKKKKKKKKARGG
10443	24344	A	10524	7	415	RFVCSSTIKVLRLDLSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSVNYDIIS T
10444	24345	A	10525	321	442	TSFSFLFFF/LETEFHSVA\RELCGTI LVHCNCLCLPGSSNS
10445	24346	A	10526	477	3	IEGLLPNRKDHTKNPSCVRHQRPFVD KTTKMGKQSRKTGNSKNQASASPPKER SSSPAMEQSWTEKFDKLEEGFRGSIY SKL/REEIRTINGKEVKNFEKELDENITR ITNAKSLKDLMLKAEAQELRECTSR AASANCVAVPQAFDRSHGVQ

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10462	24363	A	10543	3	414	HSSAHAYGTYESGSKRYLQRPRTAEL KKALKEKKNRLLQQRKSVTSSSSSR DSSARDSSSERBETSTSSSSSDSDTDES SSSSSSAYSTNSSSSFDSDSS\SR GRSTSDSSADD/STNEESELE
10463	24364	A	10544	240	509	TFISPIGTPLNGEFCCKNFGI/GKFR MKVACQIETLGLSFFFTESRSVTRLK CGGAILAHCKL
10464	24365	A	10545	275	2	GCSRFDTAIFLMGPVPEERKLLFEKNK /DCTCMFIAAHFVPAKMWIOPKCPISN EWIKNPVTHIYIHTHTYMCYIYIYTHICV CVIHIYI
10465	24366	A	10546	233	2	WSWMATOSVLPOTAFTELKKNYSCTOET PILFYFLKQSLPLSPLEKSGSVIIAHCN /LQ/RPGSTTFPASAKVERTTGA
10466	24367	A	10547	2	420	KKKIPNKGCLKRTKAFKLTFFMLQRR TPPAFFKGGGFLDFFNPLPPSKGNPPI YSWERFFPRFFKNWAPVKANLLSFFP FSIFWRTGSRVIAQAGLELLGSSYPAS CLFESWDSRR\DHRRARTI
10467	24368	A	10548	190	1	AASTFFACVCFLEFFVFETESPSVAQ AGLQWHSLSLQPPNVLG/SGNFPPALAS PVAGNC
10468	24369	A	10549	155	1	ARGEKYFLEIGGGFFFLVFLRQSHS IAQAGVQWCD\LNMQPLPPRVK
10469	24370	A	10550	223	392	RFVCSTIKVLRDLSDDRNPCFLSTLN /SLAVRKDERYKAYFTK/RPDPVYDIIS T
10470	24371	A	10551	183	3	WQKLLFLFGTESCSVARVGVQWRHLSF KPPFP/GSSNS/PASASRVA\TGALHA RLIFVFL
10471	24372	A	10552	297	10	TDEELLMEERKKWFF\DMASIPGEDTV NTDEMKT/DLEYINLVDKVSAGFERT DTNF\ERSSTVSKMLNSITCYKII/F/ RERKSQMQWTSFLSF
10472	24373	A	10553	509	3	LLTDRTLSCRSVGVPCVRCQCA\LLG ASQLG\SRGSGVRDPLEAVCFPDLQ RFGRTALFKAVROGHLSGLRLLSFV CLCPAPRGAVRGTOASLSCGGLHPVRA SRLLCLPKQAMWVGP\TSLPPCSL ISDCCASSQRDS/VGVGPSKPGAGYNLV VRRF
10473	24374	A	10554	262	453	GWGILITANLVLVFGGSLISERIFFPSL ATGFCVSQAQGVQW/LIIAHCSEFLAS SD
10474	24375	A	10555	112	372	KKKGGGPPFFFFFIFFLIRQRAKLVVL AFNRRLGRKPD/IFYAGVGKIVKKYKS GFFIELVTTCCGKNYLMCALAVIDPRDSN IIRS
10475	24376	A	10556	50	358	RFVCSTIKVLRDLSDDRNPGFRLSTSN SSLY/EKDRNKAYFTK/RPSVNDIIS T
10476	24377	A	10557	203	350	QLHADRVSRFATHAECRGVIMAYFNLL PH/FKRSCLSLWSWDYRHAP
10477	24378	A	10558	98	387	IQDTDLRGVRYRDKKREKDSPPER EGEREKEIKORKKER/ERKKERKKEST HOKE
10478	24379	A	10559	237	3	EVFFKINIFELSCSVTQARQQGDHGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QPFPTG\SSSPPTLASQSAVITGVNHRT QSGLT\FSQPKQKALGKMCISGG
10479	24380	A	10560	37	359	RLKCGPVIAYCKLEILGSSNTPTSTW VAGTT/TCHHAQ
10480	24381	A	10561	170	3	RPFFLPWGGKFGVSVFFFFLVFFFI GSHSVP\RLKCSGTITAHCSLDLGGSS
10481	24382	A	10562	1	388	LPPEPLMVLRTANLVAMAFGSRITLL\LA FALLCLPWLQADAVQTEPLSMLYDHAM LQAHRAHQLDIDITYHELEETYIPEDQKI SLLDHSQTSFCLSDSIATPSNMBETHQK SNLEMRISLLLIETWLE
10482	24383	A	10563	224	392	CVDPIKWFPLETATROGCPLS\LFNTV LEVLAATAIRQEKIKDP/QIGKEVK
10483	24384	A	10564	185	2	RYFGGPDSPQNGKTVFNLPFFFTFRV/ HSCCPNSNGTISTHCNCLPGSSNSPA SASQVA
10484	24385	A	10565	175	324	APGYGTYRVLCKILLRLRHKNHLN PGRGCSSEPRSHC/ITPAWTE
10485	24386	A	10566	3	367	HELLWSTIKVLPLYLRSDRSPGGVISTS NSSLC/EKDKKNKAYFTK/RPSVNDIMI ST
10486	24387	A	10567	128	391	GETCEGVYGPQGGGKQTKWVFSKSKDEG PCSKTMDVGLGSSPQIFLKKRVFFFF FETESHVTRLECSGTPTG/HCNLCYGP TS
10487	24388	A	10568	251	485	SFLKRFPLKGVGHVRCQSA\LLGGASQ LGYSGVADPLEAVCLLEDLCLCAGRTT ALFKAVRQGHLSLQRELLPLFSY
10488	24389	A	10569	176	3	FVEFPLKKGGPFLKCKEKGFFFFFTSEM ESRSVT\RLCSCGA/TISAHNCNCLPGS SNS
10489	24390	A	10570	212	386	RFVCSSTIKVLRLSSDRSNPGRFLPSTN SSLY/EKDKRKNKAPFTK/RPSVNDIIS T
10490	24391	A	10571	134	489	SLFFLPSPRDRWGLTOSTEMPPSWKFGP REIRSPILLAMLHSLLLQPTAFLCPSSTL LLSLKPDLSRTGSLFLSFFSFLYFEACS VA\RLKPSGTISAHNCNCLPSSSDSPAS AYIVSG
10491	24392	A	10572	1	470	GQSGRIPLLLTLDLEKPVSLLSVTNLY SKNSAQFSTILQTLSPFATFTPSPIPL SSAYFFFFSDRVS/LLSROECSGLNLG AHCRRPQPPRFKRFSLSPSS\SWGLTR HTTTPGLIFCIP/SVEAGFHVAQTLGLE LLSLNSNPASA/FPKCWDHRR
10492	24393	A	10573	242	410	VLMRMQIYFSLHNPIFFFTGTGSHFIA/ RLCSCGMIPAHNCNCLPGSSNAPASASQ V
10493	24394	A	10574	236	1	ARTFFIHLKASCGDNATITGVLWHRATW CPSVLLDRDLSLSEVCEILCIHAC/VMR IHEHTHTYIYANTHTHTHTHTHT
10494	24395	A	10575	241	35	RSSYLIIFNFVETRSVAQPGKLCCCSA WAGTPT\SSDPTSSSQSAGIIGMSNL FLOWLIIDQAGNIN
10495	24396	A	10576	294	72	PKNEKSPFLSFFFLLLSTRFYCYAQAQK LK\SNWQGDPSALASRVAGTRGVHRHTQ LQVSNFYKVLAMHSGSOL
10496	24397	A	10577	1200	1625	PDGWSYSSGHSWLPPEASNGKRAWSSCW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, =possible nucleotide insertion)
						VFPQLSPFPQAPPSPATHLGPTFPPLA/SP PQAPPPATHLGPAPPPLSSAP\PPPD TLGPAAPPPSSSGDPDFRYSP/EVPPQ LSPPQAPP
10497	24398	A	10578	226	325	ERHTHTPHSHTRSHRTLTHTHA/YTHTH AHTHA/YTHTHAHTHFFS
10498	24399	A	10579	108	320	TINVFLKVNVMKLSYLRFTNRNCSFFFL AGVQGDHGSILQLOPPG/SSCDPPSSAS RVAGTTGAYQHTQLIF
10499	24400	A	10580	1	288	ARGERERERERERERERERERERERERE REREREREREREGLSFFFSRGGGKLW CVC/RPSARPERERERHAFVSPPSLQKK KKVFGREGTSLFPYPCGSLRR
10500	24401	A	10581	1	476	REWGGLSLPRLCESVLTACSLGSLGL KRPSCLRLPSWKDYRCAPPSPSLNLFV ET/GPHYVAPGWSLLGSSD/PPPLASP KCDYRHE
10501	24402	A	10582	210	346	PHCSITHSVKRIQANVHKHQRTYGSVI PHILPHVLKKT/PSLRDF
10502	24403	A	10583	316	461	LPNITLGVVLEFFVSETGCSVTHAGVQNC DEHGSLSQCTFG/SSDLPTSD
10503	24404	A	10584	172	383	NLDLYLSYTIKNSKWTIDLVIAKTIK LLE/KNVAGENIPDLGLGKEFLD/KTQK ALS/TNKIKDKINFTR
10504	24405	A	10585	273	374	GPGETAHTRNPTSLGGRGGAIT/R/GOE FKTSLAKM
10505	24406	A	10586	150	344	KLKCKITIKLGIRISFAVIVVVEIGPHF CYLGVVQW\PIRTHPGSSDPPASASQSA GITSMSHHT
10506	24407	A	10587	199	3	SFSYIRVHLGHKIKTRHKSACEVYANCK ARGIITGIKKR/RWPGTVAHACNPNTL GGGRGWITRLV
10507	24408	A	10588	216	1	PRGAPTCMRQSQAL/LGGVLQQLGTG/V RDPLEEAVCPISLKKRCAGRTTALFRAV RQGRSLQKFLPLFLV
10508	24409	A	10589	190	3	ISAPQWAAFEKRFFIYRAPA/LKFMIF FSPPFGVPPFFPTFFFFMESRSVARLE CSGVISAH
10509	24410	A	10590	369	40	KTERNSININKNDVHTKTPSKGRQHQR KADKSRMRKNQHKKAENSKNQNPSSSP RDHNSSPARKQNMENEFDELTEVG/RP KVGNSSSELKEHILTPCKETKNRTGW
10510	24411	A	10591	114	398	RFVCSITIKLRDLSSNRNSGRFLSTNS SSLC/EKDKRNKAYFTK/RSPVNDIIS T
10511	24412	A	10592	132	1	ILYLWCVCVCVCVCVYLLIL/CKVL SCLGEPALSGAFQMS
10512	24413	A	10593	3	287	IGFITLRVGLLYLLLYLYVYVFFQVNYI VFILVLAFLKRNLLRYNTALNVEEVT REKISHYFI/NSYIHTVCKINKMD
10513	24414	A	10594	2	363	RAEVGVMAFLYLLLLSGALGLTDTWAG SHSLRYFSTAVSRPGRGEPRIAYEVVD DTHFLRFDSDTAIPRMERPKPWQEGB QNW/WTTGYAKANAQTRVALNLLRLRR YNQSEAGE
10514	24415	A	10595	156	3	NGLELSDSDGCIALLFFYFETEFCS/V AQGVQVQCDLGLSKPQPLGFKPTRP
10515	24416	A	10596	80	306	MDEELLFRDEQRKWFLEMESTGEVAVNI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						V/EMPIKDLG/YRRLVDKAVPGCERVD FNFEISSTGWVWNLTPAIPVL
10516	24417	A	10597	232	389	ILCWVFCCECCCCPETFVLVIOAGVHWC DLDSLQ/SPPPGSSDSPASAS
10517	24418	A	10598	463	154	MGQGGKPRFPLFFHFFPIYFFFLKQGFSL PRVQGRACKVPGTLASWGQKILLPQPPR /RVQENCLNPGGGGFSEPKPPSPFAW GEGGSLKLNKLNKKTTHIC
10518	24419	A	10599	208	38	LGPFQGFPTAFPPFFFTETESRSLAQV GVQWMDLGLQLPPPG/SSDSPGLSKKF LL
10519	24420	A	10600	200	3	CQPELSCMRC/RQSLGLGSLSPSGMEVR DPVEAVCPALAEKRCAGRALLVRICCS LQSQAGTFK
10520	24421	A	10601	73	427	RVVCSTIKVLRDLSDRSNPGFRLSTSN SSLY/EKDKRNKAYFTK/RSPNDIIS T
10521	24422	A	10602	193	401	GEVSLSPRLCNGVISAHCNFR/LPGF KRPSFFFL
10522	24423	A	10603	181	395	RFVCSTIKVLRDLSDRSNPGFRLSTSN SSLY/EKDKRNKAYFTK/RSPNDIIS T
10523	24424	A	10604	384	10	PRRPGCEVCHLQDLSLVTDRLRYSGRLRS DCTLSCDPMBAVPHNSLSCSHYRLKPA SGITWGCKCAGFTSFELEFKMESHV\T RLCSCGALSVPNCNLCPGPSNSPAGGS LGPSSSRPPWTT
10524	24425	A	10605	215	379	RFVCSTIKVLRDLSDRSNPGFRLSTSN SSLC/EKDKRNKADFTK/RSPNDII
10525	24426	A	10606	1	163	QTHREFAMVLPADKTNKAD\WGNVDA HAGEYGAELERMFLSFPTTKTYFFR
10526	24427	A	10608	283	2	IQKHGLIRCPQETPFKNNDVGNQKVEG RGEKSIQIL/YFFFLNS/HLSRPLE/ CSGALSAYCNLRSLSHSSDSP/VGDTIG ACHHTQLIFLFLVE
10527	24428	A	10609	144	327	CSWNSWFCGCVRVSTLIRKKNNFFEFMEFR S\VAQAGVQGRDFGILKPPPG/SSDSP ASASRV
10528	24429	A	10610	137	1	HKCPSDDEWDERV/WCMYTRYKCSALT KEIMSPGKIWMLENIMI
10529	24430	A	10611	201	334	SFFWRFCFLRGVPSRVKQCCQ/LGGSASQ LGYSGVDRDPLEAVCF
10530	24431	A	10612	146	2	KTPLKGLKRVPPFFFFFTETESCVTQAG VQWHNIGSLQVPPP/GSRHSP
10531	24432	A	10613	205	259	TTMPGLSFCTRTKSNKNLSPLTLGDSAR VDLFLYLLFRTIFQNF/CGRDKVLCC PGWSQTPELKQLICLDLPKYWDHYEPL CLAYFPALQNLTKI
10532	24433	A	10614	153	2	GVLMVSDGVLSMLANLFFSFLFF/LFET QSHSI/SRMCECSGVISAHCNCLCP
10533	24434	A	10615	213	8	KPFFPPFFFFFLFFFLRNGSHCVVSGY/C KGTIYVHCOLELLGSSCSPAPQVSGIT GLICASIFIEE
10534	24435	A	10616	146	1	ILTRIDYWNKTLFFFEPEKFS/VLPR LECSGALSACNCLLPASSDS
10535	24436	A	10617	208	2	NNFWSSSKYGYFSSETESRSVTMGH DLYSLQPPPP/GSSDSPASASQVAGITG SCHIAQLILVPIVE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10536	24437	A	10618	120	2	SFFFFFETEFERSVAQAGVQWHDLSLQPPPG\SSDSPSL
10537	24438	A	10619	162	1	SFHWKRLRLGAPGMCRCMSA/LLGGVSQ LGYSGFWHPLEAVCPFSDLTLCAG
10538	24439	A	10620	193	419	TFFFFFETESRSVAQAGVQWRDLGSLH/S QPGQOSETP
10539	24440	A	10621	313	460	KPGLWRGTRSQKQVLFFEPESHVSVA/KL ECGGTISAHCNFCPLRPSDDFA
10540	24441	A	10622	243	505	PTGCPKQEQVQAMLRPVVFFVFETQFN S/VPRVCSGTTISAHCNLRFPGSRDSPA LASRVAGICRR/CATTAAQLIFVLVETG FCHLVG
10541	24442	A	10623	67	430	LARRTWKNQHSSTHGCDLFFFFFFF LTKKGVFFPPGGGHRHFFINIKFLN YKRFFFCLFEDVLMISVGFDLAFVFFFP WRGGFYSLLRCV/LTFLALGAPLFAPM FFLFLFGEEL
10542	24443	A	10624	3	207	PGGQLGSECSGVRMDDEVL/TLKSLTIG ESGVGKSLLLRFTHTDFPELAATIDP SSVVNPARNAATP
10543	24444	A	10626	151	380	KMLFGQVQWLTITIPALWEAAGGSE/LRSSRPALKRKSETSSPSPCQKKKKKK KFRPRAGQMLEVPPFPGRVGAG
10544	24445	A	10627	210	3	NFCQVKGFQKQKSSQIKGFGNKKKKKG SFFFFFETESHSTV/RLECSGTIIVHC SLDFPGSSDPPTSA
10545	24446	A	10628	237	2	LCPLSGAGSCSPYIDVYTEVGNVNTFTI LTNTKNTFGPLFLIIFFFGETESLSIA/ RLDCSGAISTHCKLCLPGSRHSP
10546	24447	A	10629	1	352	RGPLSTQDYISKALFLLFGFLLLLLL FEVRSCLTQAGVQWCHSHSLQSPT PG/RSPDPASAS
10547	24448	A	10630	48	200	ATKPKNFLFSETKSSSVTQAGVQWRDL SSPQPPPP\SSSDSPAPAN
10548	24449	A	10631	209	376	SPLWKFCLRGVGVQVCRQSA/LLWGASR LGYLGVRDPLYEAVCPFSDLCAGRIT
10549	24450	A	10632	141	1	AGGFFFFLFFLETESRFA/RL/QCSG AITAHCNLCWGSNNYHAS
10550	24451	A	10633	18	522	PLYSLTRHRTPREA/KDNLKSTQLLSVI DAISEGPIEGPVDGLKSVLLNSTPVLDI EGNNTISGVTVVFRAGEQEQTPEGFES SGSETVLGTEVKYDTPITRTITSANIDR LRFTFGVQALVETTSKDRNPFSEVRLLV QIQRNGWVTEKDTTKGKTTQYLASV V
10551	24452	A	10634	127	2	NLSPLFFFFPETSRSVTOAGVQMSDLS LOTPPP\GSRHSPFK
10552	24453	A	10635	336	452	RIFFFLEETEALSVAFAPAVQFDLGS LQ SPPP\GSSESPA
10553	24454	A	10636	259	3	GTRIFFFFNSSPLSFPVQKKSVSFFFF SF/LFFFFFETESRVT/RLECSGAISPH CKLHLPGSRHSLASATRNVLRLPWRHGA SCA
10554	24455	A	10637	96	413	GDNTSQSAILINYIFFFFTFLF/ETG SHSVAQAVRLEYSSVITAHCNFLRGGSS NPPKKKKGGAVLKDPPWGGQSLPLATY YFFPYRGANKNLLGDWEGPLFV
10555	24456	A	10638	180	473	CYMGKRAWLVLNSLLTLKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKKK/EMPVKQKNRGRALYKK KKGGRPPFIWDPFFFFFLGGGKKHPGG FFRKKFFPGGGKKKK
10556	24457	A	10639	312	480	ETVDSGSDDDVNAEMATKDSSEYINL V\GKVAEPERTDSNFE\RGKMSKSI
10557	24458	A	10640	2	516	MKPLENLSOTASLARGATLLRPVLRRLC GLPGLQRPAEEMPLRARS DAGPLYSHH LPTSPLQKALLAAGSAAALYNPYRH/E ERPRISTSTLDLQKLSLPEGS LGREYL RFLDVNRVSPDTRAPTRFVDEELAYVI QRYREVDMLHTLLGMPINILGEIVVKW FEAVQ
10558	24459	A	10641	56	455	PLCSYIQTIFYHSKFPNSNQISLVHTIPLS KLFGYFSQLYSIYSYLCOHFIIHLLSIFI TVFCIVFYWVFLISVPMYICVCLCTN VCVCV/CCLW
10559	24460	A	10642	272	33	GRWFLFLGPAKYFLTGGRFSPDFGFLK INPPFFFFFDDTSHSVAQAGVHWHL GYLQ/SPPPG\SSDS PAPAIFHHTV
10560	24461	A	10643	285	1	MGNFLKRFKNEKKFFPILRAHPFNFF PGKSPFKTPRALPLGVPPKHPFFFF FSEBESSVARLECSGMISAHCNLNLH LPGSOYSPAL
10561	24462	A	10644	100	466	FLKFLREVPSPRVQCSA LLGPTSQL GVSGVDRDLEAVCPSPDLKLCARTNT LFKTVROGHLSLQRFLLPVQLCPVRPG GVYRGQASLSCSGVHPVRASPPLCLPK VPPPS
10562	24463	A	10645	260	460	LKPHAERETIDKRLPYSPFFPFETESC FVAQAGVQWHDYSLPPP\PGSEGSRA
10563	24464	A	10646	360	504	QIGHICAYVEKTELRIFFLFFFRQS CSVT\RLCESGTILAHCNCL
10564	24465	A	10647	241	45	WEVEVPRAVPCHLKRDYFFITLFLFLF FEMESYST\ELCESSAISTCNCLCPFG SRDSPGIPPH
10565	24466	A	10648	76	462	FLWEYQEKAHILWSLFSKLLISRSRFTV KEKVRQKPGILFIYLPFEMESCSVAQA GVQWRDLGSLSPQKKDS/DQSKAITFV EGINSKRGWGTGPHF/HCSLKMIFLI
10566	24467	A	10649	3	359	QTQREPTMELTPADKTNVKAANGKVGAG AGEYGAZALERMFLSPPTTKTYFPHFDL SHGSAQVKGHGKQVADSLTNAEASHEDYM LNALTALNDLHAHKLWVDQVNFKL\LSH CLLVTLA
10567	24468	A	10650	266	3	TPEKKKKIGGLGAPFFGYPKKIWWPNFF PFKKTITKFFQFQVWGAAPPKSFPPFF EVESCSVAQAGVQWRDLDSLQSP\GS RGSF
10568	24469	A	10651	278	461	KKITCGFFFDITGSCFVAQAGQQWRDLRS LQSPPPG\SSDSLTSASRVVGMHRMRA VF
10569	24470	A	10652	161	456	VFFPPGGENLAFVENKTTLSVHNFMTRT AUCIMENYKCGCWGWTIGFMPCNLESK RVQSLN\KVGQFFKWLNVKLLVGLAIFL TGICPKKLKYVQGY
10570	24471	A	10653	91	486	PCFNHGHNTNMYFFSLSLTLPFFVSLK PVILAYKTFSPFITRVLLQRRHRQKPV LDGPNGVDDNNILGSIICVSLIKIFFLTE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SCFVAEAGMQWCNIGSLQAPRF\GSCHSPGISPPVLG
10571	24472	A	10654	267	470	NLHMRCEKEQNPNKLSFKDLFGLGLWLWFPFCFWRRLITLSPRELC/RG/MIPAHCNLCLPGSGHSPASA
10572	24473	A	10655	775	1401	TFPSQIRYGLRRKRNLSLSPRLECSGAISAHMQRPPPGFTPPSCLSLSSSMHYRRPPRPAICVCVCVCVCVCLVETGFHRVNDQGLDLLTS/I/PPASA/FPKCWDYRRE
10573	24474	A	10656	287	454	LFLIYFLYFYETECHPLAQAGVQWRDLSSLQSPPP\GSNDSSASASPTVPTSAM
10574	24475	A	10657	212	64	LFLSKFYFFHESSCSVAJAAQWCDLGSVQPLP\POSDDSPASAWGLD
10575	24476	A	10658	368	473	GFIDHTRRERPECF/LTDEWIKGMHIHTTEYYSA
10576	24477	A	10659	358	1	TLAVECFCSAGFEGGKLTFFFNRRGRETFLALVKTTPPGKARGPVFISKNKIPEFKQPPNPNPNSFFFPFETESHTIARAGVQWHLCSLQSPDPG\SSDSPGRNSLQRTETIAPL
10577	24478	A	10660	2	235	KRDLIRHYPKEDIYMAKYILK\CSLTMTHTETLIRTTMRHYLLIKVTIFKKTDMTAVGVHICNPNTLTGHGRGIA
10578	24479	A	10661	9	538	CVTVIRIPSRPTPLSSDSNSNPRFLSTSNSSLY/EKDKRNKAYFTK/RPSPVNDIIST
10579	24480	A	10662	374	38	SPLWLKHLRGAPGCIRCQSA\LLGGVSQLGYSQVRDPLEEAVCPFSDLKPRAGRTTLFKAVERGRLSLQKFLFPVOLCPAARGVYRGROASLSCSGLHPVRASRPLCSR
10580	24481	A	10663	268	47	ALIPLSLITISAFHLLLETVSTSSPKMECSGAITSHCSFNLDPSSPPTSASR/VIGTIGARHQALMFIFYC
10581	24482	A	10664	64	451	FSSERKSHMSLT\LNQKLEMIRLSEEGLSKAKVGQKLVRLHQTVSQVVDKELKLLKIKSATPVNIGMIKQHNLIADIEKFGMIWTDCTSHRVTLCQRLIQSK/ALTLFNSMKARGKAADEKLEVRNG
10582	24483	A	10665	355	474	LYFYFIFPFTESCSVAQAGVQWRDLGSLQAPPQSRDSP
10583	24484	A	10666	317	481	GHCTCQWCTFFFFLPRDRVLLHHPGNSAVTQSWLTAALT\FGPKRSSCLNLLNDWD
10584	24485	A	10667	57	329	VKNTQWQKDSLFKNKRV\FKNWASYVRIKLD\LTYSYAKINSKWKDLNVRLEIVKVLOVEYPSFKILNGSVLDPVFVYSGIFAHLHMGEPH
10585	24486	A	10668	86	468	ENYKIPLMGGKNFLLEPSPIDPFFFFFRGLTLPLRLKCSGDHCSLQRPPLPKRSCL\GFPKCWDYRNEP/CVFR
10586	24487	A	10669	254	25	GSHICKVPAAYISNTCTSSHDGDDGVGCGSSGSTHPSPVADSFVVVETVSL/SVTQAGVRWCDLSSLPFPPPGI
10587	24488	A	10670	206	3	YGRPRKLCNIGLKSGLDPTHWGQHRVTSFFFIIMETDSRSVAQAGVQWHLGLHPPPPG\SSDSPAS
10588	24489	A	10671	20	355	GFTSQSELLYSIDPITRPTQVTIGISA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						QSYCRVHVHNRVYDLDVESOHFNPAGPAIKGSVCSTIKVPGDVSSGRSNPGRFVSTSNSSLY/EKDKKNKACFTK/RPSPVNDIIST
10589	24490	A	10673	112	359	NKAQQCVCHENHFKLKIDANTLNKIKVWRNICSSPNQKKYGLAILNLDESGFRSRKDTGDEE/HFIIKKKSVIQEDFSIINIYA
10590	24491	A	10674	317	2	TGPGFFFPQIKKVFPPFFFLKIFFTQKFLVSFWGFKTIKVGPFVFFPKGPQPRFSPFLGVQAEKFFPPPPPPPPFFFCERGSHSV A/RLECSGAISAHNCLCPGFK
10591	24492	A	10675	240	495	DHRPEKTSSTCQAGEVFLGLFVFPFRSSTDWVRPAFI/MEG/HICPTQSTNSNINPVWKHPHRTQDNVVPNANSPHGVKXLMHKLI
10592	24493	A	10676	271	484	NPAGQTCRIKSPFFSFPEFTECSVTQTGVQWHDHSGMQPQSLGP/SDPPTSANSSA
10593	24494	A	10677	364	121	KQEVVRLSHNALCNDQASPLPGSGHKKSKQKLSKAAPCAGSSKKHL/HKECKWHTHVTHTHIHTHTHTIHAHTKDRFA
10594	24495	A	10678	354	539	FFFFFVVEESHAIAGAGVQWCHLSSPHL/SPPPGFN/DSPASASSAGITLSSSVRL
10595	24496	A	10679	123	853	RWSLCHPRLE/CSGTISAHCK/L/RAPGFTFCSLSLSPSSWDYSAHHARLIFPVFLVETGFHHVSDGLDLLT/SG/IPPALA/FPKGWYDRE
10596	24497	A	10680	251	30	ASLGVSAPLCIHVSPCPNPGDLGKTWVVGCGFFFFEMEFHS/VLPRLECNGTISAQCSLCLSSSNSPASASRIFF
10597	24498	A	10681	203	1	NFFAPGKLGPPRDSLKTAPPPFFFFFETGSRVA/EAAPV/W/COLDLQPPPTLPDS DSPNSASGVAGITG
10598	24499	A	10682	237	397	DSLTLSPRLECNGISAHVNLCL/RLGSSNSPASAS
10599	24500	A	10683	8	388	LYMCWFRPGFLAHNSHDHGYSLTLCSCWASGLKKQP/CRLSKKKKKKKKKKKKKKKKKKKKKKKDS
10600	24501	A	10684	201	463	IYWEDIVQGIADVRLTSRKHNSKFLGEC LMFGQGFLFFEMDSHAARAGVQWRSLGSLRPLPPG/SQVILLPSSDS PALASRVD EIAVG
10601	24502	A	10685	151	1	PEKNKKTQKAPPPPPFFETGSPSVAQAGLQWRSHSISQNEPP/GSSDP
10602	24503	A	10686	165	3	CVFVEDIISNPPFFFMETRSVAQAGVQWREHGS/ASRVAETIGVHHHAQLIFR
10603	24504	A	10687	292	384	NTEIGWVWMLTTVIPALWEAAG/EITRSG
10604	24505	A	10688	161	365	RPFCWIRTSRWCWRYRFDGSTIKVLRLDLSSDRSNPGRVLSTSNSSLY/EKDKRNKAYFTK/RPSPVNDIIST
10605	24506	A	10689	286	3	QPSVSVSRVICAPAPFGMGSLSPQLQCVIVNFSRVTHTMKSSAVLFIPLFSLFKLEL/REASPLVSFLPQMLRIKWE SBNLVLCLDRG
10606	24507	A	10690	169	2	SDTPANWPRKRVFPFGFFFFFTESRPV T/RLECSSTISAHNCLCLPGSSDSPASGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
10607	24508	A	10691	240	406	DGIRLSFFFFFFETKFGPVA\RLER GTIWNVNLHLPGSRDSPASASQVAGIT
10608	24509	A	10692	343	3	QVPLNLSLHLKLMFLPGCINGSLSQFL QFFAQISPYQTGFPSFYKTSIYHNSLHQ YLSFLPYFIFLFFSFFFLKQSHSVS \RLCSCGMVSAHCNLRITATSTTQVQVI LV
10609	24510	A	10693	196	3	YDAGHTKTLHPTVYVFLPCWNECKM VPRWKIVRR/FLKKLNTKLYDPAIFP LSVQKELRT
10610	24511	A	10694	245	391	KTYGQGVAVHFGFRREDHPLRGVQDK PDOLKEPVSTKNTKLVN/SWVL
10611	24512	A	10695	252	389	KTGQKVLFFFFETESRSVAQVGVQWRK RSLQPPQVQOTSDCPASAS
10612	24513	A	10696	385	1	FPNKAKMYSKNDKNLCHRGKDTLLNKC WESWIVTCTTMKLDLSLSPYTKNPKMI KD/LKTIKILGENTKKTVDLIDGLHK/NM SKTSKAMTKILDLLKLSFCPAKEIISR VNRKSTEWKVFASYLSN
10613	24514	A	10697	296	430	KHTQARRGGS/CGN/RQHSGRPRRADHL RSGVREQEPQPGKPHL
10614	24515	A	10698	280	468	DYLCI/SLSTYLSYLSYLSIITHQFIY HLFIYHLSNLSISIFFTKWS
10615	24516	A	10699	15	393	RSVGVLGVPVRCQA/LLGGDSQLG/SQ SGVRDPLEAVCRFPYLQCTGRITALF KAVRGHLSLQRLLSF/VMLCPAPIGG AYRGRQASWSGGLHPVRA/SMLLCLPK EAWAGAPPPASLPPLS
10616	24517	A	10700	176	1	DWTINFTFLYNFKPSSMLPYLSHLFRT LR/MWPGAVAHARNPSTLGGRGWIMRS GDE
10617	24518	A	10701	494	80	FNKKDIHSDTFSEGHQLORFNVETLKKM GRNQCKKGENPKNQNASPKDHNSSTPR EQNMKNSEDELIEVGFRRVITNSSEL YKG/DVLTOCKEAKNLENRLGKVLTRIT SLEKNHGLMEVNIQAELCEASAGWR
10618	24519	A	10702	264	410	KKGFLTFPPGGGG/PQKPPGFLNPGG QRDSFFPPPGGNTGETPPGG
10619	24520	A	10703	125	3	NRNGKGV/QWLPVTPALWEAEGRSP EIRSRDQPRQHGETL
10620	24521	A	10704	184	2	RIRVLAPCRHLPRAPETWPKRPPFFSFF LFFPQTQSHSVA\RLCSCGAI SAHNSLNC FPPRP
10621	24522	A	10705	187	406	LFLMKFLRGVGHVRCQSAL/LGASQ LGSSGVDRDPLEEAVCLFSDIQLRAGRIT TLFKAVRQGHRLRQRLIL
10622	24523	A	10706	82	410	TLRGKQKGIYFNRTDWRREALRQSLSLFN FTIFSNFLASLHKPEMETELKGSFIELR KALFQLNARDASLLSTVSDPSFCRKFS R/CSKCGQ
10623	24524	A	10707	390	2	SKDCRTAKIAACSFLNKLRSAGAPARCK PELSCMRCLSA/LLGGVSQSGGTGIRDP LEEAVFPLAELERCVRSAALFRASRQE HLSLLKMHPLPLPSGALSQADGSFYK PLTGASAFLEMPQCOERR
10624	24525	A	10708	229	392	YSWNRQMHSAHAGVQWCD/LVSLQPPQ PG/SSDPASASLAARTTGAGHHNQLTF
10625	24526	A	10709	193	2	RYLCYQDHRVILLILLLLFLRWSLTLSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RLECSGTTIMAHCSLDS\SSNPPTISASQAAGTTGACYH
10626	24527	A	10710	180	11	LLFFPETRS/HVSQTVVQCGMISGHCNLRSGSSDPPLASRVAGTTGKHQINWLSR
10627	24528	A	10711	234	408	MKLIMLKVILFPQIHLQIQPNFYQNIFF FETELCSVAQSGVQWNLSSLQHEPP\GSSD
10628	24529	A	10712	312	470	TGPHCVT\RLECSGAI\TAHCSLDFAGLS TSPTSVSQVSGTTGT\WMLKTIILS
10629	24530	A	10713	64	392	PKNVIRISSETSLYASLFLQMGGRQK/ CEPQPKKKKKKKKKKKKKKKKKKKR G
10630	24531	A	10714	169	427	NNQKTNKMGVGSFYLSIITLNVNELNA PIQRHVAEWIKKEKKKKK/DPGICGLQ QTLFFYEDP/HDPLRLKIGW/RKYPS RGTOXK
10631	24532	A	10715	176	410	ARSSWGLHTAVFVAFFSLRPLLEIFLDR DTRCSPPAAFFETGSCCVA/RLEGRGA ITAQCSLNLGSSNPPTSRSVA
10632	24533	A	10716	234	389	NSGNMDRYKDVQNTIQNPICWFTVAHA CNPSLTGGROGQIL/RQGFETSLA
10633	24534	A	10717	190	2	GPFFPHGGFLRGFFVNTI\FPPTFFFF FFLRSLSLVAQGVQVQCDLSSLQPLPPG P\SNSPCQ
10634	24535	A	10718	201	1	WPLFLPKMFFFKFRPHMGSPSPVGAQA KKKKIFFFLTGSHSVTRIECSGTISAH CSLNLPGPSH
10635	24536	A	10719	195	419	EYHTSLVTCGNPCVYRNNKINQTSRRK VITKIRAELEIETEK/LQGSGETKIWF FEKINKTGLELLGSSDPFVW
10636	24537	A	10720	218	407	GKKNLAFKKKKKKKKRKSQSPSNMNS AKIEARTNIKLVVHGWKNCEIDA/LQ KAPGDNA
10637	24538	A	10721	231	409	GTQLHLGGSFFSEKELSPCFWF/MFALE EMEACSVT\RMECSGTVLAHCNLRFPGT SNSSA
10638	24539	A	10722	40	401	PLCPSSESGNTLMASDDPSTPAVPPPNL THPPLCLSKSHLPLRPKQGLPSGNLLQL PLTLIPLLGAPVACWQLPQOCTLSTFF FETKSHVQAQGVQVQCDLSSLQPLSPG/ SRDSPDSAC
10639	24540	A	10723	210	14	HVMGLLLFLINKLTVNVFGLAGFWCLG FFWFFSFFETRSGSVT\RLECSGMISAH YKLCIIPGSH
10640	24541	A	10724	347	462	TPFFFFETKSRCDIQAGVQWCDLCSLP PSSAPDSDCP
10641	24542	A	10725	169	386	DKXQAKTIKWKGSFSNKKWCWNNCIATG KMKLDP/YLTFYK/INSKWIIDLSI
10642	24543	A	10726	257	54	ELFFFKRGGLTSLPSKLENGTUTAHYN LKLLGSRDLPTSASF/SAGITGISNPAR LFTYLN\THLOT
10643	24544	A	10727	2	401	NNYDRAETGYQVMYCNLTFFYCLQETHL TCNDIYRLKVKGRREIMQIENKRVGVAI LVSDKDTFKPTTVKKLHYIIKSGIOPE DLIILCTYSPNIRASRFKRIPLDKKEI A/HTVKVGDFSISLNLRSQNT
10644	24545	A	10728	154	1	PMCSLILGLSGGII\FFFFFEAFCSVAQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10645	24546	A	10729	34	151	AGVQWRDLGSLQPPPG/SSDS PRFPVPSLLDRGLQLMRQRLRHRAHS NGFVIGSKQIMKLLKNYVRRPVG/VAVA TMEDPPRPYPRSHIEDDFNYGGSVASAT VHIRMGSLVENNK
10646	24547	A	10730	2	408	VFLITVTRLTICRSVGVMWRSTPDLVCLG ISSGGCRTANIGLYQMLLPDHSSGSFCL RGVPGHVRCSQA\LLGGPSQLGYSRVVD PLEEAVCPFSDLOLHAGRTTTLFKAQRQ VHLTLQRLLRFVWLCPAPRG/GVYR
10647	24548	A	10731	274	89	ENIPTVFNPPVCSPLLMQPG/CEYPL CKLCLKLHKHVRVY\FLFFFETETPSHV ARLECSG
10648	24549	A	10732	251	1	TFQMMKCFPSHRKIFHNLDDKASYKIVY KEDPFSPSLSSSVLKNFFLETESC SVTQAGVLWCHLSSQLPPPG/SRDSF
10649	24550	A	10733	375	1	APFPPLWVRGSPFPLVFFPHKPKLP AEILGFKKERKWSRKPCFLPKVKLLVS VMPGLELQIFKFIGEPPFSPSLVGRKP NPLFGPVFFFFFEKESRVA\RMECKGT ISAHCNLHLP
10650	24551	A	10734	82	398	SFLWKLRLRGVPSHVRCSQA\LLGGASQ LGYLGVDPLEEAACVPFSDLOLPAGRTT TLFKAQRQGLNLQRFLLPVQLCPASR GGVYRQGRQASLSCGGLHPVRAS
10651	24552	A	10735	2	341	TFCAISWLESGVEDGPRSRISYRSTFF FFFKGAPEPKVEKGRPKPLAPTSLPGA HGTITGLSGWTTPS IGGWQPPPPPRENK GEHPAPVAGDTTQ\FKKPPFLKVFPF K
10652	24553	A	10736	171	1	RVPYLLAFALFVDTSPPFVSQAGVQWCD RSSYQSQTSG\SNDDPASAYRVAGTTGV EHKTTVTKTKMEEMADSGSNMLRTIIF LFLFFETKSCSVT\RLCN/GSISAHCN LHLPGSSNS
10654	24555	A	10738	252	413	GLLGLQNFYSKVHLTKAHLKCKSGWDAV AHAYNDITLGRGSEW/QEFTSLTNV AGSTSRCT/QEISDLLEHLQENCLNPG GRGCSPEQSCHTPAWWTETQK
10655	24556	A	10739	101	249	IGLFPVHTMKNYHYHLCHHHHLQHMH HHHCHCHYHS/HHNSHQPPPPPPPP HHHHHHHLP
10657	24558	A	10741	119	425	IKPHLSMERTHLFLMNCWAHQKQCFK ADFVITDDIKQLCPQSWWTRAGLPLG AGRGSGHMLSHHFWPRHADILYGLVD QPQQGETPSL/LKNTKSSW
10658	24559	A	10742	112	2	GETFFFTGSSSVA\RLCSGATSAHNN LHLPGSSKSP
10659	24560	A	10743	188	3	PPPLFFFFFFFFFFKSGSAT\RECTA HCNCLPGSSHHPTSAYQVARTITDVCNH AWLIFV
10660	24561	A	10744	176	3	SLYSKNNPSHLLFLPTPIKFFFFFET EFRSVAQGVQWHDLSLQPPPG\SSD SP
10661	24562	A	10745	250	1	GPRRIIFLKEFYPRFVGKRNPAFGFFS GGKKPGPPFPNRPRIKFFFFFETFRS VAQGVQWHDLSLQPPPG\SSDSP
10662	24563	A	10746	155	3	PPHPFFNPLPIKFFFFFETEFRSVAQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, =possible nucleotide insertion)
10663	24564	A	10747	157	1	AGVQNHDLSSQQPPPG/SSDSP
10664	24565	A	10748	157	1	TPRPFFFNPPPLKFFFFFETEFERSVAQ AGVQNHDLSSLOPPPPG/SSDSP
10665	24566	A	10749	153	2	TPRPFFFNPHPIKFFFFFETEFERSVAQ AGAOWHDLSSLOPPPPG/SSDSP
10666	24567	A	10750	157	1	PPPLSVVTPAPLRFFFFFETEFERSVAQ AGVQNHDLSSLOPPPPG/SSDSP
10667	24568	A	10751	155	3	PPFFFLFFPRPLKFFFFFETEFERSVAQ AGVQNHDLSSLOPPPPG/SSDSP
10668	24569	A	10752	86	406	NTFFFFFTPLTKPFFFFFETEFERSVAQ AGVQNHDFSSLOPPPPG/SSDSP
10669	24570	A	10753	364	469	SFLWKLHKKRAGPCMCRCRLA/LLGGVSO LDYSGVRDPLEAVCPFGSPKLGAGRTT TLFKAVRQGHLSLQKFLLPFVQLCPAPS TGQEGRQASLSFGGLHPVQSSR
10670	24571	A	10754	250	61	GQPLHSLD/SHWKKSEDFCFLWPFHSEN VSAIHQDH
10671	24572	A	10755	66	446	GEKKKKRPRVFFFFFETEPGSVT/RL ECSGVLSAHCNLR/LPNNDS PASASRVA ASAKLG
10672	24573	A	10756	252	482	SFLWFKCLKGVPVCRCQSA/LLGGASQ LGYSGVRYPLEETVCPFSDLKLRAGRTT TLFKAVRQGHLSLQRLLPVCLCPAPR GEAYRGRQASLSCGGLHPVRASRPLCLP TALAMVGAAPPSL
10673	24574	A	10757	205	488	RLPRQPVKRWVAGVRGCCVGVVSKSLQ RSTLDWQGFPGQRCGLLFFFTLCH /TRLEGNESAHCDLCLPGN
10674	24575	A	10758	272	471	PLESLRSLGPLSNRTASSVFIYIYY IYIYIYIYTHYTH/HHHTHTHTHTHT QVIFVCVVLKDRVLLCHPRQAGARSW PRTSASQROEM
10675	24576	A	10759	17	342	YSYVLFFPLGTIESCSV/AFSAGVQMIN HSSLQLOTPLGKQSHLSLP/ASASFVA GTTGMRYHARLIF
10676	24577	A	10760	42	498	GTLSSGAQVLIGRIESIVVGLKPNWALG GCPSPRAVHLLASSDWRPSLDQGAEW KKGAEANGHKKR/GIAVISDQIDPKTKTI KGD/KKSHYVMIKGPICQBAITINI
10677	24578	A	10761	1	305	EPRERGREKEREKERTEERMEDRERKA EREREREKQEREREREKQERERERK EREREREKERE/RHEPGSL
10678	24579	A	10762	364	2	ASWDDPAHNNNFHFGGVVAHFFFCRL DCPWPAPRPAPR/VLL/TPAAAAAAA AASRPEKKRAEENVAIPPRKRPWRWEE RRGPRKGSAPPGAGARRR
10679	24580	A	10763	152	484	FPQKONGYLLPLPKPTGLCGKGRKRLG FFLNYFGKKKKRGRELQPPPPCQIWTG SIYRGSNGYFFFFFWQVSLALLPMLK CVRGMIRVHCSLDLVGSPNPTSSASQTA RTTGTCHH
10680	24581	A	10764	208	420	RFVCSSTKVLRLSSDRSNPGRFLSTSN SLSY/EDKRNKAYFK/RPSVNDIIS T
10681	24582	A	10765	319	85	SFLMRFFLRGVPHVRCQSA/LLGGASQ LDYSGVRDPLEDAVCLLSDLKLCAGRTT ALFKAVRQGHLSLQR
						GKLLNNNRFCGSKFGQIMFFPGTESPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: In US 95/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						ITQSGVRWHDGSLQPP\PPGSRDSPAS AS\RGITGARKHTQPIFLVNSNS
10682	24583	A	10766	122	3	KFFFFFETEFRSVAQGVQWHDLSLQPP PPPG\SSDSPSL
10683	24584	A	10767	240	86	RAPPPFFFFEMESCSIAQAGVQWLSLGLL QAPPP\GSCHPASASCLEMFSKI
10684	24585	A	10768	244	85	RAPPPFFFFEMESCSIAQAGVQWLSLGLL QAPPP\GSCHPASASCLEMFKI
10685	24586	A	10769	35	296	EUKSPSARQPPRLGSEHRLRAAASGR EVQCGPPGQPPCPGGGC/PPPGSPDW EVRSPSARQPPRLGGEPPNSLRTGHDDD GGFV
10686	24587	A	10770	260	484	MDEELLMLNEQRTWFLVESSPGEDAVS IITLARTDLEYDMLNLEKGAAG/LERKH YSFERSSVTDKILSHNTACY
10687	24588	A	10771	248	393	TOEGKKLINWNPQVAHACNPSTLGARGG RTTRGOLETK\LANKIKPCL
10688	24589	A	10772	239	2	SFLWKFCLRGVFGVRQCSA\LIGGASQ LG\SGQSGVRDPLEEAVCPSSDQLRAG RTSALFKAVRQGHLSLQRLLSF
10689	24590	A	10773	158	455	LFFTLCPSLQHIATVMLEGLKGPKSIQ PIFWVLQGTGP/HFLVTPVR/CCLPLL KLFLCLLVFGMESPSVPHAGCSGVI SAH CNLCLLGSTDSASPSRV
10690	24591	A	10774	166	403	KKTFLGEPFLFWGAKKKKFGKKNPGFFP RG/IKPRVFFSRFFFGPPPKGFPQKS FFLKSLPGFFLFGGCPPPPFFFFFFEM ECSNTRLECSGVILAHNCNCLPGSSDS P
10691	24592	A	10775	208	1	RLCFFYFRKALLGKAQIKNIATFFPRKGS FFFFSETESRSVAQAGL/LDCSGAISAH CKLRFPGSRQSPAS
10692	24593	A	10776	192	29	IFRKEFFCLNFFLLFFETESRSIAQAGV QWRDLGSLKAPPPG/SRRSPASRTGV
10693	24594	A	10777	275	490	KPGFFLLQMAKVYIFFFFMEFCS\VA QAGVQWHDLSGSMQHRPPG\SGDSPCLP SI/AGIPG
10694	24595	A	10778	340	3	LKVVPVKPSTLLGVKKVFFPGNKKKPF LALFFFRPPGEGSTFALQAKPTPRV VPALGPFKNQSPSLPFFFFFFETKSCSV TQAGVQWCGLRSPQMPPO\SSDSPASC L
10695	24596	A	10779	313	1	ANPFGGSGGDFPSSRVFFPGPKNETP FFKNKTTATKTKGNKGWAPS PHRGGEK KGPAALMDKKGNLWPPFFFTESHVSVT\ RLQCSNTILAHNCNCLPGS
10696	24597	A	10780	116	422	ILEDNTIQTITETLAREVQIQTTLRNH FTLTGMAII/RKTDNNKCWRECKIETL ICCWRECKMLCNEVGTALEIVWQFLQSL NIELSYDLAMPGFIIFFRE
10697	24598	A	10781	120	418	TQTGTAPQLHLASRWLSRSGGLTSSPQE IPKLFWISIESPLGSKHLSLQVFCFLV CSFVFMESCSVARLECSIVISAH\CTL HLWGSSHFHASASRA
10698	24599	A	10782	134	1	SSFFFLCQTESCQGVQWHDLSLQFPST RAQA\LSLPSSWDHRR
10699	24600	A	10783	2	435	CSHRGDSSSYSQLSGIRAGDLGGGKDI FRLLPTTLNI PAKGSEYDVVCVUTHERMC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LC/SCLFIYMCLCMCHV/HYIHEACVF MCLCL
10700	24601	A	10784	432	161	FSRAGFH/RVSDGDFLLPS/CLPPLGL PKCWDYKREPPRPANKLMCRQVHRKCTW LFIQIGSTLFKTNGLSAVAHANPNTW GGRGERIA
10701	24602	A	10785	270	442	NVRLRLGLALSPTLECRGTINAHCRLED PGLMQSSHLSHRVAGTTG/TCHIAMLIF KFL
10702	24603	A	10786	12	424	LIQLPRLECSGAIARCNFTY/SLGSGD PPTASQ/VLKTGVCHHAQL
10703	24604	A	10787	350	3	DSSSVQTNKGTGGQVLSLDILCAVKA SV LVIIPLHNALSSWLVLPALFWKSWQVGK SQQAHSVSGLC/MHYRSHTHAHTSPH RHRHTTYTARANTHTTQMLSAYLPSKQ PSGLSL
10704	24605	A	10788	155	3	HAFPAFCIRNRLECNQVILAHCNLC/RL LGSSDSPVASQVNOIAGACHHAQL
10705	24606	A	10789	188	2	RRLDLSLQPPRGQD/WRGCIYTHHTHT HTHTHTYTHVNGWKRHHVPGKMSANG ESRGAK
10706	24607	A	10790	19	405	IRFTTISVERGINSVLASEQRLPWDCI ACSQQLVVQQTWGPLOPFFSLGMDHR PTFRDLSNEPAPGAVNVSGLTSTPLPGA SHGLLVFFFEFETESHFVAQGVNSGDLRS LPFPFPG/SSNSPVSA
10707	24608	A	10791	157	1	KPGFPFPIYEGPLKTFPFFFEFERSVA/ RLECSGTISAHNLHLPSSSDSP
10708	24609	A	10792	157	1	QPRPFPFNRPRPKFPFFFEFERSVAQ AGVQWHDLSLQPPPG/SSSDSP
10709	24610	A	10793	83	387	SFLNKLHPGGAPACMRCOLA/LLGVSQ LGYTGFRDLLEAVCFSELKHAGRTT AVFSAVRQGLSLQKFLLPVQLCPAPR GGVRG/RQALLSCHRLHFV
10710	24611	A	10794	204	419	KGVYGHSGSFSPAPLACFRDKTLFPVS LWKEFVHSPWCKCTL/PQPLNKTWVRYLK NFKMR/PIPYVEIPLLG
10711	24612	A	10795	207	2	RRGFTMLVGQNSLDPSTSRSAHLSLPKC WYRCKP/PAPS/LREGFSYLLHSLHP TPAPGSHLWALIC
10712	24613	A	10796	2	237	FFFLRERILLALSPLRECS DANMHSCL NLPG/FSQSFCLSHP/ SRWDHRHMPPYP VKFGIFVGDRLVLPFKLSYI
10713	24614	A	10797	342	40	DRVFFCSPLRECSGAIARCS/LRTGGL KQSSHLSLPKCWNHRCRPPPARCSLNE SHSAKWPGQSTDSACEVQPTSPPTP VFYPTLLSPSAGHGGR
10714	24615	A	10798	209	2	CSVLAVLNPECIYVVWLELLAHDP RP LRVCPKSFFFETKFCVSAQAGVQWHD LG SLQPPPG/SSNSP
10715	24616	A	10799	142	2	IFFFFEHESHSVARQGVQVMSDLSLPP PDP/GSSDSPASATSPNQS
10716	24617	A	10800	276	2	ILFIITIRNTCCCFLLKESRSCSVTQARV QWHII/GSLQPTPG/SSNPASAFQVA TGAHHHTSLIRNTLIIINWEKNTKLSG CTSMHFRFL
10717	24618	A	10801	12	364	LHHYKTVSGIYKCLCVLNGPPTFFPDPF LPPLGLPYSLRHNNIEISPINNPPIASK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YSRERMSCISLTLTNQTLVMIKLNESLL KANS DHKLCLLR /SVYQVVNAYEKFL
10718	24619	A	10802	235	3	HRPSEDLDLPPPHWAVMRAPQYPSWDTRE GGPRSPFLFLFFFMESYSVAQL/EGTI SAHCNLCPLSSSDPTSRALCSL
10719	24620	A	10803	349	1	NQTPFFFFFGGTETISTTLCS/YGLLI LLKYPEVA/ESASQRDPENEAAVMRWLE GFGSAQPPSAPAKGQELDPVVGQRFPVS PDDHVPWPYTNVALLLEIQRFISVVKRTL TLDTLV
10720	24621	A	10804	365	3	IDVCHVCRVKRQVRGFCQKRYRWISPVY PHKCGWHRVVNTPPPHICETEWLVIIHLA QEH /TFSLTGRHTHTHTHTHTHTSKL APPASRALFGVAHVEAQKALASPSSORY LATIMFVQPCI
10721	24622	A	10805	406	96	CPPEFSEESPRLLKFRVGGYLTPOVSKC GLGVVRIFKVFWSPEKQVQTSLFFFSKT GSHSVT/RLECGDTILAHCDLCAFGSGD PPASATRVTVTVGLPPPCAR
10722	24623	A	10806	58	369	FFFFKGDRANNS/WGERCLLNKGWDI WISTCKMKMSTPYLTHTKISSKGLKDL IIRAKRIHLKKYIGINLHDLGLK/DPL NMTPKLATKEKIDTLDPIKK
10723	24624	A	10807	126	1	KEPFFFFFFETESCSVAQAVQRCNLSS LOHQPTG/SSDFP
10724	24625	A	10808	204	415	HLGFDSLTTCISLSDGLKYKATVFLVFF FERESNC/AVWAECNPGISVNCNLRLP SGSSPASPSRGVEIT
10725	24626	A	10809	168	2	KISKRPFFFFFFETGSHYVA/KLECSGV ITAHCSLDLFGSSNPPTSASWVAGTGT
10726	24627	A	10810	97	389	LAVSPSLSLSLSLSLSLYLGLPYSLR SNIEITPINTPAEGSCSSERKGMHSL FNEKIEVITLSAQMSNTKIG/RKLDLL CH/TSQVNVAREKFLK
10727	24628	A	10811	24	416	LEYIARRYLGVVWVWVFFFLNLRQGEKSR GPPKFFPRGFFSTRNGAPGGPWGPLE WGGGPVPGFKQKQGGA/PKKNRFPK GGLTQNLPLFKTPIENKGPPTRGFFPS GPPPKKAGPPPIFRVGGP
10728	24629	A	10812	60	435	KKRKNFPKKISPPVYPLKMKKTPPLAV KNQTPPV/CCFPEAPSLKKPPRGLKKG /WGNFPPLVLPQKKKKDTAGVAILVS DKKDFNPTKIKDKXHYINVKGMQREQ LGCPDANVPS
10729	24630	A	10813	618	1519	FWFGVNCXSVCPPLVLCLFVVCNCR GVLRSRSMGQKQKPTSLGTMKHKKG FKGDYSVTMTGPKLRTLCEDWPALEVG WPSEGSMDRSLVSKVWHVKCKGCPDQ FFYIDTWLQLV/YRPPPY
10730	24631	A	10814	179	15	KVKRLKTPFFFFFFETRTCSVAQARVOW HNHNSLQPPGPKRS/PTSVSREAGT
10731	24632	A	10815	61	422	NCFFLKGPPFLFFFFFFFLLQIVET YKFAPLPMQEFRLPRLDKNGAISAH CNLSLSPSSWDYRNLPRLANFPLFLVET RQPASA/PLTCWDYR
10732	24633	A	10816	170	440	RGSLSLPRLECSMTTAHCDLKLSSS NPPISAPHIALG/LTGLCHHTQL
10733	24634	A	10817	322	443	FIFIFYPFTRSHAVAQAGVQWRDLALL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10734	24635	A	10818	134	3	QPPFP\GSSDSFA KKAHLPPFFFLFEGTESHSVA\RLCSGT ISAHCNLCPLGSSVS
10735	24636	A	10819	76	245	FLLRKGTROGGPLSS/LLEINIVRDVLAR AIRL\EKIKIDIQGKEAEISLFADMI IF
10736	24637	A	10820	233	440	FFBFGALKRWKSMTHKKVRGKRTTLNG GGIKAAKTASLKKHLQGWKVMAMANKL LRGERAN/FPPRIRG
10737	24638	A	10821	293	402	RNPPFFLETEPHSAQGEVQWNCNLSLQ PPP\PGS
10738	24639	A	10822	168	1	PLRGLSDSSLGIMKRMATDLSLQPLFP G\SSDSPASASRVAGITDSHHHAWVIF
10739	24640	A	10823	97	405	LCVNICFNPFWLGVEMLNHIIGVGLTFF FEMESCSVARLECSGSAISAHCNLL/LFP SFGSSDSPASVT
10740	24641	A	10824	186	2	EPGTISLVALKLQWPRR/SDHLRLAVR DQPGQHDTPSLKNTKISWAQNAQAPVI PALEPV
10741	24642	A	10825	199	1	KRTQIGGAPGGALFFFFFTGTGFPFVA\ RLQCSGNTQAQCSNLGLSSNPSPALQ VTGTFSACP
10742	24643	A	10826	252	381	GQEEFFPFCSPVQAGGQWNCNLSLQAPP PG\SHSPASASRVAG
10743	24644	A	10827	77	427	IQVHCMSFPFVPMACIPRVSSFTSWVF HNLFPSECPGLPLVPASSHPRECVCCR PCTSW\CPWLWPRPCSNSPV/TCVPCL PCLCTSEIPSCVPWP/WTYSSLCFMSHV PDSPCPLP
10744	24645	A	10829	20	518	SFAFSLQLLHTTSTFAINSCEATLLPL SVFL/RAQTLTAPCQTRGPRGRDGRSG SSSPSGPKATKSSVERRRKSFDSWGHFR AA\QRLMDNAERSEAGVGLQREDDEDA PLCEDVLODGDLSPEEKI FLREFPRLK EDLKNIDIKRALADDIDKTHKKFTKAV
10745	24646	A	10830	351	3	LHFPFQLHQRONTKVMLRASMQHRSRT HGAPFLHQDEIQTRPRLRSAASSGSPLL SDHILSTLPFTCANLSRRCSSPCSC SCLRA/CCTCFHDLSTLIHARTRTHHT HTHTMY
10746	24647	A	10831	8	376	GMLPAHLADVLRHNSVGRPKHMRVMAGA LEGDLFIGPKAE\EHRG
10747	24648	A	10832	336	38	GVATEGVGEAAQGGEPQPEQ/PFPQPY PPPPQQQHEEEMAAEAQA/AGAPMDDG FLSLDSPSYLVLSDRAEWADIDLVLQNV GENPVQIILYSDKYTLWK
10748	24649	A	10833	206	1	TYFFPPFPGLEFFIAGIFFFFFLFTGSH/ SSLRLCSGIITASCNLNLPDPNDPPAS ASQVAETTCATMY
10749	24650	A	10834	226	376	RISQAIISFYFPLFETESRSVAQAGAQ WSDLSLQPPSPGV\SDSPALPS
10750	24651	A	10835	213	1	DRVILLSPLRGCSGMITHACNLHLPLWFK RFSCLCPPE/SSWDYRCPLP/PPLRTSV FLVETGFHHVQAGLR
10751	24652	A	10836	351	447	RENILWLTFTVPLALREAKAGI\LEPRSSR PAWAT
10752	24653	A	10837	71	472	SASTAPHAFVKVLVVKGG/K/KKKQVLK FTLDCHPIEDGIMDA/NSNTYEQFLQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						ERIKVNRKAVNLGGVVITTERS KSKLTVT PEVPFRRYLYKYLTKYLLKNNLCDWLC IVANSKESYELRYFQITQDKEEK
10753	24654	A	10838	37	382	SRCIMAFYLYGTRSPFLWKSPLYLVGVP GHSYVS L F V A G R C G V R N Q R L C S V K T M S P N T K A T N V I A K A R Y L R K D E G S N K Q V Y S V P H F L I A G A G K E R S Q M N S Q S D H K / L A / P V R N A V
10754	24655	A	10839	313	617	KFFLYVQFYVARERERSRS / VNCGLYQ HCYFRTL
10755	24656	A	10840	309	511	WEQGSWEHVLOQAPCSLYAFRTHAYTHF HTHTHRYTHLYPH / APTSL
10756	24657	A	10841	269	450	TPWFLKKEFFFLKWSLALVAQAGQWR DLLGSSDSP / LQPSRPKQFCSILPSSW DYR / PC
10757	24658	A	10842	420	1	LERGENGTDRRRKGLSHCHQPMDSVLE PLCHPPLLVMTMBEETMLPFDIGSSMY KAGPAG / DDASRAMFPFSIVRCPWHHGV VGMSQKDSYVGDEAOTKHSILTLKYPIK HDIITNE / WDNMEKIWHHTFYNKLVHVP CI
10758	24659	A	10843	431	1	GEHSWASDLAEDVTKVTGRFLGFLWGL CSGNLSFSGCVPLGAPAGVPFWVPFQ GGA / SWWKGFPWTLLHLLRTWGLAGG VGRSLGRWRAPGNPGSQGGGAPPAHQ ATGTPRSRTGSTGGISTVTILEGSHVSG MGIR
10759	24660	A	10844	55	297	QRWPGTLLGVQPG / APPDSTSASGSGGA RGGPVPTLEGGNTGSRKWEDPCWGSQNS PSSDGSKPPGGLTSCVDCDSRLSE
10760	24661	A	10845	109	427	QTGFSAAGLLEFARGPLQTLFAWVFAAV AAEQQIFVNRCCCLIVPLBFCFLRGVPC CVRCQSA / LLGGASQLG / SRGSGVRDPL EGGSCFPFDLQHLAARTALFTA
10761	24662	A	10846	17	416	SFLWKFCLEVFGRARCLSA / LLGASQ LGYSGVRLDEBAVCFPSDLQLRAGRTT TLFKA VRQGHLSLQRILLPFWQCPAPI GGVVRDRQSLSCSLGHPIRA / SRNAV TQASAMAGAPPPDPLPCSSSN
10762	24663	A	10847	265	429	LSGASCLFSLFVLFALLLLSLFSFF CANCVPWSLSPTLPLTVLHFL * RPIS CF * VNSNPKNLT * FMVNPQGMKIGLAL ERICICGCSLVFPEALLETSCQNLFCTY ACAGVLSSVYDYLALLAVSFL * FFSL FFFLYLYLFLFALGASLGLYLLLYFLL LCCISYSLF
10763	24664	A	10848	12	462	QTLGTRMEGLFATFIAPTLGLPDALL IILFPPLLPITS * YLINRLIITH * LV KLTSKQMITIHTNGRT * SLILISLII IVTINLLGLLPYSTFTPTQLSINLAMAI PL * AGAEVIGFRSKIKNALAHFLPGTGP TPLIPILVII
10764	24665	A	10849	2	462	TLTAFGTMKREAFITLLCLFTSANSRG VYARDAHKSEAHRKDLAEKDFLALVL IAYAQYLQCCPFEDHVKL * NEVTEFAKT CVADESAETCDKSLHTLFGDSLCTVATL RETYGEMVDCCAKHEFPYRYECFLQHWD CPNLP * VVRPEVD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10765	24666	A	10850	164	1	RGFQVRGE*NSGRETER*ERE*KLARE RAIGQEREREKSREAGRERERERKKE
10766	24667	A	10851	417	100	MMLVVGNLETRVWSQAQITPCTQRSS FFPVLNAAIFRSKSKVLNCLCYFLNLT FSWDLIPILFPLSHYHYHHHHHHNQY *KS*QWSANSTRFQGLDKNSV
10767	24668	A	10852	339	3	ETTHSEARRGRSAASCRGSLRRGRFP ESRRGRGAAPVCPRHVLL*GAQSKQAAV AGKRSGRTHASRWPKSLTPRRRRISLK RALHFQQSADSPSVSRIPPHGVGSS
10768	24669	A	10853	1	373	LQQKGMKRKAGQSEMAPAGVSLRATILC LLAWAGLAARDMYLHPHLVIHNEST* EQLTKANAGKPKDTTFIPAPIQAMTSFV DEEALQQLVVLVAALDVTVDKLMAMVT MLAIFLGFRIYG
10769	24670	A	10854	1	423	VYCSFLKIKTKMKHLLLLLCCGFLKSSQ WVTEGFPFARGHRLDKKREAPSRSL PAPPTTCGGYRARPAAATQIKVER* APDAGGCLHADPDLMW*SPTCQLOEAL LQLERPIITNTVDLNNVADSQTSSSF L
10770	24671	A	10855	343	3	RGCEAHLPRSEGPAGSALAQPMVYCYT FAGTLITAISSH*FFT*VGLINMLAFI PVLTKKINPRSTEAALKYFLTQATASII LVIAILFNNILSGQ*TLTNTTNG*SSI I
10771	24672	A	10856	147	1	TRTPTGQCVPKSMFLGAVHSCNFIITL GG*GRRIT*GPEFDPISLANMV
10772	24673	A	10859	189	422	NHTMDDFERRELELRHKREEMLEAERI AYQRNDDDEEEAAR*RRRRARQERLQK QEEESLQVTDQVEVNAHNSVP
10773	24674	A	10860	90	273	SHOEIQNSAMAPRKKRGGRGISFMFYCI RNNDQRYMT*RL*SGIGWMLSSGRMGY ALPG
10774	24675	A	10861	25	411	APCAKPCGDWRSRGLSVAMSGCNARIG DCCSRROGSHL*N*IPTDWPLN*FFLTS AKVKECFPKKESYISQTVY*SPG*KM*T *DKEHPRYLIP*LCIQFYHLCHVTGTGG GILKKGDEIYIAPSGV
10775	24676	A	10862	33	302	SRRTATLIYVDMENGEPGTRVVAKDGLKL GSGPSMLALNGRSQVSAPRFRGTNAPP SLPATIRALGTVNRATEKFVKTNGPLR Q*QPRS
10776	24677	A	10863	1075	1521	YCHTGKGEQLGERFCBGVSRRGPAERGS DSQTPWFWPLCAAGTNSMCTSSGSSSG AFSSWPCWTAEEPAARKGEPAGSSSP ATGAPGRCHRIILSRGAGSGAGVCSCL AESGL*ESSSPGRSGQ*PQQRHPQPNG LPAPPTSV
10777	24678	A	10864	245	418	TSKLAFPISTIPVIYANKVCP*FSKKKKK KKKKKKKKKKKKKKKKKKKKKKKKV FFEGPGFFF
10778	24679	A	10865	132	398	LNMGGDKPKPRKGMASYAFVQT*REE HKKKHDPASVNFSEFSKKCS*RWKMSA KEKGKFDMAKADKARYEREMKTIYPPK GETF
10779	24680	A	10866	115	455	LLTRNMDRLILLAGMGFLGSGQGPPTDAP AVDTAEHVYISYLLALLMKLKHGRAGVEM

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						EVWGLMLGEFDDDYTVRVIDVIAFMQS* TGVSAARVDPVIAQMSMDLMTQTKPEM D
10780	24681	A	10867	64	483	QGERFAAAMK*SLTLLSFLLLAAHVLL VEGKKVKVKGGLYIKVDSE*KDTLGNTHI KQSRPGNGKGFVTKDHTNCIWAIVTEQE EGISLKWVECTQLDHEFSAWAGNLTCLC KLTDIEIVYWKPVARNLLQLQNDIMYSPQ
10781	24682	A	10869	229	1	DTTLKLGRLITLQWHLSEGKSHMSETL NQK*RIKLKSKCSKAKELSQKLGCFQC VGSQVWHAKEMLLKEIKSAT
10782	24683	A	10870	934	515	KKVLLCLFGLGCGGVILAHGSLALPGSS SLHLSQLSSWGLTGM*VDARLIPVYFFR EMGSCHTCQAGLSYNSSSIPTPLVSGNV GTTGVSHRAQLAPVFCFCFVLVDVKAL HFGQENRIFFFFLFPGGSRDEDRVA
10783	24684	A	10871	373	424	EFTKTNLAMG*CLKSQHLGRPRCANIMR LGVONOLGQHGHEIPFLK
10784	24685	A	10872	1	469	RSRSGLSLPACDRPSGASALATCETIFS AISCDFWLPAPSLRLTPSCQPTMSSQIR QNYSTDTAAVNSLDNWYLQASYTYLCL GFYFDRDDVALBGVSQFRELAEENREG YDRFLKMQNQRGGRALFQDIMPDAEDD* GKTHNAMTAAMGLETK
10785	24686	A	10873	244	2	NIYSCKETFSVFLLAITHVYHFLVGRGGS QGTEMLWHRVLDLRYRQAGHSGSHL*SQ HFGSPRQVDQLRYGVSDQKRGHGE
10786	24687	A	10874	83	427	ISLNMIRIALNASSTIDDDHE*SFTRH NTQTEAQEAKAFALYH*ALDLQKHDIRI EESAKAYHELLEASLLREAVSSGDNENG LKHPLILKYSTYKNLAQLASOREDLLET AME
10787	24688	A	10875	94	1	KSQKACNPSTLGG*GGWIT*AEQFTTSL ANT
10788	24689	A	10876	2	413	GVTRGFNMRIEKCFCSCGPIYPGHGMFM VRNDCKVFRFCCKSKCHKNFMKRNPKCV RWIKAFKNAAGELTVDNSFPEKRRNE PLKYLRLNKTIDMANNVEIKKKRQA KFTMRL*KT*ELPKQDDYQEVQLN
10789	24690	A	10877	65	417	RFAAGATPEARAWPTDVIAAEKEEMD LPDLASVFCGRILSMVNTDDVAAILLV QKNMLDRFEKTEMLNLFNNLASARLEQ MSERLLRHRTTL*DMKFDLGLSLFRPRT LEWKL
10790	24691	A	10878	4	442	APTIDAMGHFTTEEDKVTITLWLGKVNVE NAGRTLGRLLVDYPTNTHRFDSFGNLT SGSVINGNPKVKAHGNVLTSLGDAIKH LDDLKGTFA*LTELHCDKLDVDPENFKL LGNELETDMAIHFGQDFTPEVYAYLQNN VTVVAN
10791	24692	A	10880	1	419	GKHIRQVHEEKETQGRINIEHYLGNML AKNLLFEKEREAEKEKSYEIPTKNIQG QMTPIYPVGMNGTGPCS*KQNRPRSTV MYICHPSKHEILSVAEVTTCYEAVIL TPLLCSHPKYRFRASAVNDIFCQSLPG
10792	24693	A	10881	54	335	REITFMSGALDVLQMNEDVLKNLAVIT HLCCCTKTDSPMEQIIYGS*TEIYISIKL NRT*QNLMLAVP*NYDI*NHDEVTMTF

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10793	24694	A	10882	216	3	NNTLQMFEF MSIKSMSTICLLKKKGKHFQIRGK*NSG RETERERERERKRARRARGQERERQKT SEGGREERERERKKE
10794	24695	A	10883	3	390	GELKCSKERCCQSMASRSRTIWIIGAPFL KGQPRGGVSEGPTVLIKAGLLEKLKEHE CDVNDYGDLPFADIPNDSAFRIVKNPRS VGKASEQLAGKVAEVKRS*ISLVLCVN LGGGLECLCGHAKVYSR
10795	24696	A	10884	3	375	STMRWIFFLLCRAGRALAVPQQESLPD ETEVVETVAEVTVDVSGANFVGGEVGE FDDGA*ETE*DVVAENPCQNHCKHGKV CELDENNITLMCVQDPTSCPALIGEVK VCSYDTLTFYSS
10796	24697	A	10885	95	2	KCTQGPSAHAHCNPNTRGGRGWIT*G QEF
10797	24698	A	10886	1	114	MGFHHVSQDGLDLVL*GACFSLPKCWD YRREPTILAH
10798	24699	A	10887	1	368	EPTMELTIAETNGKAARKVKGAHAGEY GAELERMEFLTPTT*TYPPHFLSHS AHVKGHCKKADALTNAAHVDDMPNAL SALNYLHAHLRLDPVNFLLSH*LLWT LSAHLHVEFT
10799	24700	A	10888	336	9	FRGQVIPAIFFPFOTSLSYFQGGPN* TPPFQKILKTRGGGKLLDPQTRLRQ KREDPLFPGV*NCN*P*SHPPWGTQNP VSKKKKKLKTSSIFVHRVMSPI
10800	24701	A	10889	3	362	GFLLEAPLEMOELQ*PMNRILQLTIAEQE TFLTPALLLPHPQTYTASAVFLAKPD T*PKDVGILALQVHPAQYEDQTDLENY NNVKALKYTEDLQOTLMGFCVQEDINS LCLTVEQP
10801	24702	A	10890	66	333	TLPGNIGISFVERVMEVLRPOLIRIDGR NYRKNPVQEQTYQHEED*DFYQGSMEC ADEPCDAY*VEHTPOGFTTLRAP*LY TPIVG
10802	24703	A	10891	405	49	IPWMGTERTASAQRDVAGPARNACPL PEQCFPGPAEWOTPLTPPGSC*LRPGER ERHGPGCWGPRLRSSGQTHPPSPGCA N*CPCHHQQLLAGGVAVFYKLFYRYG NSPKWDL
10803	24704	A	10892	2	197	POGRVLTWTAHLAAMAPSSRTSLLAFA LICLPLWLQAGAVQTVPLCLFVHMLQ THRAHLQVIDTYQLEETVLPKDHVGF LHDSQTC*PSDSIPTPSNMEETQOTS L*LPDIPADGFCPLDALASKGWCRPNR SAMHAFPLPYAPNAPSAPTGH
10804	24705	A	10893	3	334	DQLPEPLKVLNTAHLAAMAPSSRTSLP PYALL*LPWLQAGAVQTLPLVSRFLDHA MLQAHRAHLQLAIDTYHEDTYID*DHK *SFLHDSQTSFCLPDSIPTPSNMEET
10805	24706	A	10894	3	341	LLTPGVSDAICYILDSGYIIMSDTFTAY VIG*REFVNG*HATVRFPAVPPVALPW LGV*WDNPERGTVDGTHEWTVYFKRHS TGGFFIRSNKVNLTGDTFTADKNLYVLD Y
10806	24707	A	10895	25	351	AMIQTRDLQGGRAFLLKAQOD*RLDEI CTQLLDDLKYSNDELPLSRLEGFEKYM

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						EPDLIGNGHIDIMYLKMLLYKLAVPQTD LQLPRSIGEVYSGSGETISYPDFLM
10807	24708	A	10896	364	38	FSQFKIAQFLKKIPFPFGSPFPQNGGNF LKFSKFFPNKRGFPFHPFF*KRGPFFCP KWGPQGHIGAHGPPAPQGQKIPFPQVFK KMGIKGTPPPGPPFFFFFFFSW
10808	24709	A	10897	136	3	STLKH*RGWVAHACNPSITLGRSGRI T*GQQQPKTSLTMMKP
10809	24710	A	10898	193	269	GNKYCLTILLLLLSFKRQSLTLLEPL ECSS*TRTPQKGSLLNFS*VAGHCV CL*SQLIRLRWEDHLSFGV*QHSDEL HHCITLTWATE*DSVS*KITTTTTTK
10810	24711	A	10899	316	374	CCCCCCCC*CCCCCCCCCYKETF QQ
10811	24712	A	10900	38	206	VYCVLVFTICTLLCNTSLGLPHPEFF ETESCCVQAQGLQWIIHC*SLRLPHRII
10812	24713	A	10901	364	2	DYGHISPERKHPREGSMVYLNCRRKKK RKKNLSTKILNPQSPFIL*KPNSARK S*QKEITKIGADSLIENKRIEKIYIN ETMSWFIETLNKIQQPLARLTMIERKDS TKFRNERG
10813	24714	A	10902	132	3	ATSSPWGYSAYVAIILLFLYFSNKLAF VLYGFV*NYFLQEI
10814	24715	A	10903	234	352	NFCFFETGSCSVT*AGVIMAHCSLDLPG SSNSLTSVSEE
10815	24716	A	10904	250	356	TMEMMLDKKQI*AIFLF*FKTGDKAAET TLNINNAL
10816	24717	A	10905	280	322	QT*SLILVSLIICATITNLGLLPSYFT PTTQLSINLAMAIP*AGAVVIGFRSKI KNALVLCTSTPLPTSTMLPVHMMTSSD IHPKI*SIR*QTCIQHRLMLKLC
10817	24718	A	10906	271	365	KWRGQVVAHTYNPSILGSRGGWIT*GQE FKT
10818	24719	A	10907	135	358	LRYKLITNPKLTLTLCGLIFLKGNTVNI QCNGVHM*YQHPGRPGQDCLSPGIQGH GQHKESLS*KSLSWS
10819	24720	A	10908	107	212	IKNEGMGQVRNLMFVIPALWEA*VGGT EVSHSWL
10820	24721	A	10909	165	383	PKNRPITPLKRSSISNPDFQKSLRPLG TPMGPHFKRGNSYDENLENLCPVGNK GPGSH*GLLTCTCRGF
10821	24722	A	10910	119	291	GGYRFYKDTF*KGFWPLTLFILLKPL AGHGACILWSRMLRPL*EDELGLRCL CSELMLCTLA*ATE*DPVS*KVRLALN FVYNTKTPSRAWCMFVLATHEAEVGG SLESORSRLQ
10822	24723	A	10911	283	2	SDNTTDTFLPFTYKIFPITWEGGETWK KNPRNSRLKKTLSRTETIAQIPLKNLWP GMVAHACNPTYLTGD*GGWVT*GQEFETS LANMARPC
10823	24724	A	10912	1	360	PHAFGTMKVTFMSLLFPLSWANSRGGF RONAPKSEVAHRLKDKNGKNFKAWG*MA LAQNLKQGFENHGKLGKEVPEFAKPGV ADDAENGDKWLNTLGNLYLAPVAVRE TYGERAEC
10824	24725	A	10913	270	361	SKTWFGTVAQTCNRPRTLGSQGGWIT*GQ EF
10825	24726	A	10914	157	1	VFFQLSLAWKGFSRFFVFETSSHVA

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10826	24727	A	10915	1	357	*AAVQWRDLGSLQAPPFGPTFFSS LEEWGPEREFEEKEKGNKKKKIKNS TPPKPKARKGEEKPGPFKRAITTFVAR IPLFCLKGPLWSPC*IGRSSPTPGSKG HTGAPNCPCCPLAAPPKDVNPNPKMVE AVKNPIL
10827	24728	A	10916	102	471	PSTPIILTSSYPHYVXSSVSTFTFIISLF PTTIFMCLYQEFIISS*HLPTTOTTHLS LSFKLDYFLIIPILLTFLVWTSIEFSL *YINSNPINQPFKYLLIFLITILLIT ANNLFQLFIG
10828	24729	A	10917	2	138	REPTMVLSPADKTNVKAHVKGVAHAG* YGAVVFLTWTLVNSID
10829	24730	A	10918	178	393	LVLCTVLLMWRHFHDSLSILKAQDVT NLSNFTVLRGETGSPSAVHTSNSTLGG *GKWITQGEFETSIA
10830	24731	A	10919	278	124	TWADAGSSNETPFLLLKPKKLT*GGGVC LEQVVLGRVRPKNPFNLGNQGFN*PKFR PKTSTWGAQNPF*KKKKKNNKPK*NS RHTPP
10831	24732	A	10920	221	243	TIIGSLPLDIKYSKFLKTVAFQAQW VIPALWAEAGRSPEVGSPRPA*PGSLK VHVDNNWESIN
10832	24733	A	10921	33	292	GTWMLERHAVEVQCVLVSELVIPSQD KPEQC*DHVLI*VLILGKGWI*ISGA LEKKKKKKKKKKKKKKKKKKKIKITGS FI
10833	24734	A	10922	108	3	KLAVYGSVCL*SQLLGRLR*EDHLNLGH GGCSEP
10834	24735	A	10923	106	2	KLAVYGSVCL*SQLLGRLR*EDHLNLGH GGCSEP
10835	24736	A	10924	195	2	ASLFKSQLNRAFIYLFYVIFETGSL* PMLVCSGVITAHCNLHLVSGDPPTSAS QVAETMVL
10836	24737	A	10925	127	2	YVCILNKLGRGPMVAYACNPFSTLGGG GWIT*GQEPKTS
10837	24738	A	10926	639	282	PFLSIKGWQOFMPFIPTPWGLKQEDHL RPGRLDQPVQNSKTSLLKI*KLARRGG ACL*SQLFRKPR*ENCLSTGELKPKGGI FIRLVQNKIPTTRGEKRQSHGTGSYQCP KIKKKG
10838	24739	A	10927	1	363	ALLTQALTCRQAAGAEAPHAGATPSLMFP SLPQGFRCDCSPSDAAYTMENTIDKKQKQ VILIFKFKMGHKAQQTENINNAFGPPI ANKGTVQWRFINFCRKDESREDDE*YAQ PSKVATDQ
10839	24740	A	10928	53	379	TEARLLTLYLLPNALLNHTSPPLMFAD RRLFCNHIDIGTYLLFGA*AVVLGTA LSLLIRABELQOPGNLLCNHIVIVTA HAFVIFIFIGLPIIIGGPGN*LFPL
10840	24741	A	10929	180	350	EFMAKKTESFGFKRCGP*I*NVISQRG TLRFRAGLFFMGPEFLRLGENLLEIPRG A
10841	24742	A	10930	361	379	RRYWWLG*VQWLPMPVIALWEAKGRSP KARNL
10842	24743	A	10931	121	543	HRNTGSTHASAHAYIHVHTNP*PLTGA SALLMTSSSLAMGIFHSITLLILGLLTN TLTIYH*WRDVTRESTYQGHHTPPVQKG

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						LQYGIILYIT*VFFAGFF*AFYHSIL SPTPQLGGHWSPTGITPINPLKDFLLNT S
10843	24744	A	10932	227	339	VGGVKSQVQLLNCHFSR*MKKKKKKKKK KKKKKKKKKKKK
10844	24745	A	10933	64	409	DQRNKAHLRAHLKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK WAFPLPLKKKRVGENFLKKNF*WGGNI GGQISSKKYRGGGK
10845	24746	A	10934	2	362	NKLSGFPYKGVYTL*PULANPLAQLVIY STIFAGTLIALSH*FF*VGLIIML AFIPVLTKKINPRSTAAIKYFLTQATA SIILLIALENNILSGQ*TITSTTSQS SLIILRAM
10846	24747	A	10935	154	3	GCPLSFLFLNIVVKVLVRAVMQEKIKS IQIGLEVK*SLITDNMILVLYGN
10847	24748	A	10936	250	363	TAWPGYLYSFSFLY*ETTKIWLGAHA CDPSTLGGG
10848	24749	A	10937	199	339	NVLGILLVFRITVBIYKCGRWLGTVAH TCNFTSLGCGQRTT*GRE
10849	24750	A	10938	130	240	KNEQDPRDL*DNCKWPNHIVGVFEEDK DNGTERVED
10850	24751	A	10939	35	235	FILVENTKMKCICPLLNMIYAILYLEVP SVFL*EENKQ*GITEKKKKKKKKKKKK KKKKKKKKIKPGLL
10851	24752	A	10940	179	12	DQFGQHNKTLISQENKKNSSWQCCV*P QLLGRRLRWEDCLSPGGRSCCEPCHSG
10852	24753	A	10941	297	278	INQDNELTLINSSSKQIKHKNINQTLRT KMNENLFA*IIAATILGLSATVQIILFP PILIPITSKYLINNRLITTOQ*LIKLTSK QMITIHNKGR*SLGGD
10853	24754	A	10942	3	318	FGGGRGVNYPDAFVLSVLLPSRLFFH LFPHFLPLPPFLGLAPYCFLL*YF*K* *LYYSQSIIFFFYREMKNKLLVFWAINL FFLYYYNYMEMWTLCYWN
10854	24755	A	10943	190	3	KLSHKQSVYFKTFFI*KNHVLK*KNLW VYPNDKFFFF*FESLALSRLQCNQITL AHCNLR
10855	24756	A	10944	281	1	KKWLFSSSYLYNGLFLIPFLRVSGF KGKFWKKFFFLRARGALFWGSLKGF GFVWFF*F*DGVSLLPLRECNIIISA HCNLRFGS
10856	24757	A	10945	169	319	NGVEDAFKNVLGWAQWTVSILPALWV KVGSPEVRSFAPTRPI*KYGFRIGTVG YICNPSTLGGQRRIT*GQEPQNTNPNM VKPC
10857	24758	A	10946	312	1	FARFOLLKSWDFQ*PLDPVWGFPPKRE PENWLEFEIFPFLIIMAKKKLKSFLP FPFLG*FKD*GQKTPFFFFETVLSLLPK LECNGAISAHNCNLCPLGSSD
10858	24759	A	10947	208	329	IFTGDRSRNNRIG*ARKLTPIVPSLWEA EAGGSLEPKSLR
10859	24760	A	10948	116	374	FYFGYLLFFFCFFEMAPCSR*SWASRG QSFCNLIIFGSSDLYSAFVRVITGAR DHACIIIVFVVDGGCVDTITSGLAGWL RG
10860	24761	A	10949	264	434	QLAFCTDTLTSVREQCQBL*KCVKARKR IELCDEQ*SCRSHTD*DCDELDLFLHA

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10861	24762	A	10950	226	429	T NFGFRLDKTVFFSKIRINAWAQWMPVMPV PELWEAKAGGIT*AQELETSLSNIVRPW LYKKFKN*VWVC
10862	24763	A	10951	188	433	YSAEWKIDLGIEVFWGKMTYKQ*FFWF VFKFLFF*RGRTLSKLEWMSVITGHC NLDDLGSRETFAFAFQVTTIGSCHS
10863	24764	A	10952	298	445	LFSKCSSKSIKEEGPGVVAHACKPGTLG GROGWIT*GSEFESSLANMVK
10864	24765	A	10953	244	1	KTFQGLVVFCLFKRSPLKGTIGVSGMVL ICFFLKSRLNLFNPRGLQQRKNFFFFFF ETDSYSVAQTGVQ*HNLSLQPPSC
10865	24766	A	10954	199	3	QETKKEQNKENQTK*RSTRKKHROGTN KTKERGERQTPPVGNRQPTTLGHHARPR RRATTSRA
10866	24767	A	10955	157	3	YSYTFSPITTTSLIIQTLSHGAGACL* SQLGLRLRQDNHNLHGGCTRA
10867	24768	A	10956	263	357	GLSLKVLTVQGLGVAHACNPSTLGGRGG *IT
10868	24769	A	10957	333	2	KWKADMLIPLVIXSFFLIGFFPKMFTNSK RYIFLLQLLAQHSSFFSIRCMEL*WPF PFPLCTQSQGNQPS*LAYCRLDNELIF PFPEFETFSHSCPGQISAYCNLCG
10869	24770	A	10958	130	228	GSSFLGSSPSVAQAGVHLPDHSSLG*DK SPSVQKMSKWIGCSGACL*SQLRLRLC QGRISP*GQACSEP*SGRCTPAWATEGD PPKKLLPYTTDS
10870	24771	A	10959	250	3	VQACSTGALYORRNAEDEFQATARPISG FTTSIAMRLMLLTCSGHNWVADLAFSG IMP*GLFFPSRONLALSPRLCSARA
10871	24772	A	10960	199	326	VLGRMSNOKNYTLLARM*KIK*NNTR CWGGCGATRRIIHC*QECRI*KCQPSL WRTV*QFLNTLNR
10872	24773	A	10961	323	3	LLFPHLEDNQH*YVFCYHNLSFLQFYI N*IIQLVVFVWLLMSIILKSHPCHPFS K*LSVTVFFFRQSRVSRLWESGAISAH CNCLDPSSSDSCASAS*VAGSC
10873	24774	A	10963	120	3	PPPPPP*EMRSCFVAQARVQ*CDQSSL *PSTPLGKQSSC
10874	24775	A	10964	168	441	LTPVIFALWEAEAGRSPEVRSR*SPF
10875	24776	A	10965	19	207	APLKLNAVAMELSLGQWDVSRNLWEIFL KKGDTGRVQWLTVPVIFALWEAEVDRTE VTSVTRC*PLKLNAVAMELSLGQWDVSR NLWEIFLKKGDTGRVQWLTVPVIFALWEA EVDRTPEVTSVTRC
10876	24777	A	10966	209	1	TKSALSNMVTTHIGLCKNFVCL*DRV STVQIGVQWHDLSLSLSPRLKDPPTS ASRVAIGTGMHLV
10877	24778	A	10967	109	1	DYLSGV*DDQGQHGKTSLLLIQKLAR LVGRTISS
10878	24779	A	10968	141	2	GLAMLRLENIFRPGTVAHACNPNTLG GRGGOIT*QGEFKTSLSC
10879	24780	A	10969	175	348	LVYECKHLICVFNTSLFFPH*TCYK*RG VLWLGVEVAHACSPGLTGGRGWIMASGD RD
10880	24781	A	10970	108	2	KTKKLHMRSGVVAHTCNFSTLGG*GGWI T*GDGSC
10881	24782	A	10971	184	2	SFLWKLHLRGVGRVRCQSPATRGASQL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
						GYLGVRDPLEEAV*LFSDLKLKAGKTTT LFLV
10882	24783	A	10972	245	339	SQISGPGTVAHACNPSILGGRGWIT*G QEF
10883	24784	A	10973	295	340	KRVFF*ARKKNPFLSPLWGLTLENPLGF RLFLNPLFLGLKISQFFFPQI*PLAFFF WGTLPKPLNKLKFGPFFFFFFF*DG VSFCPCGWSQARKYIEINISLSTCPRA
10884	24785	A	10974	186	340	KPLTIIRKGFHFNFPQ*SFVFLVCYC FDTESRSVTLECSGSGSAHNL
10885	24786	A	10975	253	491	FLECTSLKKRVRHFGQHSKAPFKELQ TTGRGALLQSHLRLRQHECLSPGVG TYSEP*LIHCTPANVIEGDSGXK
10886	24787	A	10976	141	1	SFSFFKFSPTGDMIGFF*HFFFLRRSH SVAQAQGVQWCHLSSLKCPRA
10887	24788	A	10977	3	138	HEETGFHLVSDGLNLITS*STHLGLPE CWDYRREP*PGREGDF
10888	24789	A	10978	186	323	YESRSATQAGVQWCELGLS*PSTSRPQ* FFCLNLSSITWYSLGAPS
10889	24790	A	10979	183	3	IKTLFPFFFLRLSLALLPRLECSGTFS AHCNCLLGSDDAS*VAGITLCTTTPSPM QLV
10890	24791	A	10980	309	55	KNFGPNWVKFLGGKGGEMAFGLKFFPPF FFFFEKESWVFQ*MQWGFRLSLQGP PGVTO*ISRLGKIGGLFPPKKKKRERGN M
10891	24792	A	10981	637	838	SQHLGRPMRVDQLRPV*QDPQGHGEMP SLLRIQR*AGHGGTHL*SQVLRRVRQDN CLNSGGGCGSE
10892	24793	A	10982	275	2	RNRTLKMEFLSWFQFWNLLNMIREFKN VKDTSKSMENDSP*WHELFKELGKINA FDTFDSLVRGKFSDSIHNTFDHM*RTK EYNARA
10893	24794	A	10983	98	346	GHGHATRLGCLVLT*SFPHITALSVSGTN DAEDCCCLCETQKPICGYIERNLLYLK DVCVRPAVV*VVERVYSLISRYSLNRD
10894	24795	A	10984	30	410	LPFTGRPKRTRTRGFSSTNHDTDGLTYL LFGA*AGVVGTAVALLIRAEGLQPGMNL GNDHMYAIVTARAFELIFFVLPITIG GFGN*IVPLIIGADPMAFRINNICP*L LPSLLLLASAIAE
10895	24796	A	10985	141	360	QTLRTKMNENLFASFIAPTILGLEPAEVL IILFPPLLIPTSKVLINNRLLITQQ*LI KLTSKQMITIHTNKRT
10896	24797	A	10986	3	347	HELRTKVNHELIASFMGPTSGLGPAALL IIL*PPLLIPTSKVLINNRLLITQQ*LI KLTSKQMITIHTNKRT*SLILESLII IATTNLLGLLPYSTPTTQLSINLMAI PL
10897	24798	A	10987	46	317	KSMTPKIRKNPLIKLNLHSLIDLPTFSN ISA*NFQSLGLGACLLQITGLFLAMH YSPDA*FAPSSIAHITRDVNG*IRYL HANGAS
10898	24799	A	10988	245	1	VSCLEGLKLTNRKDIHTKNFVHHHQPR PKVDKTTMGKKQNRKTGNSKQTASPF PKK*SSSPATEQSWENDFDLREE
10899	24800	A	10989	255	1	SCLPWANNISVQNGHKKTLVITFTFFPI GSFHVT*LLGPPLILISPPRIFFPETG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						SFTVARAGVHSGATSAACNLRLLGSSNSA
10900	24801	A	10990	166	307	GEKFWGPLINGGLVGRSSWASCVQLELL *EMVFRHVAQAGLKLSSSNPPASASQS AGITGVSH
10901	24802	A	10991	109	330	TNQPTKKEREAGKKVKELERERERGRK KRKEQRKNEKERR*P*NMD*RRIRERNH SFDVYELFLICGLLNLHV
10902	24803	A	10992	244	326	GRYLGKWLGDGPA*AVVLGTALSLIRPE LGHFAILLGLIDLISSVIVTAHWSILLV RVIPITIIAGPGN*LVPLIIGAPDMAFPR INISISF*LLPPSLLLLPPPT*QMRAGV GEREVVR
10903	24804	A	10993	101	2	KTFMARFVGTCL*SQLLRPRQEDHLRL GGRGC
10904	24805	A	10994	177	1	TPSLLFFVNIITCFCLNPGGGGYSEQKLC LCTPAWVTE*NSISRPSQNSRQSRQVN HLF
10905	24806	A	10995	214	326	KEERKNPRAIRVVP*PWGFFPFLFKETSL FLFVFRFHWGYPFGAFAFTQKWLVP* T*VULFFFFF*VSLRPLECSQVISAHCN TFIPGSSDC
10906	24807	A	10996	184	379	LCGMVYHFFSILLYL*CKLFSSPKLEF SSCCPLECNGTVLHRSRLPASGDSPT SASRVAGHGCTCL
10907	24808	A	10997	136	3	GRVDGQHIMTHQSHAYHIVKPS*PLTG ALSALLMTSGLAM*FH
10908	24809	A	10998	274	363	PWAYAEPLTLHDATYSCT*SLIRASFTL FIA*TLRLRLP*STPTTQLQNLNAMA IPL*AVAPDIGYSSMITNALSHLLPQCT PTPLISILGIIETVSLLIQPTILGVRR ANIT*CHLLMHLIGSATLSIST
10909	24810	A	10999	305	1	NLHTPSQIPLT*PLPNINHNHLTTT Q*IKYLILIPSNLFHNKPNLKATYVSP SPNLHLPPSSSNSPASASQVAGNAGARY AWLIFVFLVETGYSLLV
10910	24811	A	11000	154	2	IVVGILQSRRCGRSL*SQHFRPRQADC FTPGVPDQYFTLLPEVVFLLV
10911	24812	A	11001	142	367	GVCLYQRISITYIKTKKLSQGLFYPLL LLLF*EGGSHSVTKLECSGGVSAHCNLC LLASSHPFTSSSQVATG
10912	24813	A	11002	60	385	QNTLLSHTLRAHLIENLHREFDRTILG LPA*LLILFFPLLIPT*YLINRIMA NRH*LLIKLSERMIITRNISGRT*SIIL VSLIITATIANLLGLLPLYSITRT
10913	24814	A	11003	214	83	SKKSASFLLTFNVFQVLNSVREERIRY TEMEKEIKLS*FVD
10914	24815	A	11004	241	368	SVLL*PSP*PLTGLSALLMTSGLRWF HFHSITLLILGLLTNTLTIVQ*WRDVR ESTYQGHHTPPVQKGLRYGIILFTILEV FFFAFF*AFHYSLAPTQL*GHNPLT GINPLNA
10915	24816	A	11005	3	396	HEPHALGMPLTADLPMSASCSQSLLL LHLLHLPWI*EARAYQAAGCSKLPDHAM LQAHRAHQLTIDTYQVEETIYPEDHKY SFLHDFQTSFCFSDSIPTPNTSETYQK SNLELLRISLLIESWLEP
10916	24817	A	11006	156	335	PGCCCCFLFF*LVYCCYVMMLYFYVLY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						SPGFYF*YWIM*YFRLVYNLYLVLYL LYMS
10917	24818	A	11007	107	2	KCSSSKHPTKEDSQITNKHIEKCSS*LL VRBMQII
10918	24819	A	11008	129	412	KTRSGPKKTPGQKGTPLPKKTPKITGP GGALKPFPGGGFRDENPLNLDKGGSSG PKTFTTFSPNGKK*NFQPKKKKLLYPG KIFFPWWKNI
10919	24820	A	11009	63	268	CTFKFKNHCTSTQSTT*LDREKKKKKK KKKKKKKKKKKKGGPL*KNFSLKG
10920	24821	A	11010	154	422	NEFSFFFFFKPKPFFFAQVGGQVRNWG *LKPRPPLKKNFSGFASGEAGITGGVPH PG*ILVF*VKAGFHENLVNSETGNQF ACASQ
10921	24822	A	11011	23	375	TRYLTIKIKKKKKKKKKKKRGAFLPK TPWGAPFFPGSAIFIFFFGGFF*TPLG FFWETLFFWGKILGHLSPKILPFWGKK NFFWVKGKKNLNSPFLKIFFLVFFKK FFPPG
10922	24823	A	11012	151	361	ACTTTPSSFFSNIDTVSLCCPG*VFGHN NSSLINFPFLRSWYRPHAPPHAFHF ILIRSRVVAQGLEFLALRDTPISDCPC TVHYPPSLAN*SVFFFLTQSFVSLPRL KRK
10923	24824	A	11013	146	378	NFVVSIEFLHICY*ISYFICLIKVL* *KKKKKKKKKKKKKKKKKNLKGAG GGKKFLGGGKNNSFFRNGGCF
10924	24825	A	11014	82	264	TEFLYTTICNSAILYL*RNKVLFSF INTEKKKKKKKKKKKKKKKKKKKK KKKKKKKKIKERT
10925	24826	A	11015	381	2	GRALFTLLKGFIRHPQMPFFPLRVFPF SVTGISIRQSGFFIKRIVFRL*IAL FLLPFLFPFFSFFLKIGTYSVAQCNGM IIDN*NFELIGRRNPSTASQIAGNTSA Y*HTQLVFLCEDGI
10926	24827	A	11016	1	251	PNCIVHSLRTGLNFIILLLLCFTF*F LNKNIIFESQKKKKKKKKKKKKKKR GAPLKKTPGGPKFYPASKKKISPKQGG
10927	24828	A	11017	234	1	DINIKGSWVKIPKPSVLSQLCFNSKI FPN*KLIKKNENEPGMVHVCPNSTSG GRNGQMA*GOEFKASLANMAKP
10928	24829	A	11018	107	342	FQLCYGIVHCFPLFMQHSSEYKSTDHRA SSKCHTVQSSQLSTSAFKQ*THKKK KKKKKKKKKKKK*KKGGASF
10929	24830	A	11019	264	1	CFKPLLFYPGIIKAVNLVSTASATFH KF*YVTFSS*KKFLCVGKGTGSHSTQ AECSGTIKAHCSLELPGRGDTPTPTSRV AARA
10930	24831	A	11020	1	288	RTGTSSRSRAATLFFFFFPPKGGGFNG NLPTTFGLGNKKPPLNLPGGPPLPHG GLKKGPGAPQVPPLFLKKPQTSPP*GLR EGPPPLKKFYLF
10931	24832	A	11021	115	287	STCEISFGCSRGCCWDYLMWVESHFYF *FLETECCSVA*AGVQWSNLSSQLSHF E
10932	24833	A	11022	186	1	RPKVDKTKMRGRDQSRKA*NFKNQKASS PPKEYNSSLAREQNMWNEFELTEVGFR KSVITN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10933	24834	A	11023	180	353	IFCFCIFSRDGVSVVC*PGWSQSPELMIH*NTKIS*AWQRVPKIPATQGEAEAGESLEPG
10934	24835	A	11024	155	1	POAREGGTCLQS*LLRRLRLQEDRLSPGV*GYSEL*SCPCTPAWETERLV
10935	24836	A	11025	22	325	KLILLYDPQLTFIFLNTRAVVAHCAFCWPFIHFVFGNYGFVSCCLTFIFVYSGKADLFFPKKKKKKKKKKKKKKKKK*KKGGRLKNSWGGPIFWGFPK
10936	24837	A	11027	127	259	GQVQLTPTVPLTLEAMVGGSTGLRSSRPFSTP*PCIVMILYG
10937	24838	A	11028	37	408	IASGALFFFFKAAGKRGFKTEGAYQRQRTIFKNKKRRREKTRGNRLGNYNKNGRLGLKTPRGALGGPYLDKGPLRGKPPFGGTLGGGPKIKIGTL*IRRNYPYIRRYNRPKKRQKNN
10938	24839	A	11029	146	3	LLVLKDLPRIMRVASPTYIYYIYLYIYIYIYTHHTHTFIT*VLFC
10939	24840	A	11030	268	435	LMCLRNETH*F*VVE*WLGAGAHNCPKTLG*GGRJA*GQEFETRLRNIVRP
10940	24841	A	11031	322	2	KLPHLQQQQKVCVYFLKNGKIGHGGVCL*SQRLRRLRQNNISNPCCASAWTQRDSVSNKKKKKKKKKKKKKKKK*HTKMSPTKADTKSTHCCGRV
10941	24842	A	11032	251	380	HKRLRTIYFFVFLKKKMSFGLVGHYTNPSTLGGQGQIT*GRE
10942	24843	A	11033	64	324	FWFFFFFFFFFFFLNPPGGKKKKKKPPPLGKKKKRKGKGGKFFSPPPGGGGGPKKISLKRVLKFF*NPPGGTKKGGPFLIPPSP
10943	24844	A	11034	420	534	CPGVVAHAYNPSTLGS*GRQITIDREITILANMAKPH
10944	24845	A	11035	196	1	KNGHSLPPGPKGTTPPPKKKTKFKINLS ELGSKKAYSWPGTVVHACNPSTLGG*GGWIN*GQEFE
10945	24846	A	11036	10	248	PSDR*LFSTNHKIDIGLYLLFGA*AGVLGTALLIRAEGLQPGNLLGNDHIYVIVTAHAFVIF
10946	24847	A	11037	32	405	DYVSKRKKREKRNIVILETSISSHLVEWMLCSRYHPLIKRRSSVRIILALLCPQKVRDMS*GIGSKKQCWDSWLSIWKMESDPFLIPYPKINA*RLKDLCEINLKIIKREYLDHYRVKKV
10947	24848	A	11038	337	448	KNPFPGFGKNPFFWGGPPGPPPPPKMGFGKKKF*FKRSKKKKKKKKKKKKKKKKKKKG
10948	24849	A	11039	307	415	RVCSTIKVLRLDSSDRNPGRVLSTNSLSL*KKK
10949	24850	A	11040	213	403	VHRGIKTYELNKLDPDFRQTFKK*G*RLGAVAHACDPSTLGG*GWNITLQTFETS LTRMGKS
10950	24851	A	11041	104	2	SAFFF*ETESCSVAQGVQWCDLSSLQLPPPGFK
10951	24852	A	11042	177	3	AYTAYICVCIHIVLYK*MYICINVHVCKITLYLYIKYKYNAYILHIGFPSFLHTIIS
10952	24853	A	11043	314	395	TVYTLNLSINSVCSVLLSVFHLRLHQPRGRVQLTPTVIPALWEAQAGGSP*VRISQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: of USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10953	24854	A	11044	310	403	IKTPA RGKGGKKPRNPGGGGK*ALTKKKKKKKK KKKKKKKPGGALKKKPRGGQKKTGGGK KKFLPKRGAKKKPPGDFGKQKQIGGGEK RGKTPPKKKK*GKKKLNKGGGKKTPK SGGGKKFPFVV*KKKLPPGG
10954	24855	A	11046	181	3	BGPLSLSLFFFF*QISSLLLRLLKYS TIIAHCSPFKFPSSRNPTTASQAASTTG VNH
10955	24856	A	11047	392	41	KESRSLSQGGREKGGPKFLAPPAPKFKR IFRPHPLKKLGPKGPPSPS*ILSLKKK GGPFLARNFWNSCPQGFPFPPGPKRLG FKGGPPFPLF*KKKPPFLGGENQKVKN FFFF
10956	24857	A	11048	147	307	TVIFVFLLRKGLTLRLPRLSGWMAHLK S*PDGLKQSSCHSLSSWDYRRRRG
10957	24858	A	11049	118	1	HGKTPSLQ*HK*IAGYGSACLSQQLR RLRWESRSIS
10958	24859	A	11050	54	284	RKTRRGGLHWSNLRLGLRWDDLGLRLR WEDRLSPRRGGCSEPLRCHCPANATE* DPVSKKKKSLFVEKPGGG
10959	24860	A	11051	130	340	HNMPFAHGRSINDFFFFFFFFERRGFP FCPPVGRAGTHGLLEPPFSRV*QYVY LGTVAHVCNPSTLGGHVGS*GQEFKIS LANIVK
10960	24861	A	11052	140	337	NIIMFFFFFFFETVSFLLGLLEGKGTIW N*NLCPLG*GDSPLGCS
10961	24862	A	11053	197	428	IRSINNPTVASQYSSSEKSHPIILNQ LDMIKFSEEGMLKAKIGLLRQTGVQVNV AKEKFLKKNQSATPLSI*IRK
10962	24863	A	11055	180	1	ATIALLYSLRGDYARRFHLRRKKEQWQ MVTHVYNPSTLGGQGGRTA*TOEFKSSL GNIA
10963	24864	A	11056	158	426	FFPLPLPLPTVSLFPRSPDAEPKLDCT AAISAHCNLP*PSCLSLPSACNCRRAP PRLTASASRGAGIADGVSTQCSDMVPRL ECSGV
10964	24865	A	11057	220	421	YALHLNKNNSYF*MRKKKKKKKKKKK KKKKKKKKQKNDPGGAVYKKIP
10965	24866	A	11058	162	464	SCSVGLLFLFSKTSLLSYCLLLLLTL HYVYYITY*SLVPM
10966	24867	A	11059	1	134	APENRVDPRVKTLVPLILPIITLANP CKD*YPIYKISIAIC
10967	24868	A	11060	382	273	SSCL*POLRLRLQEDVLS*GA*GNEL **CHCSDAWTEQDPVSGNHTYIHSQS INYSMIGYIHEQGIIADHKPIIAEPE DSTVPRDET
10968	24869	A	11061	298	378	SCSASPCCSSRRHWSFGC*QTCLLLAIA LRCLPWLREAGALHTGPGCRFLDHAHLQ AHKAHQLVIDTYOIEGENYIPQDQKNSF LLESHTSFCFSDSITTPSNMEETQOKSN LKLRLISLLLIETWLEPVRFLTRIVANN
10969	24870	A	11062	39	486	RPTRPDAYHVKFSP*PLTGALSALLMT SGLGMRHFHSITLLILGLLTLTLTYQ *WRDVTRESTYQGHHTPPGQGLQYRIM LFTITSEVFFAGFF*AFYHSSLAPTPOL GGHWPTGITPLNDLEVPLLNTFGILAI GGSIT*AHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10970	24871	A	11063	269	429	ATWQKLPLQIQKNYFGLGLVAHACNPFST LGGQGGRIIT*GQEFINQFANMVNTH
10971	24872	A	11064	248	65	ITIEGQAQWLMFVPIPALWKAEEAGGSPEVG SSKPA*PCDPPASASQAGITGVSHRTQ LILNS
10972	24873	A	11065	176	1	LFPPPKKVPFPGWNTQPKSICLYTITNEFF FETESRSVARLECRGTISPHCKF*LPGRS RE
10973	24874	A	11066	2	397	MVLWTAHLRAMAPGSSRTWGLLT FALLCL PWLQEGAGVQTPVIRLCDHAMLQAHRA HQLAIDTYQEPKETYIPKDHKYSLLNDS QTSFCDSDSIPTPYNMEETQOKTNLEVL RMSLEIDS*LRPAQSNKR
10974	24875	A	11067	172	399	QILYL*KYATVTTMQHLSHPIL*KKKKK KKKKKKKKKKKKKKKKKKKKTTGG
10975	24876	A	11068	192	3	PKLTPLMLRLVPHITILLPLT*LSKRHII *INTTTHSIIISIIPLLFNQITSNLFS CSPTC
10976	24877	A	11069	204	345	DKSGEHSKTSISSIQNNLRGLGAVTHTCNPR TLGGQGRWTT*SCQFQSP
10977	24878	A	11070	3	416	HELPGQLRLWLTALGTAAGASRTSLLL DPALLCLPWPVQEDGAGQTVP*SRLEDA MLQAHRSRLRGITDYQEVVETYPEDRK LSFPPDCHTYFCF*HSIPTPSHLGETLL TSNLELLRLICLVLDSWLEPARILTS
10978	24879	A	11071	108	2	PSPPFFFTESCST*AGVLWRDLCSLQA PLPGSSC
10979	24880	A	11072	400	278	KVK*LRQENQWNSRGDCSEPRSRHGTLP WITTEQDSIPKNTKPKYKIS
10980	24881	A	11073	139	3	KLACGQRAHLSFQLRRRLREHDLSPGG *GYSEPSWRYCTPASRA
10981	24882	A	11074	17	421	DHVIQGFWRMLMPVILALNEAEPGGLLEP KVQDQPGQNKCSLSLLTIKKRRRENFPG RGGTQLCSQLLRLRVGCCIDPKLHNCPL PAMMTERDPTFKRE*KQNDVLEAKNFFT ILTFMNTTEKMAVQAIGSLFHG
10982	24883	A	11075	412	1	QFFFLGVCCPTQIFGVGKGEKKKKKKRG FPPRVFFFNNPQIFSPFFFGPFFFLGK FPPFPGERFLFFSKKPFPPGVFKRGFP FPPKNFFFF*RI*FKWSPPKPFFFF FFF*DRASLCHPGWSTVAQS*LTSC
10983	24884	A	11076	279	410	VPCCVAGRDGAPGVKAHPAAQKPDWGG FPGP*SAGVGPPPIPR
10984	24885	A	11077	12	386	IAHLLLFSSYHKDTGTLYLLFGAGAGVL STALSLIRKAEGLGGPGLVGNHDHYNVI VTAHAGIIFPIIIGCYGN*LATL IGAQDMAFPRIINISFGLLPTSLLLLL AVAIVDAGARTGW
10985	24886	A	11078	412	3	LATLSLSLSLGFYSRLRYKNIKIPINN PTMASCSSKKRRTSTPTLNQNLMLKL IEKSTAKAKRLKRVPLVPVSVQVNAEEK FLKEIKSAIPLNIQMIR*QTSILIADMEK VSVL*IKDPTSYNIPLSQS*THSK
10986	24887	A	11079	78	443	RHRLPSDTCLTAAPV*PCRGSKKKKKKK KKKKKKKKKKKKKKKKKGGGGGPKNS GGGQNPAAGGKKIFFFFPGGVFNPLWIF WKKTFFWGGKISGQLSKQLSLWGEKKI FWGCGGETSF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LQAHRAHHLAIDTYQEFETIYIPKQDKY SLLDHDSQTSF*FSDYIPTPCSMETQK SNVELLRICLLV
11007	24908	A	11100	1	359	LQLPKPLTVLGTAAHLFAMCLAYATAIL GCALLCLA*VE*ARAQTPQSNF*DHA MLQAHRAHQLAIDTYHEFETIYIPQDK YSFLHDYQTSFCLSYSIATPSNMEETQ KSNLELL
11008	24909	A	11101	1	370	LPEPLTDLTAHLVPMAGSRSTSLLLAF ALLCLPWLQAGAGQTV*SWLFDRA MLQAHRAHQLAIRTYQEFETIYIPKQDK FLHDHDSQTSF*DSIATPSNMGSTQKS NLELLPISILL
11009	24910	A	11102	2	361	AHLAMAPGYRTYLLAFALLCLPWLQ AGAVQTV*SRFLPDHMLQAHRAHQLA IDTYQEFETIYIPKQDKYSLHDHDSQTS* FSDSITTPCNMEETQKSNL*LRICLL LNESWMEP
11010	24911	A	11103	8	366	PLRALWTAHLAARAPGSRSTSLLLAIAL CLPWLQAGAG*QTV*SRLLDHAHMLQAH RAHQLPIDTYHEFEKTYIPKDHKHSFLH DSQTSFCF*DSIATPSNMDDETQKSNLE LLRIFLL
11011	24912	A	11104	3	341	EPLRDLRTAHLVAMAGSRTYMLLAFAL LCLPWL*EAGAAQTAPLFLFDHMLQA HRAHQLYIDTYQEFETIYIPQDKYSL HDSQTSFCFSDSISTPCNMEETHQRSNL E
11012	24913	A	11105	240	329	RNNPGAEAHYYPSTLGGGRQIT*GRG FE
11013	24914	A	11106	2	316	HEERERERERERESAIVRCIHTQGEGLT ELVFFYTRPAPSGKLFITVYVQEHILGV GGNGLSPQLQIGVILRDGRGLAHIRCGTR NKILRLKSGGRAPDLS*DLV
11014	24915	A	11107	169	1	EGHHSGHLSKQKQKQAPFMSWVTHTCNP NTLGGRGWIT*GQFETSLTNMEKPCNL
11015	24916	A	11108	192	355	GMELTGHSTYIILNLFNFWPCVVAHTCN PWTLGGQGRIT*GQFENLWAGK
11016	24917	A	11109	145	383	EWNKDKKKYHVSQCYQSFYVAVYFRK LYIMTWITVNSALLYTELVICQGRVLV FDGPG*FWFETESC SVIAGBO*CDLG
11017	24918	A	11110	199	400	TRAGFFPPFKFLKFGPGGAPFNNLFL GGRGGGFF*IPKKIYIPLLPLKVKQT PSKPPFFFFFLLRQVLCCPGWSAMAR SRLTRA
11018	24919	A	11111	373	177	QFETSLGTMSGPSFYLNK*KSARCGHTC MRFOLLQRQSGREHLLSSGVHRCSENF* LH RCTITWTK
11019	24920	A	11112	204	399	NHFDVVYHFSSFFFFFEKRLCSVPR AEDQGNLS*LNPLPGLKQFFA*PSQE AGIIGPGHH
11020	24921	A	11113	192	16	RKTENNR*RGYGETETPAHCGRACKLG *PLNKPV*QFLKKLKKLPYDPTIFLPA IFS
11021	24922	A	11114	113	369	AGGQGNLFLQKPGPGLKGPFFLPLQ GGNYGGGPPSRGIF*FPEKGGGVKPV GPNLRG*RDLPAPPKGAHPLONGFPSR N

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11022	24923	A	11115	250	387	YLCDEHSLAPGVPHAYNPSTLGGQDG RIA*AQEPEETSLNNIARL
11023	24924	A	11116	192	1	VCDFWKPESHALTRRTSVFHLKR*FS WLGAVAHTCNPSTLGG*GFWRIT*AQEF ETSLGNMV
11024	24925	A	11117	289	202	VFYCQ*KPIRKKKKKKKKKKKKKKKKKK KKLKKKKKKMDQKKLRSPTIK
11025	24926	A	11118	412	421	RA*PTEQVTLGITEGSVSRGHINNVRHD LDVGS*HDDCAAAIKGSPVORLKG
11026	24927	A	11119	16	472	DRKKPSATHAFADAYHTGKAP*FLTGA LLTLLMTSGLT*VHLHSITLLILGLLT NTLTIYQWRVRETVRESTYQGQHTPPVQK GLRYGILFITSEALFFAGGF*AFYHSS LAPTQLGGHWPPTGITPLNPLEDPLLN TSVLLASRVST
11027	24928	A	11120	304	346	GLWHATGITP*PLTGSF*LLMTSSSLAM *FHYHSITLLILSLSSSTLTIYH*WREV TRESTYQGHHTPPVQKGLRYGILFITS EAVFLARFC*AFYHSSLAPTQL*GLWH ATGITPLNPL
11028	24929	A	11121	174	420	FISALLKSAIQNNAMFSTYVALTCTVG TAVSSVSS*PQRNMMS*VHAPAMAGR LVCHYIRVYRRFEHVCKRAVHGQYP
11029	24930	A	11122	299	466	IFILHEICITFFETRHFC*AEVHWKCS LGLLKPPPGGLRCDPSTSPSRVAGTRPS
11030	24931	A	11123	138	1	NPFENEKPPPGKGGPKGNAPFFFFFEMES CSVAQARVC*HDLGSLQP
11031	24932	A	11124	241	499	NQRERS*HLYLLYNTVCLTHGLPILITY SAYQLAIYDLLLRDLARLQADLADRR RGLQPKKRFAFKTRRKDAASSTKVDAAP GI
11032	24933	A	11125	252	391	FLSLDLQSNASLSHFTSPPLMFADR*LF STNHKNI*TLYLPGAWA
11033	24934	A	11126	45	459	AFLNKHPLET*SNHSITDLP*LSNISA* GNFG*ILGACL*LIQITGLFLAHMYS PDASTAFSSIAHITRDVNVG*IRIYHANG ASIFPICLFLHSGRLSYGAPLYSQT*N IGIILLATIATAPIGYVLP*GOISF
11034	24935	A	11127	109	301	QDSLMRKKSKNKSFSHER*RSKCLERKK SGDKKKKKGGPKKKKIGGFPFGQMKLK PFSILGGF
11035	24936	A	11128	322	2	SCHVSVSLGDRAPCLQKEKKKKKKVGG DFNTPLSIMGYQHWQARKIIIMDGT K*KITRK*KIRNQ*DLTDVYRTLHPRVK YTFLSCAYOTFSRTHIRGOAI
11036	24937	A	11129	182	2	FLPRGFQPPPVVVPGLGFLFPFPSSRD PGFPSPMPPPPPPFETESCSVS*AGEQW RNLG
11037	24938	A	11130	138	1	GWVFFLVVFSFSLFFFLR*GLSLSPTL ECSGAITAHCCLKLPGLS
11038	24939	A	11131	304	83	WKKTDIFPRGRNSARLPSDSNCSNLS LQGLSLLYRFWTYHVAITGKSQSRPOEQ VLGYHARKNSR*VHRVK
11039	24940	A	11132	247	225	KNFVGPPFLRGKKKN*FFFFGGGYKK*L LLCLVNMNII*CV*YI*HKRIISDPKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK K
11040	24941	A	11133	242	3	KKKKIIFPPRYFWAPPYFFFLGPPPPFF

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						FFFFFFFFFFFFFFFFFVF* TQFHLSPRLCSGTISAHYNLHLPSPDC
11041	24942	A	11134	361	2	ASQSAGITGVSHRTKPTHGKDT*RKPAEPEVTIH* I* ITLMSCNIESPEKVCADLIRGAKEKNLKVRRPAGPTIKASRITTRKTPCBGSNTRDRFQMRIHKWLTDLHSPDFGRVGRV
11042	24943	A	11135	1	370	IRQTFFQKRREIVGIIILCYWNVGYYSQLH*SSRMLWIFHFYRVVISVKVILVILVPHKKKKKKKKKKKKKKKKKK
11043	24944	A	11136	273	2	GGHAGQQILFCRGWILGPPRSQCCTFRSPGGLAL*FWECFSLPPALKIRFSPFLPF FFWMEFSLRSPRLCNGVTVAHCNLRLP GSNFP
11044	24945	A	11137	130	354	CQLNKISGYPENVGTYLPVLINPLAQPVYSTIFAGTILITALSSH*FT*VGLEI NMLAFIPVLTKKKKGGPL
11045	24946	A	11138	366	2	LVEMGFLRVQRNGLYLLT*SAALGLSKCWDYRREPPCPASDWVFIITSLTHALD GKEHTHTHTHTHTHTGLICQSSLGKQSGWGLSANRGQFSPFAVCLVVSFLPEVPVTSALFT
11046	24947	A	11139	228	1	CRAGRGLFAAVLIILFEPPLIPTSKVLI NNRLLITQQ*LIKLTSKQMIAIPNTKGR T*SLILVSLIIFKATNLIG
11047	24948	A	11140	157	337	HIPTPPHTTCPEPSTRHNSIYLLKRYC LLRIILSLPLQTP*PLTGALSLMLT SGLSM*SHLSITLALRLTYLTITVQ *WRDVSRHSTYQRHHTPPVQKGLRYGII VFTTSKDIVFSGLF*AFYHSRLAPTTL *CHWPPSGITPLN
11048	24949	A	11141	188	3	IPTPGGPPPLFPQKVLFPKGNPRAPPGV FFFFTDSRSVVRLECSGVI*AH*NLH FRGSR
11049	24950	A	11142	224	3	SVSSPCISNTHKVDVRSSALLQESTSSR EVMTGHPHYLIYET*LRSLAQARLACSGTISAKCNLRLPSSN
11050	24951	A	11143	262	371	SYCGPWVAHAYNPSTLGGRRRIT*QG EFETSLN
11051	24952	A	11144	244	379	TIGKQKCHAGIEFVSQSQAPWLKPVIF AL*FAEAGCSLEPSLR
11052	24953	A	11145	1397	1565	DRLESLEMHITPGVYPNQWNTNPLYFIYFEASHSVAQTLQ*RLGLSLQPPPGVGRGQGGDSGKGEGNRAMDITGGLVKG GQGAGEAFVEWKEKLRGFKVGEGBDMD KERVVD*GL*GGRERERERERERERE RERERERESLV
11054	24955	A	11147	64	286	THALATNRQIRGSGHGAMCLYSHLLRK LRQNDHLTPGV*KCLEL*LHH*TPWT TKTAKAIFFNLLKKDSWD
11055	24956	A	11148	230	358	VSVSLIIFATNTNLGLLPSFTPTQL SINLSMAIPL*AGAV
11056	24957	A	11149	81	367	QTLRTKMNKNVVASLIDPTIILGLPAEL IILFPPLIPSCDKVINNRMTTQQ*LI ELTWEQMITIHTKGT*CLILECLIMV IATTKLLGLLP
11057	24958	A	11150	257	2	SVCATITKYLRLGCFADADTORPLPPA TVKLTMFNLIATGHEFLOCIP*LFVDIV

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						PKTAENPHALSTGEK*FSYKGS CFHRI LP
11058	24959	A	11151	257	1	WRGGEKETLRCWWECKLVQSLGRTVWR FVRELKLELFPNPAIPLGSIHPKCK* LDPCTCMFIVALVTIAKMNQKPCPSMDL V
11059	24960	A	11152	17	367	NHKDGKKTTEKKQSTSPPOKDCSSSPAM EQSWTENDFDLEEGFRSSNYLQEEI QTKGKEVKNFEKN*DECITRITNTENCL KELMELKAKARELCEECRLSSRCQGLE ERVSA
11060	24961	A	11153	213	2	TFCHFFFFFFESGSVAQPGVRWCDLGS LQAPLPGFTPFPSWRQLQ*AEIVPLHRS LKLHFKKKQGVFSC
11061	24962	A	11154	1	347	GTSNHFFFLTYTVHNSDTPRNRCCLN PSLRHTSSKPLPARPHIMTHOSHAYHI VKPSP*PLTGALLAMTSGLAM*FHIF SITLLILCLLTNTLSIYQ*WRDVTREST YQS
11062	24963	A	11155	223	3	YSTNLKILRNHPIFF*DRVLLCLPGWS AVASSRLTANSASCLSLPSSWDYRRAPP HPANFCTDRFHFHVQVQV
11063	24964	A	11156	143	1	RQFLNQCPSCNFPFFFTESCSVTQAG MKWYDLS*MQPPPPFKLV
11064	24965	A	11157	149	355	LQBLPFGFKRSCLELTSWYKQVDS ALLSNVYT*KYISKTLCRHQSPFIVREF LTAMKSHKLTQVQ
11065	24966	A	11158	156	370	RSDDGCKITPRNMLGDSVLHHTVDEQ*G PNRYIKKCSASLIREMHINTVRCLT PATMATVRRKITSVG
11066	24967	A	11159	298	4	HPQVVMWRQLVKGELQAQKNAFTDSH THLCYLKCVYFCVCMVICVFCV*SR AL*SLYFLCICAKVAGHSVSGLESQH YGRLRQADHLRSGV
11067	24968	A	11160	364	285	NSWGRKIKLKGK*PPPPKIFFFKYPQS FFLSP*KKKTNPFPKRYLSPGIFLK APPLLIFFFFFFFFFFFFFWG
11068	24969	A	11161	198	406	KSVYMTLKKRGSPHERGDVAICNFFF *IHYVMCVYIHCYIYIYTHIYIYTHI QIYIYIYIYIYIY
11069	24970	A	11162	95	376	KIITKHNIARTNPYTCFIMN*LEITLQ EPKLRPPKPDKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KIRGEKIFFFFLGGD
11070	24971	A	11163	343	391	WR*LSSTNHNDILTYLFLFRARAGVLRS AVSLILIAEQGPNGNDLGGDHIYSAIDP AHAFIMFFIIVPMIIGGFDN*LLAVRN GAPEMAIPHINNISC*RLPPSLLLLLAS AIVEAGAGTG*TAYPEPLE
11071	24972	A	11164	1	158	QPMTPNKGFLSP*PLTGALSALLKTSGL AM*FHFSITLLILGLLTNTLTITQ*WR DVTRES
11072	24973	A	11165	265	466	KILTSLSFNNLLRETHQVGLLESQAKY KKTPLCTYAVCNPSITLGGQGGWIT*A QEPETSLANMA
11073	24974	A	11166	204	458	KRCLLPLPDSNTQSSQCRREQIGRAIR KILFTBTQNIKRLKTEQLKLL*SGK ITAHCNLDLPSSSPPTASQASAGITAJ

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11074	24975	A	11167	256	3	S. KILFFKPGVLSPPWGGVNFQIMPPQGG PPKKRGGPLSPKKGPPFFFFF*ESR SLLPRLCSCAISHTCNLCRLGSSRRTG
11075	24976	A	11168	1	457	HRTFSGVETPNCRGDPVRSTNHKDIQTL YLLPGA*AGVLSTAILTLTRAGLQQGN LLGNDHIYVNIQTAAHAFVLIIFTVIPI IGGFGN*LVPLIIGAPDMAFPRINNISC *LLPSSLLLLRASATVEAGAGTG*TVYP PLAGNYSHPGAS
11076	24977	A	11169	343	428	GR*LFSTNHKIDIGLLYLPGA*AGGLST ALSLLIRAEALGQPNLLGNDHIYVNIQT GHAFVLIIFPIEPIIIGGFGN*LVPLII GAPDMAFPRINNISF*LLPSSLLLLRAS GIGEGAGTG*TVYPPLAGNYSHPGAYV DLT
11077	24978	A	11170	91	2	PRQDPSFFFFF*TESGSVAQAGVQWCD L
11078	24979	A	11171	219	1	IFKSKILCLPPPEPNFFFFFFFFFFFFF FFMRHGGACCSPSYLG*GERMT*ASRV AGTGTGVCHYAWLIFVFL
11079	24980	A	11172	292	365	RI*SLGQAQWLTPVPIITLWEAKVG ICDILQILTHGITTCKMGLTLLFVSGIT FLIHHSIAIKPGV*KNPS*LGTVVITCN LSS*GGRGRIA*ARFETCLGNIVRP
11081	24982	A	11174	200	407	KIFETDVYKCSNLCWASISPSNYPG GPFLYNI.*FLSYFSFLETESHIVAPLE CSGMILAHNCNCL
11082	24983	A	11175	11	155	STNFFLPSETSGSVLQAGVQWGLDLL ASSHSPASAS*VSGTTVDAA
11083	24984	A	11176	140	1	PSTFPDVMARRVSCLSKGDQGV*WLT PVPAPAEAKAGQSPESI
11084	24985	A	11177	210	1	TDEELLMDGRK*FIEMESTPDDEAVN IVEMPMKDLIYYINVD*VVAGLRKTD SFERSSTVGMKLSN
11085	24986	A	11178	133	148	STSTR*LFSTRKDIGALHLLPGA*AGV LGTAVSLLIRAWLAQSGNKEA
11086	24987	A	11179	236	1	KFWKDELTEGGCFLLKKGGGGIFSKKK KNVFFPKKKPKGGKKKNFFFKKKKKK KKKKKKK*LFISFAHIAVHL
11087	24988	A	11180	210	1	QSLGOENLQVFFLPGF*PNYLDKGEKN IRVGKIWGHLEFFFEETESRSVAQSPRLE CSGAIAAHNCNCLP
11088	24989	A	11181	292	348	KKGALFSPGG*KNPNPPGKKKKGLPFS KKKKNP*KKPGEKETRPPPLGLGGLG GFPLAPGGKPPRNRVLAPPNPNGKKKK KTPFSKKKKKKKKK
11089	24990	A	11182	168	3	KPEASMLRMDFFFF*EAGSHSVAHAGVQ WYWCSSLQPTPELSDPLAPSSKVGGIT
11090	24991	A	11183	87	351	KGIKWSLNIQRGVQPHLSYNYSSFFSF S*DWVLLRLRCSTGTTAHSRLNLPGSSD PPTSASQAAGTGMCHCTRILF*ETGFH HAYQ
11091	24992	A	11184	55	344	TSLNLCFFFFWGEKSPFLFPFGDEGFL FGQLDRPWGIEKIFAPP*KGKRGVP PGGEEFNPPAPKGEPLS*KK*NQPGQ GAPPCYPPFLGGGAKKIFSIQGRVSN* PKRGSSPPGGKKGDFSPQKKKKQRFR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
						EV**PNSFSGAP
11092	24993	A	11185	344	190	LVETFRHVRVSDGLNHLTL*STRIGLP KCWDYRCEPPRPANTANSINFPFM
11093	24994	A	11186	135	3	IFPKVFGGPPPPPPFF*ETESRSVAQVG VQVCNLSGLQAPPPGFT
11094	24995	A	11187	305	14	IMLTISIRSRSLSTAEKGLSRIRICG RVAKYLINNRLITRE*LIKLTQKMIT ILNTKGR*SLILVSLVSVYVYHLF*G* FD*SLLLY
11095	24996	A	11188	198	1	LEQTFNMFFPNKSIISIPSGFLFKIS FFFLLFF*DEVFLLLSRLCNGTILAH CNLCLPGSSD
11096	24997	A	11189	352	3	QLCNTPLPKTNHMLTSSNANTLIYERS AIAAASPPILFPASKILLNRLITPHQ *LIKLSKQMIAPNTKGR*SLILVSL IICFEVSLISHCWVVISRLMLRLEVGI NROG
11097	24998	A	11190	270	137	CTINRLVVCVYIYIYIYIYIYIYFNYV YNLCILGHRRESGVI
11098	24999	A	11191	18	342	ACRRKRMSKFPALRATGNCYCSTFCST SFPHPK*MFYQKQKKKKKKKKKKKK KKTIV*K*SKTKKIKGLGAR*ELSLA*L LGEPPI*FAGHPLMLKWEICKRP
11099	25000	A	11192	169	3	ERSGIRIVYQD*NGCLAWSLA*KITHPW LAVAARTCNPS*PSGGRHGWT*QGEFK
11100	25001	A	11193	407	1	KRACFRLILLISTLWEAKQBNCLAGV HQPQKQKGETSPQKIKSAWHQSPRL *EVRMD*LSQGG*GYSEPCSHCTPAWA TERDVP*KQKRS*PWELASERKDSGR RNLVREMWPSQASVIVQRRISF
11101	25002	A	11194	110	412	VCGFRLHSPATLMPFLMPSYFRHSNT EIKPISNPTVASKRERKSCSTSLTNQ KLEMIKLSEAT*KAENVQKLGSLHLQKV SQVNAKEEFLKEIESA
11102	25003	A	11195	34	155	AWHEGHHVSDGLNHLTL*DACLGLPK SWDYRRKPPCPA
11103	25004	A	11196	289	453	NQPGKSPMISTTFHFMFEITLVHAGV*W LDLGLQLPPPRFPGFSCSLHLPBGWDR
11104	25005	A	11197	177	432	KWEKQAGTLGGGNFPKPKTRVGNFEK LKGNPPFLCL*KRGRKGTGPWKKPAPS GERGI*PGKGGKTGPPKFGPMKKIKRG K
11105	25006	A	11198	139	3	AMVSLSPRLCCSSMIMAHCSLGLSGSSD PPTSAP*VARITGMHHP
11106	25007	A	11199	150	492	GDPLFGHHPV*EVRRFPARQLPRLRSEE PLRPVATPSGK*GASLSGSHPIQEGGG GOPLPGHLPHPGWSGVKPPPGQSARPG GEGHLLPATPTGK*GGPQSGPHLSGGR RE
11107	25008	A	11200	239	64	YQKYYYYYFF*ETESRSVARVKSSGLIS ARCNLHLPGLRLQLCLFPTSAPVGGESH IT
11108	25009	A	11201	31	396	ILTMRETVHIQAGCGCAGNIGAKFWEVIT DEHGMDPTGTVHGDSLDLDRISVYVNE ATGGKGVPRAILVDL*PGTMDSVRSQFP GGIFRPDNPVFGQSGAGNNAKCHYTKG AELGDSVLVD
11109	25010	A	11202	85	407	VLLPHSEALEGATMPHSYPALSAEOKK

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						ELSDIALQIVSPGKGI LAADCEVGSMAK RLNQIGVENTQENRRLYRQVLFNADRA KKRIGGVIFPHETL*QKDDGVT
11110	25011	A	11203	302	115	THLDHVALIYLSIYLSIYLSIYLSIYHLL STIYLCRF*LID*DRVSLYFSGWLMQMG KPSCF
11111	25012	A	11204	130	348	GNAYGEPCSVLVORT**IPALTFPSTCL DSKFORDLVLTARTDSNFTSNTVAEIQ LTSQGESOLDGALGWQ
11112	25013	A	11205	232	62	ISARNEGFTLN*RTFFFFFSHCLSR LECGGMILAHCNLQLPGESLEPGROSQ LK
11113	25014	A	11206	161	2	KKKGFLPLLEFFCTQSTQLRLGAVAH YNPSTLGGRGWIT*GGEFKTSLAN
11114	25015	A	11207	251	3	PNHLPKAPSNITLRIRFOHNLFRGAQ TFGLQHLKTSQMKTTHINTKGT*SLIL VSLIIFIATNNLLGLLPHSFTPTIOL
11115	25016	A	11208	145	287	GFRLLK*INQKYSPLKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKK
11116	25017	A	11209	436	110	ISGRGEQKFKYFSPAPFFRGINPPPLGG E*QNQLKPP*KKIPLGSPKVPKKGSPQ KILKKGPGGGPPLFPPLGGGGGGFPF SQGFKTPPGKKKKPPPKKKKKKK
11117	25018	A	11210	217	2	DKSVLHINVTLSLSSLVHILFKYLEN K*KKNLWPGMVAHACNTNLGGGGRIV *AQEFETSMGNTVC
11118	25019	A	11211	146	3	QKVSHAQYRCLSGWYFFFLIFLETRSRS IAQAGVQWRDLGSL*PPPA
11119	25020	A	11212	187	384	GLICFYLTCTFYFYFIFYLIFYSLCYVM LCYVLCYVLMCYVMVCMYLCYVI*DRV SFCHPDNSAA
11120	25021	A	11213	373	482	MYKLRLHRLGTVAHCTNPSTLGGRGOWIA *GGEYKTS
11121	25022	A	11214	64	362	ITGVSHFTQPLFPIGGLALSPLKECRM ITAYCNPELPGSGDSCHLSLSPSWNYRY MPCWPS*LKKN**RQGLTVLSLEKDY LL*DFSLKRSFVGR
11122	25023	A	11215	181	368	CDSAVPLLDIYPTFEFKADLKKIRPMFT IALFAVAKR*KQPTYPSPIDKWIKLWAG CGSRL
11123	25024	A	11216	268	369	TTRPDMVVHTYNSSTSGGQGGTIT*AAQ FKTSLT
11124	25025	A	11217	90	3	IGQAG*LTPIPALWEKPSGGSPVEVRL SLTAPGL*SQLRLRWEDHLSIGQSSF SEP*SCPCTPAWVTO*DSVSKKKKKKK KKRKEKEKNQTPKATESPGQALIGSHS LQVQKRVYAHPI
11126	25027	A	11220	19	343	LELEVEPEDVSELQSLDKNYLSCEFLKR FLEMKYTPGEDVVNTIKMTEDLKNYND LVDKAAAGLERINFNPEGSSVGMKLSN SIAWYSEIFYERQSQFMWOT*LLA
11127	25028	A	11221	266	356	FFEMESHTVA*AGVQWCDLGLLQSLPPG FK
11128	25029	A	11222	105	2	RPVCSTIKVLRDLSSARSNPGRFI*TSN SRPRKS
11129	25030	A	11223	145	350	RKGRQLD*DLGWV*WLTPITPILWEAR LGGSLEARSSRPAN
11130	25031	A	11225	155	348	PLFFFCFHRNTFY*KSVCRFPPKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
11131	25032	A	11226	271	3	KKKKKKKKKKKKKKGGGGGANTKFLY GENRKPPLFFFF
11132	25033	A	11227	3	413	NFLSVFNFRTRICLGMCFLSIFLLIFGGG LKQQLFLAQGFFFLHYFTSSIHSSLL Y*MLDFLDLFFLYFLFCNFSVFLFCI LSKFF
11133	25034	A	11228	48	413	SPAEPHRSYTMNVKVGNGVGRIBRLV TRAAFNQSKVDIVAINDPPIIDNVMVYM FQYDSTHGKFGHTVKAENAKLVINGNPI TIFHERDSCCKIKRGDAGAEYV*STGVF TMDNAGAHLHG*ATRGIIISAPSD
11134	25035	A	11229	172	404	VFLVSCGFFFFFWEKKICFFNFGSKK RGKIGGTGTGPGKPKGNFRGPPPNKKEK GGPPPPPNFPGFLKKKFVQGGQG*KT RNFEGPPAPNPPKGGDLGGGPTQGGNG FLKKKKKKQK
11135	25036	A	11230	247	2	EFENS CSPGWQRGVMI PGVTVEDMNOQ EFIRALVALLKKSRLKVPWVDTTKLA KRKELT*DEKWFT*AAST
11136	25037	A	11231	1	372	QPKKKS VSKKKKELPCDFATPLPGIYP KEKKS VYKDNHLRLVYCRAVFTIAKIW NQPKC*SGDK*KKI*YITVTLRR
11137	25038	A	11232	311	464	TELTVEAWCELDQRLTKSRQRKKE AEMLQIQHINIVFQDSWETWKKKKC IVLVELMTSSGTLKT*VQGYKS*PRSM REFDFLFRSTSTFTLVQPKGTVLPTV TVLAYFLAHKVL
11138	25039	A	11233	64	418	KKATPRNLCKWPGTVAHACNPSTLEGRD GNIT*GQEFETSLTNMVP
11139	25040	A	11234	233	421	VPVASRRRRRCGRVGGGKAMADLKLNI DSITQRLLEA*GAKPGKKVQLHENEITG LCLEPREIFLQPIILL*LVAPLKI CGDI HGPPYDLRLFEYRGLPPKSNYLFLEDY VDRRQH
11140	25041	A	11235	343	1	PTTSMRSLRLGASS*KTAGPQOORL EPALPRRWGRSADNPSSGLRSGKNM KQTPGTA
11141	25042	A	11236	122	419	NNTHGLSHS SVGRNPGAVGSGSCMSGYK LSEGLRSLLEAVCISRAAVIKCHSWVAS NNRIHFPSSGG*KSEAKVWAGPSL*R RVPSLPLPASGGRHCLVCGCVTPPSAF TW
11142	25043	A	11237	1	379	RTPRGPKPNPGLQKRTFFLIGGRITKYL GIFGKDLFWGGKNWDTLLPKI*RSREN KNF*RBKWNLPFPYPGCLKNGARQQHFA HLLILRDTKTYLAF
11143	25044	A	11238	1	397	AFNHLHAGHGLSGAAMKSLVLLLCALQ WGHSSPHGPWLIYRQPNCDP*TEEAS LEADYINQNLPGWYKHTLNHIDEVKVW PQ*PSGELPDIEDTETTCVHLDPTVP A*CNVRLNEHAVO
						QMTFNKRGFLPFSKDLRSSHVLISPLHS ATHTRTPNGHTNHPMARSTRKHIRR APHITTCPKPSIRDNPIYLRNFFLRRI FLSLLPLOSPPPIRRALAFNRHHPAK SPRRPTP*PLTGALSALLTKSGLAM*PH FHSIALLILGLLNTNTITIQ*WRDVALE STYEGHHTPPVQKGLRYGIIITSEIF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						FFAGGF*AFYHSSLAFTPOLGHHWPPTG ITFLNPLEDFLLNTSVLLASGVSTIT
11144	25045	A	11239	267	3	FVSVRITPIYASAAATWLSYVWVWASSPN VCPGDRVALSPRVCSGTISAVRNRLR PGSSDYPA*PADGWAPPYQRCPPFRL ANF
11145	25046	A	11240	391	31	VTFEEEEEEEEEEEEEEEEEEEEEEEEEE LKNPFPPPPNPPFFCPKF*ILFLN*1*F *IKF*1*KIPGFLLNPPPPPPPPPPFP GALFPPPPF*EGVLPCSPGWSAMSHLLS EKRLKLTPRMSYN
11146	25047	A	11241	371	491	KIPLCWARHDAHACNPISIRFQGGHIT* GOEFKTSLANMV
11147	25048	A	11242	1	221	HRIDPLCRNSAKAFVFFLSTGCHRVSDG LDLLTS*SAHLGLPKWDYRCKPPRPAL NCFETISQLLNLICID
11148	25049	A	11243	382	333	TKIKDFKFTF*RWPHNISRVEAEKFLF SRGQGFPLARFPSESSPGFTLTVSR
11149	25050	A	11244	169	477	TOKDEKSTTTTKNAENSKGQSAYSPPS DCNTSLARAQ*EASMOELTEVGFRRR VIMNFVKLKGHILTCREANHDKTLQK LLTSITSLAWNINDLMELK
11150	25051	A	11245	200	462	SLTYNELCTHILYQYVA*QRS*CFQG LMSFY*RTLKNLKESSCKVALLVPSFL WKRGLWLTGADT*KPSTLGGQGGR1A QEF
11151	25052	A	11246	484	301	IFCEKKGSL*FQLLRVRNRPFPNPNNG CS*LLSSPCPPGWITE*DPVSQKKKRRK RNQVMELVSAQENKNKPRSVGLQACARS MLAFSTTPR
11152	25053	A	11247	226	458	NTVAVDWGPRCFCSLLLSHAENCMDWFT KIELFIFTNHLKQDLEMLW*GQAHAC NPSTLGGRGWIT*GOEFETS
11153	25054	A	11248	304	436	SFSRCRK*KYG*QWLTPVISTLWEARV GRSLDPRNRSRAWTMY
11154	25055	A	11249	216	451	THKYLFPYLYGNVPMPLYERETGSCSIA* AGVQWYSHGLLP*PSGLKRSSQVAGVI CLANFPPPPFLKKNSLVLPRLG
11155	25056	A	11250	260	474	DKYFLLYPLKALNVLGARINI*KVSKI MC*K*DKNMYNFFFSF*DGVSLLPLRL CNGTILAHCNCLPC
11156	25057	A	11252	193	496	MTSCSYFYL*IKDASMVKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KASDYK
11157	25058	A	11253	348	478	DLGWLKLTGVAHTYNSSTSGGQGRIT* GQFKTSLANVVKPC
11158	25059	A	11254	174	475	MHHVLLIQDIDNT*NCNLHFLSCSQL KSIQKKKKKKKKKKKKKKKKKKKST
11159	25060	A	11255	292	48	LEFLTCIRAVSHTHLAFNFTAGITTF* TRSSSNWAGTFIIPKIVTFLEFF*ER VSLKLTRLERSGAIPAHCNHLPEP
11160	25061	A	11256	347	16	TQSDAWCIYNFPAKIKSSSPHPTQ*PS WLHLVDPAAPGFWVLEPTSPAPSACTPOP LGRWDOPQOSKQCPGSRGLGQGGPPQ VGLKGAGWSQALPVGLTRSIESHN
11161	25062	A	11257	238	590	APGAYIFPQHNPTDSQVTFSLTASHL ICSPLCISVLHFGNMDDENRNAVHA RACAHANTHTHTHTHTHTLYLMNYRETL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11162	25063	A	11258	310	461	MLLKTRGRATGSHARCIFS*SLAQACP LSFGDVLQLES DRP GAVARTCGPSTLGG *GSGWIT*GREFETSLANMLKPR
11163	25064	A	11259	461	174	MGFHRVSQDGLDLIT*SSAHGLPKCWD Y*CEPLRLAPVQKLFKCVGYLVLCHGS GYMSMKVIRMPGLINSLEGGSAUVHR YWSIWEISGCI
11164	25065	A	11260	343	472	LLRELRLQKCLSGSSGGCSEPRLDYCTP AWWTK*DPVSHKQE
11165	25066	A	11261	229	3	VKMKLG*VPVKVKI*KYTPLLGYLKEL KAGFORNTCTLMFIALFTIANRMQPR LP*IGECVNNM*YHITMES
11166	25067	A	11263	163	399	KLLPSTRNLHAMEHPIFGWLRNPHATAQ G*HPLSQSSALHGRADHICVPELCTSS SSCIAGYPN*EGMFASQHRHV
11167	25068	A	11264	316	427	TNKKHII*ITNTTTHSLITISITPLLEFNO INNLFSCS
11168	25069	A	11265	184	418	KTPPGFEEKNPFFWGKKGPPPPKKNLP LGGKKKFLRGKGGTKFFFFF*KIGSSS SPPPPPGGEQAPPPPKSPRR
11169	25070	A	11266	219	13	KFFFSLEHQNFSGGGVLEFPFPEGFLP KKPKQGFIPTPLKQKIKPPPPGYSGPP RVL*KGPPHIFYK
11170	25071	A	11267	3	173	SHHARPETGFRHVSQDGLDLITL*SACL GLPKCWDYRREP RPQARKLYCLGMRTNE
11171	25072	A	11268	157	2	PVDITHVKTITVGLGMVAHACNPSTLGG GGRIT*ARGSRFLPPHWTSELR
11172	25073	A	11269	291	468	ISEGKRSFLVILHFIFFETGSCSVAQA GVQCWCDLDSL*PHIPGPK*SSHGLRLTG ACH
11173	25074	A	11270	29	478	GWNPNYQDDIGTLYL*SGARAGVLGTAL CLLIRAEIGQPGDILLGNHINYNVITAH AFATIFFIVTPIIIGSGN*LVPLIIGA PDMAVPRINNIS*LLPTSLLLLASAI AEAGA*TG*TVYPLAGNYSHPGACVDL TIFSLHLASV
11174	25075	A	11271	61	474	PYNQGGDHAANPHLTKWRSOQTTEIC RFEFGAKQRFQCPRLHKGRSPGQRLALS QNLPSYSGSHLLSAYVVDITISKHPIN TIGWLGTVAHACNPSTL*GEDRWIY*AQ EFKTSANVL
11175	25076	A	11272	277	478	KIYQVPIKHQPRPAGVAHTCNPSTLQDR DGWIT*QGEFETSLANMNSPSL
11176	25077	A	11273	350	11	KEKTAGQARWLTPVIPALWEAEGASPE VRSSRPA*PPP
11177	25078	A	11274	138	3	NYINLYANLGAVAHACNPSTLQGRGGWI A*AQEFKTSLGNMAKP
11178	25079	A	11275	359	219	FVIKNGFPQVGRDGFNFSL*SAPLGLP KWDYDRH*PRLALFFFF
11179	25080	A	11276	262	3	FCMSLVHLFSLHSQDNYFTSFL*IPNIP SGPFLFAFQDTLQ*P*DFIYFYFETESP SVTRLECSGATISAHCNLRLLVSSNSPAS AS
11180	25081	A	11277	285	1	VKKGDSVSKI FRKKKKRDKIRLHFMIT TVNNLGIEGNLNNIKEYIKNPNTANIL NGERLKAFSL*SGTRMSFLTPTFF*ILV DTQQVYFMESH
11181	25082	A	11278	160	3	TDKEVPLINAQKRWKLFEMESIPGEDAMN

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11182	25083	A	11279	334	488	IV*MTKELQYYINLVEKVIARPE PLNTCGY*NLN**NFQPGSVAPACNPST LGQDRWIT*GQEFETSLANMVK
11183	25084	A	11280	527	356	FFVFLVETAFHHVQDSLDLLTS*SSRL NLPKCWDVRHEPQRQAKNVGEFSETRSI Q
11184	25085	A	11281	486	248	VQQLFSLLLPRLFCNGVISAHCNLRLEP SCDSSASAS*VARITGASGSQAVVLQVQ CLQPVQRGELLRVDLFLQVLVLR
11185	25086	A	11282	38	157	STGLHHVSDQGVDDLTS*STLPKCWDYR HDLPLRPAQSRL
11186	25087	A	11283	474	339	FVFLVQMGFHHVQAGLELLTS*SACLG LPKCWD*RHEPTDPAK
11187	25088	A	11284	2	462	LETTTAKRWNSVIALKRHNNSCPYKMANL IDKVCSDYSKDWFPFIFLPLLRPPYCL RHNMETRSTINPWPFSKCSSEKINEEG MLKVEIG*KLICLLCQTFPKDMNAEKFL KEIKSATPMNTSMIRKQNLRIHDMKVL VIRIEYQASHNLI
11188	25089	A	11285	65	280	SRAVEFNLLTT*SACLGPKCWDYRCEP PHPASP*FSKLLSSNLTKYLSL*DSHS GFYSFVCSGLGILIL
11189	25090	A	11286	244	488	MRIGRVPVSLVFCYVMQREGIILEAENK PSPDIESVGALIDFTASRTIRNKILLF IIFPG*GILDSFNVF
11190	25091	A	11287	345	445	KRPGTVAHACNPHTLGG*GRWIT*GQEF WTILA
11191	25092	A	11288	223	500	SPGTRPKVLECOSTLGRQAILLLGEGWL WGQSHRLGVQSQLCLVLDLTCSLSCS FQIIKLR*RPQVMVHTCNPTLGGCGGR IAQGGEFK
11192	25093	A	11289	157	22	LSCQEVRGIEGAECIWAQWLFFIIPAL WGAKVG*SPFVRSKPA
11193	25094	A	11290	305	497	KLUNCYIFRGVSVFVRELYCNKIV*WLS TVAHLYNPALGGACGWIT*GQEFETSL TNMAKPRIL
11194	25095	A	11291	478	1145	QHVQACPERPQMMGTLEERSRAVASRIGH SYSLDSQPARAVGHPWQQAQCTRVTELT EATGKILRTSHIGKPHQSPQPAARATQK LRPASQGGVQMQTKGGASNPAQIGSHV PKSSSQFSDQSNPSTVKHSQPKPFHSV PSQPKSSQTKSCSQSQSTKPSCKSTQ PKPSPQHPFKSPKSPFPQPKSSSTNP SQRKAHNSKAGQKRGKQ*RANSRL
11195	25096	A	11292	352	468	TFPGQHGKIPSLTKQLAGHDCL*S RLSPR
11196	25097	A	11293	295	24	ENIQCSKKNERQHMHNGVCTWNSNPGFV STWYVRNCLACLDTSFSTIKWVKSHDT SMGMFTAALFTIAKT*NQSTCPSMVDWN STTRTS
11197	25098	A	11294	274	429	ECEPVQTLNKKRFLKGLKLESPDAI PLKGINLKEVKSVP*SDTYTPMCI
11198	25099	A	11295	168	469	PSLGNKSETSPFKKKNLFLGFFPYFREK LVGILLKTLVLQKAGGVFFGPKNPPEKN PDPPLDSPKTFRRLLGAFVTKFPKGLKA AVVEPALV*POGQMG
11199	25100	A	11296	37	348	IKIPNKTLYFKKKKTKKKKKKGGSL KRPRGGPRIYDGARINLPHIGTAKKHE

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						GGYWEKNFHGGGGNIGTPPQKTRPLGG KNMLKRVQGEKPRPLGGCKTRSQLPSC HA*P+VQGEKPRPLGGCK
11200	25101	A	11297	93	388	DEVASDNCVYFGSSHDSQVQIGSQFT TQIQAHNLAKPRAL*NIIS* PMEMRSK CLLLAYKKKKKKKKKKKKKKKKKKKK PKYLSRQKDH
11201	25102	A	11298	61	243	YYIHRTTVYFCMN*GLKDNVVK*TIDLC LCKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKPGGGGA
11202	25103	A	11299	250	341	TYMSLTGLQNL*ETHLTHKDSHLQVK GWKNIPIFANVQKQTVAILISDNIDIK ATTVKKKKKRENPTILNIYVNTGAPKF MKHLLLNKNERDGTTVLG
11203	25104	A	11300	3	285	DAWERKKRSQMOKTTNKGAVGVSPLYST MAWNVNELNFLIKRRVA*CIKKTKSMI CYLQETNFIKIDTHRLKRWKKIFHFRN N*KLAVVY
11204	25105	A	11301	175	407	AENNPDLVLQKA*TSRGTFMP*ILLRVK RGSNSRNRNCWGWGTGMILLH*QECK LVQPLWKTVMRILPDLESL
11205	25106	A	11302	75	280	YHLNLVLVYPHPKRNVC*KKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK FFPGGKKKNFF
11206	25107	A	11303	299	3	IHASFLFRGCTIAPTVCRSRHSITSS TSDLTHYYYYYYYY*LASQSVLAGVQ WDQLGSHNPPTSAS*VAETAGASHARL IFNFFVMEVSLYC
11207	25108	A	11304	137	323	FFTVMGRHRKEKSKNDQLNLGLHDFLD NPILLF*KYLGRKKKKKKKKKKKKKKKK KQKKKK
11208	25109	A	11305	64	481	KPTRPHVYHIVKPI*PLTGALSALLMT COLSH*FHFMSITLLGLLNTLTITQ *WRDETRESTYQGHPT*PQGLRKYLI LFTTSEDLPAGFF*AFYHSLTTPPOL GHWPPGTITPLNPLEVPLLNTSVLLA
11209	25110	A	11306	142	330	FFTVMGRHRKEKSKNDQLNLGLHDFLD NPILLF*KYLGRKKKKKKKKKKKKKKKK KKKKKK
11210	25111	A	11307	259	440	RPIRDNPIYVYKSCPLRTPLSLLLPLQ PRPYPTTRALSPNRHHPAKSPSP*PL TGALSALLMTSDTLTGLHFFHYITLLILG LLTNTLTITQ*WRDETRESTYQGHPTP VHKGGLGYIILFITSKVFFARFF*AFY HSLDPTPOLGHWPPGTITPLNPLEV LLNTVRL
11211	25112	A	11308	433	3	FPFPPDIRHSRLGFFPSPGRAGFLNFAF SKGQEPALPGGYFYPSPKKKNLAFCSPP LFYWGKFGSKFSLGVGLFFP**SPKSF CQFLBNKGFFPEKFFKFFFPAGGCVTF FSEGGFFPCLLFFFFDRVNLCHPGWISV ARS
11212	25113	A	11309	2	423	GRVGDR*LFYTNHMDIGTLYLLFGA*SG VLGTALSLIRAEIGQPNLLGNDHIYN GIVTDHAFDIIFFIAPIIIGGFGN*LV PLIIGAPDMAVARINNISV*LLPFSLL LLAYAIVEAGAGTG*TVYPALAGNYSHE TFFGKFFPCLKFKPAQRGENTPGFFPFF
11213	25114	A	11310	234	1	

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						LVFFFMESRSVAQTGVQWRDLGSSN SPTSAS*VAGTTGACHHARLIF
11214	25115	A	11311	406	211	LSLFLHSLISTHGARPDPVGLVPTQDG LDLLTS*SAHIGLPPKWDYRRAPPCCFAC GFDLHLPND
11215	25116	A	11312	379	398	KT*NFTVRGSIPLNNIPMASMTFSKKK KKKKKKRGGPLKKNPGGAKFNGGRKKR IFSLKGGEKKNPGGILEKKKPFGGGKKG ENPPKKNKGLREKKKF*RGKGKKPKQKG GGKKMGSSSAKPTTWG
11216	25117	A	11313	390	489	RYRLGVVAHACNPFSTLGRGRWYI*GQE FETSV
11217	25118	A	11314	286	434	ILWYNNYISIKLLKIIYKLGAVAHCTN PSTLGGGGWIP*GWBFETSL
11218	25119	A	11315	322	3	PTFYGCRQGVF*IVTKNDRIIFSSYTK NLLRIYGLY*FYVPLLRKTSKKKTS FESNLSFK*VFLMSGTVAHCTNPSLGG RRGWIA*GQELTSLTWERFR
11219	25120	A	11316	251	389	TFPFFKEKHFVPGVGGSLGSLQAP PPGSHSLA*ASPRCWDG
11220	25121	A	11317	313	80	EYICPRCLSPGRD*PSQHGFTSLQKL QKSAGCGAHLRQGLRLRGLDRVRHCLK KRIYLSLNSLVLSNNRPOII
11221	25122	A	11318	145	410	APKTLKVALTSAAAREESTCOLVLEDEL VIFLELNRSTDRPGAVAHCTNPRITLGG HGGWIT*AOEFKTNLANMVKTC
11222	25123	A	11319	393	3	NFFKRIIFLSPPLPLIFTPPPFFPKKI PPKPLFLFGVFSQTCQISFFKNFYVPL FWFSPNPFLLFSPSRKGPPPSRFFFPK VGNPLFLFFFPFFFPF*EGVSLLLPR LECNGTISAHYYLRPRV
11223	25124	A	11320	135	1	HRDVKLEYAIRKMEVRPGVAAHACNPST LGSRGGWIT*GQEFETS
11224	25125	A	11321	282	2	NSESVLKEKGDEEEKVLSPLFSKRV LESKTFPTLHSGCKKRSYFLKITTSSFL *PRVBCSGLV IDHCKLKLGSDDPPTSA FPVARTTGM
11225	25126	A	11322	149	30	WGGGGVRLNTPITPALWKAEGGSPEV RSS*PVMPCLY
11226	25127	A	11323	316	399	STLGGGQAQIT*GREFETSLANMNPIS
11227	25128	A	11324	223	397	I IKAYQ*DVNREGI KTIITVFONKLKCI KIMIWPGAVVHVYNPSTLGG*GGWIT*G QE
11228	25129	A	11325	3	396	NYSTAALFLRGHIWGRWGLTYGSSFI YCRGLNSTLGLYPLNASSNPHRKLCKP KIVTHIAKCPIGHKIIYPYANTPNH*HH THHTHTHTL*DSLLWPGVAVTCTNHT LGSRGQAQIT*VQEFKTSIA
11229	25130	A	11326	113	442	KRYIQIRAHSEVLGHELMGTILHNPVQT IQTEWFFPYLPCLCSRYTSGSHRFPVPL LFHL*NRNNSHHHHHHHHHHHNPNC* ECCRAHSDSYAVNSDKVSGEPVAM
11230	25131	A	11327	145	3	ELDKFPNPFPCHTGVQ*CDLGSQQLLP PGFK*FCLSPSSWDYRCA
11231	25132	A	11328	189	1	KTNILLIHSKLRHLHQSSEVFC*SKSEK SNVCT*CAFSCLPKI.PWLGKVAHACNPS TLGGGG
11232	25133	A	11329	193	405	ID*QTLTKKKKKKKKKKKKKKKKKKK

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11233	25134	A	11330	209	11	AYTSKKKT GGKRGTPPTINNIFFNFF*EKGSCCSS RAC*CNGET*AHCPRLRPGSSNSPAAAS RVQETATTSP
11234	25135	A	11331	38	390	VDQSTVCRMGQSAGCGWSDKGIGAGCL K*QRQKKKKKKKKKKKKKKKKKKGGG LKKKFLPGGEGKFFFFFWGFFFGGR FLKRGGKKPGYKKNKISGHPFFFLGGG KKKKR
11235	25136	A	11332	38	326	VDQSTVCRMGQSAGCGWSDKGIGAGCL K*ORPKKKKKKKKKKKKKKKKKNRGGG FIKKI FPGGGEKIFFFFWGFFFGGG FKKRGGEENLFP
11236	25137	A	11333	1	234	RTRGKNMFAIEGKGVPTGRMGGSPIKH SFLESKNITLWKKKKKKKKKKKKKKK PHDKIKDLDFPV*NKQKNISIP
11237	25138	A	11334	244	398	INHLYSKNKDLFLLVFLFFFP*RRPG EPLLIKGWLPYLGGLNLRLKDKPL
11238	25139	A	11335	174	1	HQVYFPYKQEHYKQDSQCQYIKMNVWP DAVAHGCNPGTLGAQGGWI*GQKFERT RG
11239	25140	A	11336	148	411	LIFFPHCYLLNAPSTILYNPEKVVNLH LCVSAVCLLVVPHS PHTCLY*KKKKKK KKKKKKKKKKKKKKKKKKKGGAFFK KLLF
11240	25141	A	11337	237	453	GORPLLSFREKGSFFLLLETFCFAPQA EGQGHNLG*LQLPLWG*SNLSVSSQEV GITGAGHHPRLFFVF
11241	25142	A	11338	65	347	VCRVDDFVPEARTFFKSI*EAWNKNKI KPLLSTFSQVPGSENEKCTLDQAFIGI LEEEIINHSSCENVLAIISLAIGGVTEG KYGSVPLCLK
11242	25143	A	11339	158	393	VPCITSGIRKGRKCLPRTRENARERRD KKIPPGLC*AGKLPQEKSSWPKQVHV AWNPTLEGRGGWIT*GLEFKTT GIRPGAVAHVCNPSPLGG*GRWTSRDWE L*TSLANIR
11243	25144	A	11340	117	3	SOQGLRELGRGAFRGVQAKEMWPIKLG LVKDWKIKSLEIYFSPSPPIK*PEITDF FLGASFKEDEVFLPVCLFVCF
11245	25146	A	11342	149	30	TQIFPPPPPPGKKKKKFFFPKKKKKKKK ERKDKRKNQK*KGPGVGVSPLFPPLG GQGGGFPQGLGFKTPLAPKGPWF*KT QKFPRRGGGPKIPLFGGGGKKFPSPG GQGSNPKFPFPFP*PRGKKKNFSPKPK KKKKKKKKERKTEKTNKK
11246	25147	A	11343	120	504	GVHDCRLWDDMTREPPAAAAATACAGRP PPRREEHSQLLLLISFGQFRW*DDQVN TPNLDHLAREGVKAKYLMPLVTMTSPS HFTAITGKRSHAHTRCPSPQRPSPFV IRSKSSVSSREVEA
11247	25148	A	11344	213	399	ALVHICLTTTIQVSGLSGSKYLMRQGMV AHGCHPNLTGGRGGWIT*SQESSTLAN TVKPCPL
11248	25149	A	11345	308	3	NPTFRSGDLWVEEGSPGAGNWGCLSEQT LRAIIKATTSYSFYCYFFETGSHSVAWA RVQWYNPGCSICGSSHLPTSAS*GAGTI GMHHHAWLILFFVEE

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11249	25150	A	11346	189	433	GHCRAGTSLTLTHLGGSAMELIHLGLCLGRMKPFIHTTCIILFLFLSATQAGGQGDLS* LQPPFLGFKQFSCFSLPRSWD
11250	25151	A	11347	257	3	KWGLCPLTIKEERMGFLAKRRKIKGVF* PGLFFFFETESHVQAHCNLSLLDSYSPASAS* VAGITGACHNQLIFIFYE
11251	25152	A	11348	159	434	LSFSCRDVGTYSARAHPPTHTRVRAHTHACTHVRARHTHTHTTAHSHLTKEQGLCTLPGSSW* PGLGGRALATAQAQVHCAGITTAHPP
11252	25153	A	11349	240	406	AFKRLAKNNSMGVNRSLSPGVVAHAWNPSLGGRGRIIT* QGEFETSANMVKP
11253	25154	A	11350	163	360	FQLLQLMKFLQN* LLERLRFQNLNLLEG LACSESRRCAPVWRTEDSVSSPQPRPGAGRGSPFF
11254	25155	A	11351	145	406	PLNSGAKPTLLPWSFRPELNAFPFPPGEKEFFFLGRGFLPAPQEEAGGENIV* GKPFPFG* REFFAPPGGDGNKAPPPPP LFL
11255	25156	A	11352	122	337	ILWVLLVRESLKFFFLLLFLFLFFETDVA* AAVQ* SDHSSRPQ* PGLRGSYTS AFRIAGAIGICHILY
11256	25157	A	11353	325	416	KCVYINGWA* WLTVPVTPALWEAGAGRSLEV
11257	25158	A	11354	260	415	LEELONTACQKLEFFLSRTETKGGCLLSPLRLNIVLEVA* AVRQKEIKGI
11258	25159	A	11355	160	2	ISEISTKRNYYFLKNLGVVAHACNPST* RG* GGQTRGQDFQTSANMVKP
11259	25160	A	11356	160	3	ENLKLYNGSPFKTIWLGWVHTCNPSTLGGQGGRIPI* AQEPTKSLGNVRRP
11260	25161	A	11357	235	408	GOPLAALFFYQWHLHFKEALLHPWGKT VWRFL* PLKKEGPHDPAIPLLDIYPKNK KW
11261	25162	A	11358	11	393	QTERTPTPKPHLYVSFFPNSQDFQLGGKLTNRKNTHTKTPSVCHHQRPKVDKTITKIGKQSRKTGSKNGSASPPPKCESSPATEQSWTENDFDELREEGFR* SYNTLLKEEVRTHGKEVKNLE
11262	25163	A	11359	283	475	FMVSVSIXVYFFIPIFLFFEMESCSVTQAGVQWHDCLSLFC* VLASSPGNSSPVR
11263	25164	A	11360	266	407	LEIHHSKTL* FWLGIVARACNPSTLGG* GRWIT* GQBAEILANIVK
11264	25165	A	11361	93	1	DVLSILLPLECNGAISAH* NFRPLGSSNSS
11265	25166	A	11362	131	377	MEEMIKGRGLSKPPALSSYLTLSKSS* LKRVARRRLFLSKRSLSLDQVAGFFVCLFVWDRVSLCHPCWSVVFQSLTALT
11266	25167	A	11363	212	392	QAECEALPIGVKEFPKILTHWLGIVAH TSNPSTLGG* GGQITWQGEFETSANNA KPCV
11267	25168	A	11364	141	3	NELWLNHQNVLEWLTQVAYTCNPSTVGRWIT* V* EFETSLGNMVK
11268	25169	A	11365	215	384	ANFNIRPETSLASKCPSEKRSKTLPLLN OKLEMI* LSEEAITSKAKTG* KLGLLHQI
11269	25170	A	11366	48	373	EPWTRKEVLKISSSLKTHCYLSLCTLLMPTLECTAAIMAYSANLELPSTSCPTTCA S* VAGTTGACHRAPTVLKIPLRDRIFFF FFTNVTVPNCHTPADPAIFANAR

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11270	25171	A	11367	310	2	GLTCLNRENAYFFVIRQISMSCLEKEKP ARYSSPYAKSVTRGEKKRRQFFLSRAPPI PFLFFI*IV*AESRSVAQAGQWLHFS SLQTPTP*RTSDSPASAS
11271	25172	A	11368	303	50	MFALTNRGVGQSPVIFLGVFLSKMGFT CFKGFSRFKVLVFFLGVFSPFFFLRAR VLLCCPGWSPPTLGK*SSCLGLPQCVLIT
11272	25173	A	11369	109	419	QSNASLSHPTSPPSLGVADK*LFSTDRKD IGALYLLFGA*AAVLCTAISLFLDLDLWG QPCNLRLNDHIYTVITAIAPAFIPFIG IPTIIGGFGN*LVPLIIGA
11273	25174	A	11370	112	258	GGKFGKSNFTSAGQQRNTFFMGPPK*NS RAGV*QRGEGKNPGVTKLNRL
11274	25175	A	11371	823	1078	SGHFGMPRWADHLRSGVDQPGQHGHTL SLKIKQKLAGRGGRCL*SQLRLRLQEN CLSLGGRGCSEPRSHHCTPAWATQ*DSV S
11275	25176	A	11372	184	420	IKQCKNLFALVKELVOLLWKTWQVFLK KLNIELLCDPAILLLGIYPRELKMYVHT KTCT*MFIVELFKSKK*KQPTC
11276	25177	A	11373	234	44	LATTIDRLALSDSALPPLGIYAKCKKS VYQKDNCTYIFVAALFTVAQI*NQPKCP STRTRGS
11277	25178	A	11374	73	456	PPIGSPLVYFIPSPALSSPOAPRMGSHF CLIPASCHPEPLETDFLSLLPHTFCLAV FTKERFSPPPPSPYPRF*KFLRS*KFSF FLPPFLFPGGTVLCLSGWSAVAQSWLT AASTSLGSSDDPTSTS
11278	25179	A	11375	43	456	EFFHHVQDGLDLTST*SAHLGLLKCWD YRREPPRPASDGHY*TDATGSLPSSGTT *IRTKPSQAPASWGLWNLAHPPRSHPS CPMANLICSTLSSFDGGSPTGGPGWC LGLSGSPARAVFKDSSCSLPLATGI
11279	25180	A	11376	288	484	EWVLASVGGSGYGVCCPFLHCFTFFETE SRSAQDGVQ*CDLGGSSSLPPG
11280	25181	A	11377	129	1	NFNALNLI RAGAVAHAYNPSHLGGEDGR IA*GQEFETSNVTA
11281	25182	A	11378	307	1	DSSETPSLGLAKFWHRRRPPCLALFLTL NQKLEMLKLSBEGTSKATR*KAGFLCQ RVSDQVNAKEKFLKEIKRATLVKTQMMR HQNSFIADAERKVMAMMK
11282	25183	A	11379	200	397	CISLSHSHYKDLPEPTSGFIKKRLLGSH WLGAVAHACNPSILGGQRRIT*GQEFE TSLASNVKPC
11283	25184	A	11380	167	1	SNGLYSREARMVQHTHREPGVAHTCNP STLGGHGGRT*AEQLKTSIGNIVRCP
11284	25185	A	11382	12	395	AHSSFLSLDLSVFATCPHPRATFTQTHH FSTLLPSALYPK*DYFKKKKKKKKKKK KKKKKKKKKKKKSGGA
11285	25186	A	11383	160	2	TMEMMLDTK*I*EFLFPEFKMGLKAAET TQNIINTFGPGTANEQTQRWFNK
11286	25187	A	11384	274	389	GGAQWLTPVPIPALWETKAGGSLE*GOAQ WLTPVPIPALWETKAGGSLELKNRSLG NMVKPP
11287	25188	A	11385	389	37	WSYESSWSFIFKSLFSLFMISAYDM*YA SQILFTPKLYRTHPYPLLVFLILSLV LLETGSRFVSRLECGGGISAYGSPK*LG SGNPPAAASLSSRI PVVIGSCWSDLAFN

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11288	25189	A	11386	214	374	PEFEM KGGGRFXGSKFTSPGGGKNFFFGA/K* NSRAGV*KRREGKNPGVTQLEKGVG
11289	25190	A	11387	142	410	RFVCSSTIKVRLDLSDDSNPGRFLSTSN *KKKIKKKRGAFFKKKNFYRGGGGKY FFFGAPKINFLGRVFPQGGGNPGRSPF KGAWG
11290	25191	A	11388	144	1	CLSNEDSIKTPKGLGTARTCNPNSTWGG RNGWIT*GQEFKTS/LANTVK
11291	25192	A	11389	167	2	RN1SSHLLNMAITQTNNNWC*GYREY ITHIC*WFKMMQLLQKLVQKVRHT
11292	25193	A	11390	2	412	SDOVQDAGRLISSEASLGLPTATFLLC LPTGFALCTRVPGVFFLLRTSVILREGP TLVTSFYLNLYLKDVLISQSHWGLGLQP MNFGETQFSL*QKLV*KEKSMMPGMVAH ACNPNRLGGQGLIT*GQEFKTLILA
11293	25194	A	11391	1	206	TGRLAGHRVSSLPTRGGRAEAPLTSRTG RLNQDGLNLLTS*SARLGLPKCWEYRRQ PLRLAVISGFLT
11294	25195	A	11392	262	388	VSK*KKKKKKKKKKKKKKKKQ
11295	25196	A	11393	78	414	ICFFFLRAPPPPPPPPP*TKIFFPPFAL NBMNFFFWTFPPFLGGIFLPPPPFLEG GGGLASPPGGAFF
11296	25197	A	11394	238	11	IKWETAGRSSACL*V*LFERLRRENFLN PGVHG*DEI*HHCTPAWVTVRPLSKY INKNK*ARLAARCGGSL
11297	25198	A	11395	340	1	KHILVPPFINVSEIQRYSLV*HLLPVGV *NLFFLEFLSKKPVLCM*II CHEIISP PSKPKCKASHLSFV*KKNSNLWLGAVAH ACNPGTLGARGGRIT*GWEIETSLTNME K
11298	25199	A	11396	363	245	QMDLNRHLSKDDK*MANQCMNRLTSLA IRQMIKTIMI
11299	25200	A	11397	292	2	DPKKEAGRGGAQL*FOLLRRFKRTHLN PGG*GCSESRSHSPAGATK*NGVSKK K*Y*APKEERHPRFVLVEPRVPQVSPG SQTYRQDHSRVP
11300	25201	A	11398	121	321	KKLPTHSKSDVMFLKIETVSWLYCPG WRVMAHCDLLGGSSKPTAS*VAETS GTCHHARLIFL
11301	25202	A	11399	118	394	QALPQPIVLLILLQFFFFF*GTGFCFV AQIGGGGGHYG*LEPPIRGLKPSSRRTL RGWD*GGHNAQLILGFEKTKGSCFVV QAGLKALA
11302	25203	A	11400	273	379	AEPGVVAHSPNGTGLCGGGGTT*AQEF YTS/LGNM
11303	25204	A	11401	360	38	KIFGQARWLTPVIPAFNETVEDGSPVUG RSRPA*PS
11304	25205	A	11402	254	404	GFAGHDHFMITPSKSTEIGLGAVAHVCN PSTLGGRGWIT*RDLETSIA
11305	25206	A	11403	161	3	ILTFITQYIKINLRGAQWFTFHPALW KAK*SGLLLSRLSPAWVIGDGL
11306	25207	A	11404	1	170	MGVLLSLPDLGNGVISAHCNCHLL*FT FK*PSCLSLPSHNYKVPDLATFLY
11307	25208	A	11405	249	3	NAKSRQVTSIWFTVKEPHLYLNCPS Q*NEMAGGOSIFRKKHLLDPSLEHSGMT THCSLDLPSSDPPNSASSVGGTRH
11308	25209	A	11406	70	401	CGKHGWNLIHSLNHLKYLILLQMANL

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						FISQFLLTVCVSEPLLF*YCHQIIKVGRL HEVQMGRGTHKQEKMFPTMNDNDVCPG VPAHACNFTTVGG*GGWIT*GQEFNT
11309	25210	A	11407	257	389	GGSLQKILRLPLVAFLEFSFFFFSETES *SVVRLCNGMISAHC
11310	25211	A	11408	364	420	SCPFGRPRQADCLSSG*QWLTPVVPAL WEAKAGRLRLSLR
11311	25212	A	11409	312	413	TSQWPGVVAHACNFTLGGQGGWIT*G REFETS
11312	25213	A	11410	283	425	HEGKDYVHMLGAVARACPSILGGRGW IS*GQEFETSLANMVKCL
11313	25214	A	11411	389	3	CRIDGLFNLVFLRLVWVKF*VIFFLSY FSFLVILQPLTYMLNCTFF*QILNLP TLVLLTKILNTLLSTENYCHFSLLYCLE FWFHPIIKHKMYNLFLL*FILIFILRQS LARSRLKYSGTISIH
11314	25215	A	11412	267	3	QEPQEDTSELDELRLSLCKKRGGLKQG DTRDNLKRVVVEDTKGKAANWPGAVTH ACNPSTLGGGGWIT*GQEFETLTNRC PRV
11315	25216	A	11413	3	281	GAWSRIPGEGSLASQAQPPSLYLPVN PQ*ISLSARKKKKKKKKKKKKKKKKK KKKGGGVLKKIYFPFPRGKKKFFFWGP PKKTGGGGF
11316	25217	A	11414	275	2	KTAHFOLFNSDFKFGSRNPGQSWSPRA KQSFCTOALLKYFLK*MNEMKLNKRSRG AVARTCNPTLGGGGWIT*GQEFETSL ANNAKPR
11317	25218	A	11415	319	1	RNLGVQVYEVVLYVYKCSVSSNNMKM KRDLLVI*VPGIVIHLYRLIKENPELY ISLFYSMRSLKKLTYPGVAHACNPN TLGGRGWIVCSQEFETSLGM
11318	25219	A	11416	121	428	LSCDKWGNRDMTKMLSKELKKKKKKKK KKKKKKKKKKKKKKLGDDEEDKE*QSSW GGGALIKNLPSPRAAGFFLLSLKRYK KLGAAYVILIGKKTILWL
11319	25220	A	11417	79	253	KIFNFQSNMLNNNSHTTRINNYFPGR RNLTVIIPFLWEAKAGRSLEVR*RFSC P
11320	25221	A	11418	180	4	EVGFMKPGLCGVFLPAGHSVALTIVQW CDLGSQHPHPLGSRDPP*ALQIVGNTR RVP
11321	25222	A	11419	154	3	STLKDKENOKLSIQPTMAHVCNPTSLG GRGGWIT*VOEFEISLNNMVKP
11322	25223	A	11420	436	478	ATPLPH*RKTIHAALFFFPFKGSFVLS PRLECS*KIWAHCSLPPNISNPASS QEGGTT
11323	25224	A	11421	143	398	AAGFWFVLTIRFLRQLRSLPRDCCFFA KSASQPRPP*FKRVCLSLPLKSWDYRP DLLCAAGLVVWVLSVSRHLHNEKNQPP P
11324	25225	A	11422	1	138	MVFHRVQDGLLELLTS*SAHLGLPCWD YRHEPPRPAHSYFLLHK
11325	25226	A	11423	2	390	LELPILLNLTLLFLFLILYIYLVFSPN AFRLFITIVLESFIFLLVSPKPKYS LILSNAPVLCMISPPPLFSLSTTRI NKKLDFWLGAVAHAYNPSTLGSQGGWII *GQEFETSLTNMAKPHL

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11326	25227	A	11424	267	414	VFGITFCIKNFPGWVAHACSPSTLGG*GGRIT*ARQFETSLGNMVKPC
11327	25228	A	11425	189	73	HQDGLDLLTS*STRGLPKCNDYRHKFP RSARPNWVAP
11328	25229	A	11426	318	33	KKTISSSHARGKLGSKFAAPFFFF*TGSCSLAQAGVKWCSSSSMQPRPPGLK*F SASGSAGITGMSHTRPITAGFLAKLKK KSNSTGYGGAHV
11329	25230	A	11427	291	393	DRVSLCLPGNSAVLFS*LTAQISWAQV IFLPQP
11330	25231	A	11428	51	399	KRVARQNPNNGQGGWCSCSPIYQGSR AQGENIYKLLGSGEWPGQLIIDVEREQLEDWRQGDGRGMWMTKARVHKGPGLVAG TCNPTSLGGRGRWIT*GQEFENSLANMV KPCF
11331	25232	A	11429	242	420	VKKKKRGRFRFGSKFTSACLQGISFFKG APKLNSRAGF*QRWEGNGLVPGQFNRF GAHP
11332	25233	A	11430	77	405	TKRGDSSFFLYRIWIIDSVMKNWQSKAA ARAAFFFFLRGTLFLPRLKKGKVGASVI *NFCLRGSGWSPASPSKEVMEGACHSN GLFFVFLFKRRFLVQCKEFTKTRAN
11333	25234	A	11431	121	439	LPLTSSGPEPLAISFKPTSPGLSGW IYTHGPSPEHSHLMPAPVNNKACRF FKT*KKKKKKKKKKKKKKKKGGPL KKKKIFAPPGGEIFFFFWGPKK
11334	25235	A	11432	109	283	LTPWNLDSRCEIKNGKQCEHNLNLGGG GCSEPKSHHCTPAREKRNQSVSK*INK IK
11335	25236	A	11433	296	1	FLKKFSKGFSLPHLPONLNFPPFK*K CPRAKKDIPPSF*KISSLFGE*GFTG SRPPSLNLENPPKRIFFFFFLDRVSHC RPGWSAMASSCPRV
11336	25237	A	11434	385	418	QSEFLSQKQKTK*E*SWLGAVAHACNPS TSGGRGGWIT*GWEFENSLTNMVKPCL
11337	25238	A	11435	3	405	LLHQGRMLMGQWNGRHTKLLMRENVGK FPAEPSCSALGVWLQALACYPLVLRQ* ANHWKKKKKKKKKKKKKKKKKSGG G
11338	25239	A	11436	221	3	KHEFQTIQMESMK*NTS1K1CIYAS*IQ DCLRYQWQRPAAVAQAITEHFGRRPRQAD HLRSGVSDQPGQHGT
11339	25240	A	11437	288	366	KMFFSWA*WLMPIIPELWEAKAGGSL
11340	25241	A	11438	160	370	LWYHFPVRDGLTLTVYQLKAIKRLTL LKSRSGAVAHCTNLNLGGRGGWIT*GR EFETSLANMEKPHL
11341	25242	A	11439	230	404	MQHGQVGVIYSGGGWRPVDKKNSQLGTV AHTCNLITLGGRGWIT*GQBFKTSLTN MV
11342	25243	A	11440	302	54	LSGWFLTPFPKGGGFP*NGGAPGFF PPPFPNPPRGLGGPKKKKPPPPG EGKLVFLKAGAPPPFFFFFPPFFFL
11343	25244	A	11441	271	416	KRTLSTELQYNNCLLTKSKITFK*KKKK KKKKKKKKKKKKKKKKPPSLP
11344	25245	A	11442	254	392	SVGTGWTWSSCCYKTKCTKQKLARH GQTCL*SQLRLRLRQENS
11345	25246	A	11443	390	150	LLKNQKTLGGFARNFFPLGGPNNGVPKA GNGWPGPPGGTPTFFFNKQITPPGGGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11346	25247	A	11444	122	1	P*FPPLRGGGGPNFLYPGGQGH
11347	25248	A	11445	272	403	PAPLFFFFFFETQS CSVA*AGVQWRNLG SLQPPDDGTGL
11348	25249	A	11446	70	397	RPKVDKTTKMGNRQSRKAENSKNQSAASP KPDHNSSPAME*SWM
11349	25250	A	11447	3	401	LCHCAPAWATERDPVLGEKKRRTMMSYCH PPMRMVEKKIVGDIKC*GYGETGFLTH C*WECRMVQIL*NIIV*QCLKNLAVHSPY ELAIVLIGIYPREMKYIFTKKTSN
11350	25251	A	11448	333	1	HASAHASAHASAYRLECAVPKSSFLYPS SFLLVSNFPLNILDTTIGPKATETLPI KHVMHDIYSMQLSKKTFYNYFFLLSLNV FYFVLSCCKRRKRSLQGMVSHICNPSTL GGRGRWIT*GOEFETSLANMA
11351	25252	A	11449	104	402	KSGCTPKPGQVFLPFLOKRTAKIGSPKPV SPPRGKGQFPFQGLRGFY*FLPPPQGV EIFFFFF*DSSHSVTLSPREYSGMNTA HCSLHLPSSNPASDSHIASTGTCHH
11352	25253	A	11450	198	2	VVCRFLGGVSLGYGMVMDFFKEAVCL FSELKHCAGRITTAI FRAVRQCLSLKNF LLPFFQLCPAHRGGVL*RQ*ALLSCGGL HPVRAASRPLCLPTQA
11353	25254	A	11451	171	3	KYKFMAGLGGSC*SHHFAFRPOODGLS PGV*NQPGQHGTFPSLQKKVSWANWHAS VEAAGEQP
11354	25255	A	11452	177	461	TPPPRATSLFFFF*TESHSVQECNGTI SAHCNLCPLPGSSDSPASASRVAGITGA
11355	25256	A	11453	247	3	PMTGGKYISNSTCSKPNLSPLPLKTK TKNMEHFRLTRGDCLSPGV*DPGQGRG KTLQLQKISQALWDVTAAHVVVPLPTR ERRRSLSPPTG
11356	25257	A	11454	328	57	EGECOGIESR*ILHLKGRICWHINYLIKI TKIKN*VILKMYQKLRPGAVAHAYNP SALGG*GGRIARAQELTRGLNIVR
11357	25258	A	11455	70	435	EVHSNICATLSTHQMKITLGTGRHQHIS *GPF*EGEVLTLSTKLECSGVIMAHCNL NIGGSSDPLALVSGVAETRGASVYLLAI CPKVNK
11358	25259	A	11456	112	401	ATRAKLHLKKKGGRKKEFFHHQCGQPT PALVPQPRTHPIFKVSIPLSKNREQL PTVTQTSLLPLNSHWGQVA*AGVQWRN LRFSCSLSPSSWDY
11359	25260	A	11457	198	3	KCWDYRREPCFAENICIF*LTFFPLGK KLNQSGFFFFFLKGSVLVPLRLKGGGAF LFN*NLTLQGNKNSPASPS*RAETLGLG PHAKLWFVFLKK
11360	25261	A	11458	179	1	EKTSVKQSGDSNKKANLEMKTNKKSLKR *GVVAHACNPSTLGGRGWIS*GREFT SWTNMEKP
11361	25262	A	11459	210	5	FFHYMNHIVCEYTTITLSVINNSGGPRA AHAYNPSTSEDRTWP*AEQFTSLANMV KPH
11362	25263	A	11460	139	2	RLIHFFKNNLFSGGGSTA*GQBEFELI DNTVRPHFLKK*KISQVWCMVVVSATQ EVEVGNGLSPGV
11363	25264	A	11461	388	272	RTIALSKLFFFFFKOESHFFLPLMLECSG VISAHCNL*LLGSSDLIS
						S*KKKKRGRFGKSMFLSPAQGNPFPM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GPLKSI SLAVV*QRREGKNLGAPHITRLGAHPLFAGWHKTOGAEF
11364	25265	A	11462	2	387	CVVKSNNKKAPPVCAALRFRWKDDMDDEM APGKHGGLTSKVQSGGLMGRYTGPLTK TENSILLKNPYFEAGHSGSRL*HQHLGR PRMEDYLRPGGQGCSEL*SSHCTFT*VT EGDPVSKLKRITIFGG
11365	25266	A	11463	325	398	SLPTAVACAPRPS*GSGIPELKTNLAG VILEDYLDIKNGFAKVGVLSCILATGST LFLGKVGPPVHL SVMIAALGRVRTTIT GEPENKSKQNEK
11366	25267	A	11464	174	2	YLETLFFFTGGRSTQAGVQNSHFGSL QTPPPCPSNSPASA*VAHASADAWADA W
11367	25268	A	11465	103	411	TDVELLLMDE*KKVLELETTFGEDDVN IVKMTTKDPGYSINLVKAVSEFPIRHS YFERGSAVGKVLSHSIVC*GEIPRIKHS PLMQQISLLTFLTFYFSE
11368	25269	A	11466	291	404	SOEGVKIKRQGTVAHTCDSTLGG*GGR IT*GQEFKTS
11369	25270	A	11467	64	236	THASGLDLTS*SSCLGLPKCWDRHEP PRPARFSSFYSGSLNLYLAKI IKRDAFC I
11370	25271	A	11468	278	416	NPQISCLQKHVGAHAVHCINPSTSGG*G GRIT*GQELKTILNMVK
11371	25272	A	11469	178	325	RPEVKKQASCRDPHVRVGLLPVCSDE RVPQKKKKKKKKKKKKKKKKKKKK KKASSGGARF*KKKKKKKKKKKKKKKK
11372	25273	A	11470	264	60	DINHQSWSLGRWTPLSWSISQREDRR GFSASTIYIYIYIYIYIYIYIYIYIYIHT YT*SYHFNQNT
11373	25274	A	11471	95	399	DFPHLLFLPLSQFCTACCPVPENRCPH YFPLIFSALCWEMNSRISHSNTARVBQC CKVFKILQMKSVLGQVQWLTFTVIPALWE AEAS*LPETRSRNQPGG
11374	25275	A	11472	139	2	NHVSTKLSLHVAHHCINPSTAGGQGG IT*GQEFKTSLATWAKF
11375	25276	A	11473	179	3	RAKMNPFQVC*GFLPVFPKILFIWPLRK GVFPFPPNFFFLRVSLCHPHWSAVARS RL
11376	25277	A	11474	282	12	KYIRNE*IVLPIYVFECNRNYSWCPCGWS *TPELKRSSCLCPSCWDYRHEPLCPAE MNKLDRLNKMDDTKWQIQKQGNHRTORQ DNKII
11377	25278	A	11475	145	3	VMQLRDTDPQGAHVAHCNPSTLRC*GG WIT*GREFTKGLNNMEQPC
11378	25279	A	11476	61	397	PQTPLRKQSYHVSIPFSDWSYSWIYHRL VNPGRETDWATYSGGNQLQENKLNTP TDSTLWVSLCCPRLCSEAPADCSLNL PG*SDPPTSTSHVAETTGACHYAQLIFG
11379	25280	A	11477	156	3	FIFLKSSQNSY*KCNPGAVAHACNLD LGG*GGWIT*GHRPKPTRRPRV
11380	25281	A	11478	224	383	CWVCLIHRAFLAPRPLGCO*QKKKKKK KNKKKKKKKKKIDS RGGG
11381	25282	A	11479	339	58	NFKNKLFCASGYLDSKDSQHYIIFIR WSLALLPRLRWEDCLNPGGGGSEPRS Y HRTPAWVIE*DPVSKK*IK*NKIK*KQQ DWLRHDKTF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11382	25283	A	11480	244	407	SFGKKIGFLFGFKKFNNGSYGNYYKINR RFFPFLGEGFSPIVVF*NLETRITGGG LLETTTKTTFNMLGRKLGSFLGPRSLTAA PTGTTIKLITGGFFQFWGKVFPRMYIFW KDEWKKGF
11383	25284	A	11482	308	30	SPQKNFPTVSGFKNLSASFGQKAKPRF FLNQFLPLGIMGGGRQFPLLRVRPNC FNPFGKRCN*QKLGPCPPGGPKETVSKK KKRERQQ
11384	25285	A	11483	226	407	NHWKK*FWPKVANTYNLSALGGQGGRI T*GQEFETSPSMRPHAS
11385	25286	A	11484	10	411	QPTIYFLSLRISLFWFHINGITQYVAI CVLVLVSCNHSRFLCAACDDDFIVFLW LNNIPLCGYNILCHSICFNWRTITGLFW LLAII IKL*TFVKKKKKKKKKKKKKK KR
11386	25287	A	11485	184	1	TDEELLPMDEQKKWFLEKKPTSGEDAVN IFEMTRKDIECYVH*VDKAAAMYERIDS NFLSN
11387	25288	A	11486	435	222	AKNLNRHFSKKVI*MASRRHKRCSISLT IRET*IKSIIR*HVIPGQMTFIOKTDGM FGSVSPLKSHHLKL
11388	25289	A	11487	317	408	FRPGTVAHACNPSLTGGQGWIT*GKEF KT
11389	25290	A	11488	340	469	GKGDTKCHLWLTGVVHACDNTLGGQGR RIA*GQEFKTSLSNM
11390	25291	A	11489	38	389	KRPTSLKKSNFCSLQGGFFFGLSQKPGK SNRS PGKKNPFSSGGKAP*KG*KI FL SPGLGSSPQKPHLLGLGKRYLTLEKG GCRDPK*CPCFPPWAGEGNPFSSKKKKQK FPFFG
11391	25292	A	11490	235	2	FVLNWLMPKLHIFVTEFRRLFAFPEFL* FLCPVLSTFVLLTSGSHVTVLAECSGA ISVHCSNLPGSSDDPTSVLY
11392	25293	A	11491	25	417	GTLCIRIGFTNTSHCWILKENSLFFFF WETKYPFAPQADGRGNLQ*WNPSPG* RGS PGPTSRRKRGGGGGPGVPIPFKLR KNGVPGGLKGPKSLAPGIGPGPKDR GLRGGPPAPGLLKKNPKVW
11393	25294	A	11492	234	438	MVVIIAQQCDCTECHY*LKMAKXINFM LFIYHTHTHTHTHTHTHTTRERGPSYI YGVVSFKLTHL
11394	25295	A	11493	344	477	CFTMFTS*IKT*KFNISQVLAHTCNPSI LGGQGGRT*GQEFKT
11395	25296	A	11494	35	482	GIPGFHHVGQNGDLTLTS*STHLGLPKC WHYRPGPPRPAISITPST*AYLLGNQKI GVTHFLAILALFSSGTKAMISPKYVCII FYLLVEHLGCFYFLAINTATCVCVYKL FDITYMQVESHA THEFISYVFFKILCSL SIRLYAVLL
11396	25297	A	11495	307	484	LSPSERHELKCVLWFGAVAHAYNQSTVG GRGRQIT*GPEF
11397	25298	A	11496	487	349	FLIKTEFHPHQGGGDFDLTL*FARLGLP KGWDYKGEPLRLAFWHPF
11398	25299	A	11497	224	417	ASGASALKVELCSFSRYKTIYPRKRRYA RTDGKVF*FLSAKCEITFLSFFFFFL EVLFCSPG
11399	25300	A	11498	17	411	KRLVFGGRGRTDRFISQYV*AEYVSINL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						LIPLTKKKKKKKKKKKKKGGALKKKP WGGQNTKGKKKNFFFLRGGKKFPGDF KKKNFFWGGENWGKPPPKKTPWGKKKI FKGKGKGTTPPYFCLKKMG
11400	25301	A	11499	117	370	VSESADLAWSLGICFIEFFPSDADVAGL ETAFPLGGWTGSCSVQPGV*WCHSSSL QPRPSGPRQSSCLSLPSSWDYKMPCL
11401	25302	A	11500	244	1	EELFECYSCSPTFSSDFLTPLLLIT* LLPLTIMASQRHLSSSEPLSRKKLYLSL ISLQISLITITFATTELIIFYIFET
11402	25303	A	11501	130	55	RFVCSSTTKVLRDLSSDRENPGRFLSTN SSLKKKKKKGRPF*RDNSAIF
11403	25304	A	11502	186	421	SFKLKIAGITGVHHTCWLVLILNLVL K*ITFALKIMPMKSKSIDQAGGLMEVI PALWEADAGSLQPSLSLGNK
11404	25305	A	11503	1	213	GELLPLYIFA*NLPLSKLLFVLVCLC ELQPNRFIMVLCIIILVGGLFFLCF L*PCDFPPFFWRG
11405	25306	A	11504	82	6	AGWQNPWSRLRL*LPFTQVLMIFPPF YHQNFFP*KGFFFLGGLSHFFPPNKG FFFNYPQGFPSPLKKKFFFSPIFL APPGIFL*GPFRFFPPPPFF*EGVSL CHLWNSAVAILAPPAGFTPSCLSLPS S
11406	25307	A	11505	245	440	WAPCIG*QLLKDPQVLFAGYKVPHPLEH KIIIRVQTTDYSPQEAFTNAITDLISE LSLLEERFR
11407	25308	A	11506	256	370	GRKM*GHHVGQAGLKLSTSDPPALASR SAGITGVNRHAPRLNVTLYTKGTIIL YHNQYNO
11408	25309	A	11507	1	149	GCMWRTVLFAFQHKFVNFLKTLGDFGQ VQWLMRVIPALWEAEAGLPEARWRFP *PRTVLFAFQHKFVNFLKTLGDFGQVQW LMRVIPALWEAEAGLPE
11409	25310	A	11508	316	420	YTYIYEPG*VQWLTPVIALWEAKAGGS LEVRSLR
11410	25311	A	11509	136	2	LDNRLWPGAVAHACNSRTLGDQSGWIT* GQFFETSLANMKPHL
11411	25312	A	11510	167	420	PTPRSGHTALQPPHHTHTHTHTHTHR HTHTHTHTTRACI*QVRRLSPKKK PLFCLSVSQIYVGRCLLKRLLFPLRH
11412	25313	A	11511	124	415	IYISVANTILYLAHVLASIFFFKK EVLFLPPRRGGGA*VN*NLCEWG*GN FPA*PSLKKGITGALTPLGFLVFLKKT GFRHVQGANLDFL
11413	25314	A	11512	121	1	PPVKFWAPFFFF*IGSSPVAQGVQWN NLSSLOSPSCL
11414	25315	A	11513	245	13	VLFILSGFFGPDINYPSPPLQFFPAGS NHPSTLYLHEFCFYFLPIFYF*DRV SLCRPGWSAVARSOLLVPSDS
11415	25316	A	11514	434	2	RPPFFPWWGSPPPFFFFFGGEGIWGER KGASSPPVVSRIILRGGPFGGGAPPT PLKKPPLFFLAPFLGVFRFFSPFTV PFLPFFVCCKKREALLGVKGRPPFFFR SFLFFSGD*VSLCRPGWSAVARSOLTE SLAS
11416	25317	A	11515	247	390	QGLRIYSQDFFFLFKSRFVAQAGEQG GNLG*LEPPPPS*SDFMASD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
11417	25318	A	11516	269	368	FFFERESC SVTRAGVQWHRLLSSL*FLPPAFRRP
11418	25319	A	11517	256	404	NYLKIFFLRI*KKGNQLGVVAHCNLR*LGGRGGWITRGQ*FKTSKKMVK
11419	25320	A	11518	211	404	YLCFTRCSVHSHLK*VELHKCVI*MYRPH*TL*CMQVHTHTHTHTHAHTHTHTP LSGGGDCI
11420	25321	A	11519	41	232	ESVEPRRRVRPRAGITPLHCSLGDRARP CL*SQLKRLRHENLNPGGAGCRPERS HHCTAANAETEODPV*KKKSKLNPKTIRA INLKMLGALISFHLFLWGIWF
11421	25322	A	11520	146	2	LIDQGGVNLQPLRMESCGAITAHCCLELP GSSDPLTSAS*VAGRPPTRP
11422	25323	A	11521	297	437	TDHFVNRILSSCGGTFRDTWLGUVVPHAY NPSTLGGRRARIT*AOEFE
11423	25324	A	11522	244	460	NCATITTSNRIFLQLOKHKCTKWLSLSEI SWQSLISF**ICPVFFETINLAVSLRLE CSGAILAHNCNLCILSS
11424	25325	A	11523	222	1	ESKDLDFRCQLAPRNSSCFVLFPCVFPF LEIGSCSVAQAGAQWNCNHSLOPPPIA SAS*VAGTINVRHYVQLF
11425	25326	A	11524	308	424	ITFLTMFKIYLGDPDAIPLLGIYPKDY* SCCYKDTCTRM
11426	25327	A	11525	98	2	NIGGRPGVAHAHYNPSTLGGGGQIT*G QEFTE
11427	25328	A	11526	113	399	LDRFLTLLPRLREEDCLSPGGQGCSEF* SHRCVPANATE*DLLSKKKKGVLKPF LPPPSVGKPPPSPPERLFFILRPPLGG VFPPPSKKIIS
11428	25329	A	11527	280	3	PKYCOI*VLQCTIAOLFKLISYNTYTHTH THSLSLSLSPPPKVNKMLMSSEFTLTF KMYTFPGPRVHTCNPSTLGG*GGWIT* GQEFETHL
11429	25330	A	11528	284	2	FWGPKKNFSFPPPGKLGSEKRAPPPF FFFETKSCSVTQAGVWRWCDLSLQPLA WATERD*LNK*IKGMSKKLHT*VCMFRT RGRTRGRTRG
11430	25331	A	11529	134	2	DTLLPRLKNCNTHAHCSLKLPGSGDPP ASAS* IAGTGMCSHA
11431	25332	A	11530	104	1	GRGFFFFFFFFFF*EVESCSVAQGVQWL NLGSIQ
11432	25333	A	11531	157	373	CVFYTSTSLQRCYIFIGNTRSVFRCHE IYT*KNRFWASTVAHTCNFSTLGSRGKW II*G*EFMTSLANVR
11433	25334	A	11532	237	389	ICKCSKTGFG*DFQEFETSLGNVVRPCF YRKIKASQV*WHADIVLATWRAE
11434	25335	A	11533	259	122	HISPSVQRHFFLPYF*TKPHLVAQAGVQ WCNLSSLSQSPPPGPKRF
11435	25336	A	11534	164	1	SSVVSQALITLLFLKTCFWGAVAHACN PCTLGGRGERIT*QKFKETSLASINL
11436	25337	A	11535	106	310	GGDKGTVDWTDLHFFDQGRKLDHKNHDM TIHAELPHELSA*CYAFKKECISGGGSI *AEKEYIQFDG
11437	25338	A	11536	167	378	ASFFGTITTYRTLLVYVMPEKFIYIYH MYTF*RGQLVLSKLECSNVIIGHCNLKH LGSSNLPTSASRVA
11438	25339	A	11537	101	396	VNNLKQRIGLSKRGKKLLVLSIGGGG FPGAGWIKKGKPPPGFPGGLP*KRGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						GKKGNFNMKGFPNPKTLVFNQNFQGGGA KPGTGPVGRPLGLD
11439	25340	A	11538	18	361	QIGPRLY* DQNGETPSLLKIQKKKIPGF GGGGLKSQLGLGWNH* NPGGGGCRD F* PQLPWPWTNQNFVKKEGGREKKG EGRKEGGGKKKTLPGIGALNLGGLLT SP
11440	25341	A	11539	134	365	EGFQNKITGGGGPRPKTKTNFVKF* KY LKICGFWPKRPPPPFFLETRSLPFI FFLGGFF* ETKRSVTRLECSGVILAH NPRLVGSSHY
11441	25342	A	11540	2	318	TTERTYRITFGPKSETEVNDLPGAPSEP VALRLARSFILK* SFLVDFDFFLP F* KTGSCLS* PRLECRGEITVHCSERLP S* SHPTSSASOSSGGGFFLG
11442	25343	A	11541	294	409	GTISFFRTCLRWNAHTNPSTLGGGG * II* GQEFQT
11443	25344	A	11542	1	123	GKQGEPAISYDHATVLTIS* SAHLGLP KCWDYRSDPPCLA
11444	25345	A	11543	69	350	VGAKHWIMDTKIEADPGNYSGERGK RPRAEKLPCVYALYLGNGIICNPKPPC CWKGHDFIYIVCGHLYIHIYICTHIYI YFF* DGGLLC
11445	25346	A	11544	103	340	LFCAPFLSPSKLDYHLSFYV* TFLKLD LISLAPFLFWAEGSCSVTQAGVQGPS TNCNLCLPGSNPNSTASQAAGT
11446	25347	A	11545	256	354	PYPFGKPKRGDHWGLGV* NQPGQGETP SLLKI
11447	25348	A	11546	196	335	EIVARLKRSPVGRQAQWLPVLPALWAK ESGSPEVRSS* VKKICTRPGTVAHACNP STLBGGQKNIT* GQEFKTSIANMVK
11448	25349	A	11547	202	377	TIHTKGVWGNFLLVVFYONFFKTF* D KILGWARWMPPLIPAFWSEMGGLLEPK SL
11449	25350	A	11548	396	26	PPRIKKEKRSFNGAFYPPFCWNF* KKN LSLAKRPPRDSVFFVSW* GSYLPTTFL QLLRWVYLSHIANVFKHLCEPHKNFTL QHSIPYLYIIEIVSYFINRNTIYKIN MDFSIVGFVL
11450	25351	A	11549	232	371	REVPPENTIKGVQWLTITIPALWEVKA GGSLARS* KYQNWPGAVAHANPSTL GGQGGRIA* GQKFEISPNMAKE
11451	25352	A	11550	174	381	NRDEGPRYADRAEVQRLLTGTLHCGCL QRPL* RSSCTLPQGWYRH* SPSHVA GTTGISHTRLIKKAFPSOTGVSSC
11452	25353	A	11551	262	359	DYSNLGLVWMLTVPVLPALWEAKGRSE VRSS* PALWEAKGRSEVRSS
11453	25354	A	11552	70	380	LHKCSPIYINHCNNPIYGLISLYPKQLF SYENFKDFCNKI* P* IPNFELKTSTP* L EKL* NWAMARHGGSL* SQHFGRRPRAD HMRSGVPGQPGRGESPT
11454	25355	A	11553	319	56	TFLLGPPGGF* KIPFSVGPPLIFLPLK FIGEQKNAPGKNPFFGLFSLFFPFL TLSSALECSGAMSAHDNLCLPGSSNSPA SAF
11455	25356	A	11554	230	399	MMGEIINQANISVCQITIRLRHRESHLI PGGRGYSELRSYHCTSTWVTE* DSCLKK F* IFWRDGVSPCCPGWSQILRQGSTCL
11456	25357	A	11555	376	396	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GLPKCWYRFPHPATAACPVFYHYLL KIWRYSFELSCLWNLVWGLAPG
11457	25358	A	11556	176	384	KAWBVRNNYR*NFFFCCCLNNFRKRLK CFRCGADKFGKTFGSCILQYALKPTNWR EQWLTVNPTNFGK
11458	25359	A	11557	295	391	PYKLLITHHTHTHTHTSRTHTI*HTTLS LYTF
11459	25360	A	11558	1210	1753	NTWCNERLAVAFSGFNKNRSLRGMALWL TPIILALWEAEAGGPLEQPFETCLGNM VKHCLYKNLKNVSGV*DLPGHGETLSL QKPKKCVRRGGTCL*SQRLRLSWEDCL SQGGGQCSEP*SHQCFAWVTELDPSX KTKTKKFFGLPSPFLVFCFLTHIYVKNK YAFVLAEEASGKTSKLTMTVTSRNLGK TKKFFGL
11460	25361	A	11559	172	3	KCKFFFFPFSHQIKIFGGAGEMPFFFFF FFEKESRFVA*AGVQWRNLSLHPPHP
11461	25362	A	11560	143	1	GGAQWFMFVTPVLWEAKAG*SEARSSR PVCATATPPQLIPK*YGL
11462	25363	A	11561	84	2	KPLDITGGGGGCT*GQEFETSLANMV
11463	25364	A	11562	12	387	QGILLPCFMSSEERGRISYNTSFYFF FGKGGQINPQGGGQATEPLRLREPSPLG TLQGGPNGGPPPPGGQNFYFKKGGYPG GAGGVLPNGPKGNT*PPGPKARKKRGGP DPGGQKFL*NPKG
11464	25365	A	11563	230	375	RAKGKLLSESLISQSFKKPSVITCNFS TLGG*GRWIT*GLETTSLA
11465	25366	A	11564	287	55	PPDGRVQWLTPVVPGLWEAKEGGSLSR SS*SQINPVGVSVPYSLRVLR
11466	25367	A	11565	115	411	PPPPFFFLGENSEFSSFRGGPRGGGHIFW NEPPPG*GVFPPPPPGGGNKGAPPFG FFFFFP*KTGFFELGGPPPLFGPPF FPPPKGYNERDPP
11467	25368	A	11566	139	356	CLLIGWYNTGICTGGSTAKIGTFFFLRG SSVAQAGVKCSGMILCYRNLRLPGSSN LPDSAS*VAGTTATYP
11468	25369	A	11567	101	410	PLFFFFFLLKKIFFPPRGGGGGGN*K KQTPPLGGKNFPPPPKRGGGGTPPP PLLFLVP*GEGGFGGAGGKXPKGNP PPPPKGGEMGRGPPRGG
11469	25370	A	11568	417	56	EDCLRTGVRDLLPNPHNLQAGRGAR L*SQLEHNLSPGRGYSEL*SCHCSPA WATE*AYRKQNTKQNYRSSALLHLYTP MATAWIKIAFLRAGDIFLSVLSFLPNY PLFSHPQ
11470	25371	A	11569	301	443	EDTTFVCFEVECSVAQATDPSASAS*I AGIIGVCHHARLIFVPLVE
11471	25372	A	11570	44	408	RGRGHGPHSPWRRRRRLRVVEGRKATES KRRAYKYPLPALLCSHQNKNEWLDQSI KIPTGL*LK*PSFIFIFIYLFWKGLS LAPMLECRGAVLAH*HLRLPRSSLSHAS ASQAVTTG
11472	25373	A	11571	201	1	AERPVTPGPVYAEFGLQGRG*KNMFKN MQHPRWADHLRSGVQDQPGQYGETPVST KNTKITQAQCI
11473	25374	A	11572	343	1	FGLLFAFTLEYKLYESINHAHCCVCRF SSGTLHVVCNRRHPNKLDEWNSGGGGRQ DLTLTPRLGCSGVIMAHCNLVLLGLSNP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VSAS*VAGTIGAHSHAWIDKLFVVKTPGLY
11474	25375	A	11573	209	3	VGPPPKSLPGGPPFFFCPKCFPLRLKKKKKKKPLGVAYTCNLNTSGVRGKKIT*AQEFKKSPSNIVKPPWY
11475	25376	A	11574	312	430	QRYARPGPVVHVCYNSSTVGGRSRGIV*AQEFATSLCNMT
11476	25377	A	11575	125	3	NSLGPVVHACNPRSLGG*GGRTISAQEFETSLGKIRRLPY
11477	25378	A	11576	190	362	CVNNYID*EKKKKKKKKRERKKKKKKKKKKKKKK*GGGAPKKKKKFTPGGGKRNFFFL
11478	25379	A	11577	231	340	KRITRVNQDGLDLTTS*SAPLGLPECWDYTMKPCLY
11479	25380	A	11578	60	3	RMQVSV*IFPMISLQAYLIYSSSSVAAGAOSGIEECKYQFAWRWNCPRRLAQ
11480	25381	A	11579	285	406	KKGNWFGAMARTCNFSTLGRGGGWIA*GOEFETNVGDMAK
11481	25382	A	11580	121	1	NLNCPGPVVAHASNPTITGG*CRPIV*GQEFYRIANVVKP
11482	25383	A	11581	199	384	KKTFFGGYFFCPKEAGAPPL*TFPC*TIPLFFSPAPKPKRALKFFLKPKKGGFQIPFFP*DGVSCHDGHSTVARSCHY
11483	25384	A	11582	677	934	YGSRHCTCFLOATSEILFLKNPARHGGSQVQDQPOQSKTLTLRKKS*ARHNGSLSSQNFGLRQEGHLSPG*GCSEL*PRHC
11484	25385	A	11583	104	2	KRIGGGPPLFFFETESCSVARLE*SGAISAHCN
11485	25386	A	11584	349	9	GGRSLSGPRKTRVQWGIPEFPLHLGGKAKPCFPKKKKKKVGLNKHYSKEDIQMVNYMKKCSLTPRERKIKTIMRYHPSIRMAIRKIKDPKQ*GCIKGGSVVRPMYLL
11486	25387	A	11585	163	1	TAVRIKHSYTLTFLRHSRYLINVTWCWPGVVAHACNPSTLGGGRWIT*GQEF
11487	25388	A	11586	192	41	SKSKYHIYGDALQKSTVYKWTIFHEKKG*DDVKDKAHSITLSMSICEEKE
11488	25389	A	11587	30	374	GWSFEDLFPGLSPFALKGFSGEGG*PFLPFQKKRGGGGGGSPFPVLKRVRENRLYPGGGGFR*PKQGPCPSAWGAEPDLSLKKKGFGQKKKKKKVLEKET
11489	25390	A	11588	66	245	SLCFVFFVFF*TESCSVTQGV*WYNLGSLOPPPPKKKKNIKKQKKRINWGRGPKRRL
11490	25391	A	11589	243	402	FLHLKKKKKKKKKKKKKKKK*KDAG
11491	25392	A	11590	205	3	IRLLGIIKNPTFAHQ*KK*KTGEPLW*VVM*FFERLHTELSYDPAIPLLCINSTEVWLAGPPRRFR
11492	25393	A	11591	404	152	WGPHVSDGLDLTTS*STLLSLPKCWD*CWDFTRPLCPGHFAISFNKVLNITTYVLYFLYLIILHCYICPKLLELFFFYIY
11493	25394	A	11592	311	386	TVVYPLAGNLAHAGA*AGIVETALSTLIRARLGQPGALLGDQIYVNVITAHAVIIFFTAIPIIIGGPGN*LVPLIIGAPDIAFPRINNISF*LLPFSFLLLLASSIVEAGAGTG*TVVYPLAGNLAHAGASVLTITFFLH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11494	25395	A	11593	39	397	EGCPLFFVFFVFFVFFGGKKIFFPPPRG GGGAPHKIPGPPPPGPNFFPPPPPLRG GKRGGPPPPGPPFFV*KGGVSLFPRGG VFVFSWRGGRGPPPPPPQKKIFLKG PPFYKKK
11495	25396	A	11594	243	46	GLLSCCFHDSLSLSLNSL*CD*VWISLCLS YLVSIELLQCCGLIFFKRRSFWLLLLK MYLQPLSFLS
11496	25397	A	11595	327	2	FRATLRIGQFLMLWPRPYVMWSQPCSLCF CHTAKTVPTSRPLLLGFFSLPGIAHISM WLVLSTYGLGESSKVTLLWPGVVAHVCMPS TLGG*GGWIT*GWFKTSLANMVK
11497	25398	A	11596	292	384	LGTVAHTCNFSTLGGQGWIT*IQEPET SLR
11498	25399	A	11598	125	2	PFQGRSGGTRGPGFAVAHTYNPSTLEG* GGRIT*GQEFETS
11499	25400	A	11599	302	408	TGGMLGVVAHACNPSILGGRGRIIT*QG ELETRLA
11500	25401	A	11600	409	131	GRSGGVKPSGVLPKPPGPGTIPFFKPK KITRGGGPPPLPPLQVRPENCLSLGS GGCH*TKLPCCSTWGAQ*KLVSKKKCK EGGGRIYS
11501	25402	A	11601	196	330	HHCMALWVTGRPYLNIYICVADIYIHI YICVYIYTHRVYIYLLAI*YIYVYMR IYIYIYIYVYIYTHYIYIYIY
11502	25403	A	11602	41	252	TPGRARGQRLGHSSTGLDLTS*SACLS LPKCWDYRREPPRAEDDKPMF*AILSE TILVRGVRSRATPS
11503	25404	A	11603	271	440	KKKKRGGRFKESKFTSAGLQSNIFFIGP PKLIPRAAV*QRGDWNLGVTLQNLRLCH
11504	25405	A	11604	429	2	FSFFFAEKGCHCVSQAGFKLLSRDLPT SAPHILGIRLLGLRLQEDPPSPGV*GCSE LQSRLLCTPAWITTKRDPVS*KFKKQRTKT HTH*KRPKTGGDQHQYHCLPPHVMPLKV FSGNSVBGAVRTRGSRGSIPELSHAVPH AP
11505	25406	A	11605	113	2	TEATHLVCTYKN*KLGNAWIMFVPIPAL WEAEVGRLL
11506	25407	A	11606	301	3	WVMVCSVKNIALGHACGKPHYEGRGKPA EHPWSWLVLSLQKKLFLSYPLFTFL QPPSPRLT*PVFRFFFFRDRIMLCCPGW SAVVPERVGRAGNSE
11507	25408	A	11607	117	431	SCDFCLSFSLSLFFFKKGIFFLGPRG ENKGNNKIKWTLGPGGKGNRSPSPKGG GKRGGPPPGANLDF*KKTGFPQGGRGGE KPPPPGGRAGGAPORGKPGAG
11508	25409	A	11608	277	88	RRTTSSWLARNCTQGAGYHTGS*TPDL KGSACLSFPKCDYRWRDL
11509	25410	A	11609	200	27	VKLKPGDSKDPDMQVYI*ENRPARCGG SLL*S*HFGRRKADHLRLGVQDTRSSA R
11510	25411	A	11610	17	414	TWLVLMQDFENEWIVSGWGKEEPGRYF MCEARSSMDRVFFFF*KKTLLFFPPGGG GGAKIWNIGIPPPQGSPLSVAYPLGVWE KKGPPHPHKRVPPV*PGGVLFSEPN PPPGPKGVGRSSPPSPVL
11511	25412	A	11611	296	428	RIYENWRGTVAHACNPSTLGGQGGWIT* GSLKLTSTGTVAKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
11512	25413	A	11612	20	362	NFVRGVARGSRGGATRCBVGVLRFVGMAYGRSPSWLL*VKPSAASHRPPLPRAADTPGTAPAPTPTPAPAAAPALTPSSSGPGSALTEELLEQAIRRAQKGLTMTLFRLASNS
11513	25414	A	11613	158	2	LMSRTPLQQL*YTLLELELPLRLAPDL LNSGSSLKDLKWTSHNYRASKETK
11514	25415	A	11614	3	410	RSEVGLVLTWYQVNRVPWTHKAARFT RVSRRWARPRSKISESCYWLPAHRTKS* PLVRTLSGLCSILGPHFLLFSLLATDLV PLPSFALLLLELFFLPQMPKLAP* SPT KRSFSFYFFRDRVLLCCPGWSQTP
11515	25416	A	11615	189	397	YKVLFLVERKNGFFLFFFTKPCCVAPTVQGPNGF* LQAPPGLPLFSALAAPEVGTINTGTPPPPRFFF
11516	25417	A	11616	158	1	KGKPTPTKFFCQKQIFVLFVFF* TESHVARAGVQWRDLDSLQAPPPGFTPR
11517	25418	A	11617	319	425	KWLYSQAV* KWLYSQAVHTYNTPLGGQWRHA* AYEFKTSL
11518	25419	A	11618	94	2	CLTISWLGTVARVCNPSLIGG*GGHITR SR
11519	25420	A	11619	381	9	FFFLPLPLPTVSLFFRSPSDAEPKLDDAISAHCNLEA* FSCLSLPSACNCRAP PRLTASASRGAGIADGVSTQCSMVPRLECSGVISAHYNLHLPLATSLGLPKCRDCSLCPDEIVDPRI
11520	25421	A	11620	144	431	IVNVI VGKGGKRIPE* LIRCGNN* S WDRMWAEHDVLRPSSENRLRLARVCLTP VSQHFGRRRRLDHEVRSLRPACATWRNS VSTYNTKSGWAC
11521	25422	A	11621	174	449	VFSLEPLGGASQLGYLEVRDPLSEAVCF FSDLKPHAGRTTTLFKAIRQHLSLQRF LLLFVWLCPAPRGGVYRQOASLS* GGL HPVRASRP
11522	25423	A	11622	316	412	GGPSAVAHACNPSALGGRGGYS*GOEF KTSL
11523	25424	A	11623	183	2	PRQVYLRNGLLSHSKCNKIHHIIRLKR KIQPGVVAHAYNANTLGGGGRWIT*GOE FENS
11524	25425	A	11624	355	168	DLILVYCDPNAIINL* SLLRLKLWEDCL SPGG*GYSEPRSCCHSPAWAAEPDPVSK KDRNVEFYCC
11525	25426	A	11625	154	3	TADVLFLGQAGRGNFVMMKNCRPGTVAHACNPSLGGGG* ITRGLEFK
11526	25427	A	11626	412	3	IFFFFPKKDKRTGGGQKNIAPPAPPRNF LGRGNGPPPPQKFFFPPLP* IFFPRPP* C XGSIAPPPLPCLCFQKKKTPSFFFLPNGS PPICEKILPLFFKGFLLKKKPLKKG PFFFFFGNAVLLCQPCWGAQAQO
11527	25428	A	11627	290	423	VFEVFFPKFFKKNNSWGVVAHTYNPSL GQQGGWIT* SQVLRRP
11528	25429	A	11628	213	3	LSGIYSQNRNLVRYKSVYIHHIIRLKL KKHII IISIDGKPLEQIQNSFMT* KRN KLKWNEDHLRPADA
11529	25430	A	11629	152	2	FOKNRDLPSKAGWPGWVAHACNPSLIG ARGGOIT*GOEFETSMVMNVKP
11530	25431	A	11630	422	189	PLSGFCFSTWGAKORLSKKKKRSAGH SGSCLS* SQVLGRLLKQKDHPSGGRGFSF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
11531	25432	A	11631	239	424	LLNCTPAWVAKQDPVPKKRLK KEDNNRVFVIGPLGGLNELAHDKAFKTO NHHWLGVGAHACNPSTLGGQGRWTT*GQ EPTTSL
11532	25433	A	11632	343	401	AREHEHKSAAQ*GMERSVIGKICHIVATE *EREQKREERQERASENERQQESERDSK REARESERRESTRACLVKRVNQIS
11533	25434	A	11633	125	371	FQCKAKICLITWLPYAHYGLIWRHDGK QCHEKWTAKI IISCKLSPAL* SOLGVP L*THTHHTHTHTHTHTHTFSEKKGLVP
11534	25435	A	11634	235	433	ALTSFSGPSPFCSYLINTLGXNPNHIE ISTT*FTLQRL*KIIFWPGMVAHACNP TFGGQGRNIT
11535	25436	A	11635	93	385	FTLKSERRKHSPVQKKQNKIKLLSDC KLENKRFGWARWLPVPIPAL*EAKAGES PEGNGEREATEPFGSIILGFFPCTQIA HLHRSDYEPNEDS
11536	25437	A	11636	190	398	NTKKSQKAFPK*QGGPFLDPKPKASKK TKFPLPKKISTRKFRGTGWPGRGTNFSLKK AKKNLGKTRKKIFP*RPFPFSISSLFWP FFFFLFF*KDKVPLCHRGWSAVVQSOLT ATSISQMY
11537	25438	A	11637	190	380	TPKKWPKAFPKTKGKPSPPHPRKKALRK TKFPLPKQFF*NPLSLPLFPWPPFF FFP*KDKVPLCHRGWSAVVQSOLTATSI SQMY
11538	25439	A	11638	261	91	EKTLWAGHGGTCL*SQLLGRLRWENHLN LGGRG*RSRHCTPAWVTERDSVSNK*IN K
11539	25440	A	11639	1	334	FRANRTVKDAHSINGTNPQYLVEKIR RIYESKYWKEBCFGLTAEVLVDKAMELR FVGGVYGGNIKPT*PFLCLTLKMLQIQPE KDIIVEF IKNEDPK*VOCSLANIRGMY
11540	25441	A	11640	193	457	DGILLCGPWSAVAPSQLCSGTTISAYCN LCLPGSSSPVSAP*YLGQACAHPLM FVFLVYGTCLMLPLSAHHSRAANSHFS YPLL
11541	25442	A	11641	257	373	NTISCPSSLRPFVAHCTNPFSTLGG*DGQI T*AEFETCLG
11542	25443	A	11642	211	367	DTTHSPFOWL*FKSKSR*RVLDRIWGN* MLVHCWHEHVMQVLL*KIVWLPFK
11543	25444	A	11643	112	367	LQIKTIRYHHILTRMAKIQNTDITNKCYQ ECGATGTLIHCWWEFKIIPVIALNEARE VGGLEVRSSRPAMPPTRENPIPTKI IKN Y*KYKNTPIYIR*LQIKTIRYHHILTRM AKIQNTDITNKCYQECGATGTLIHCWWEF KIIIPVIALWEAEVGGLEVRSSRPAMP TRENPIPTKI IKNY
11544	25445	A	11644	310	335	YHLIAGSLGDIETRLSML*IGKAVCHNKY **GCGEPGLLHCWWEHVMQVSL*KIVC QILO
11545	25446	A	11645	143	455	KKKGSPSLWLLGRSMGGRIFP*KKVFSSG FKSLWFFFWPLWKPLSLRN*IKISFYPP AKKGGQRKAQFFFFFPRFSLAGCSG SISAHCNCLLGLSDSPTS
11546	25447	A	11646	182	458	SRGGIRFF*KRVFVSFKISWFFFWPLL KPLGRVN*IKISFNPAPKRGWERKAQF FFFFLPRFSLAGCSGISAHCNCLLGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11547	25448	A	11647	319	3	LSDSPSTS RSTKYSRPGWEPFMSWFLFLHVFSLPFRS ILGPPILLGTFLRGSPPPPPFEGKGFY GLTFFFP*EPPCEIFFFFLDRVLLYCP GSAVVSQAHSLELKKDKVCI
11548	25449	A	11648	165	2	DQSGRPKRLICARHTHTAHAMHTSLGQT* QDFV*THHTHTHTHTPLAAAGQGIN
11549	25450	A	11649	290	3	SKQNTTHWATLKSTIYPSQFWRLGSPSS RWQDGLVRLFLVCRQPPSLRILITWW EKTERKREK*DRERERNEIERNERE RERERETQRMV
11550	25451	A	11650	220	2	TPFLPKTGLTALDRTPGRDPGPRRAGR PF*AGVAENCDDPABGGSTRPLGAPGR GSAPP*RHPGPAGGR
11551	25452	A	11651	29	387	FLYFDVTVIDLACHEPHYSKMAHLIN VCVLTAPTSTSYFFI*SFGLP*PYSLRHNDI EIRPINNPTRTSQCSSEKRSHTSLTLNQ KLEMTTSLKDGMSKAKTG*EPGL*CV*TV SQAVNAK
11552	25453	A	11652	267	2	KFFFFFVSTSKLNFYPGTFPFLFLFSFF FFFFF*FMREGFATVNVGAVAGAVLA HCSLELVGSGKPPISAS*GAGTGMHYH TRMY
11553	25454	A	11653	50	411	EAVAGGMEKSMNMLPKGPDTLCPDKDEF MNEEDVDHVFVSDCRNRQGLELRDNFPQ LYYKLLKTAMVELINKDYADFVNLSTDL VGMEQALNQLSVPL*QLREEVLSL*SFV IERISPS
11554	25455	A	11654	303	403	VRNMVWLGVAARACNPSTLGGQGEQIT *GQEF
11555	25456	A	11655	356	653	SVSPCPFPGPASTLSFLVADFRRRRGVDV SQVAWQSKGDTFSSCCINNNSGNRTIV LHDT*GPRASPCYNPPI*SWLNQFPHSP WASQLPFSVASVYQK
11556	25457	A	11656	442	2	GRPLMEPVL*SEPTPACVDIQQQIM TTIDBVKACAKVGTLSAPINASRMQS IRHVVYLLKDSARPAKGAIGFVVG YKLLFVLLDREAHNEVEPLCILDIFYIHE SVQRHGHGREL*PQYMLQKEREVPHQLAI DRPSLV
11557	25458	A	11657	109	474	DINMCGRVLVLAERM*KRKRDKNYEEET E*VL*KKVRHSLQKENVAQNAPVQNA AYIDQPSPAHVQQQGLSKLPSRPGDQGV EPONLRTLQGRSVIRSAINTTLPHMLMS QRVIAPNPAQLQGQRGPPKHGICRTTTP NMNPNV
11558	25459	A	11658	342	3	ENQLKNGEHSKSSQASSPPNDHNTSLAR A*KWAGAEAEIALLTAGFGRWVIMFA ELKEHVVTQCKEAKVHDKTQELIAGFE RNITYLM*LKITTREPHIAITSINRMA
11559	25460	A	11659	204	17	STCTPLETA*SQSRPHPPPTTTPPAPVR SSNGPLSRGSSSRNSTSSWSIALATGPW THRSKL
11560	25461	A	11660	505	514	GS*GNHFPDGCASHGQFQDSDRTPGRPF CLDPSWGAQILRDWYPOEEMGLTQKQ
11561	25462	A	11661	80	374	FLFDIYNRCYLI*FINII*YLSNFD*IF IIIIYLVAIYRLCLGLFRAPRQCKHPRP QFSFNKIGTKR*AWGAMHTCNPTLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, =possible nucleotide insertion)
						GLGAQTM*GOEFTT
11562	25463	A	11662	142	437	GQRVQVFFFWKRRPFFAQQGTGGAQFR LHKPSFSGLKEIFPPNPFRKGE*RDGPP FRGDVFLRKNGVPPCCQGGSKPPADGE PFFFTPPRGNNRG
11563	25464	A	11663	120	353	QALQVMLKHVNFPPFLFPLFWKQSFVPL PRLECNAGTSVHCNLCPLG*RNFPASAQ EFRIAGSYDHAICPPASGKGE
11564	25465	A	11664	1	404	NTWSDLIISYFHPHPSAFLPRLQGLALSP RLEYRGTTITHGYSLDLWGSSDSPASISR VAGTTYRCM*PQLRLRLRENHLSPRGR GCSDP*LCPYTPANVTERDPVSKKRLRG GGNSLLSSQTM
11565	25466	A	11665	493	3	NWTVDVLPGHARQ*LGSPGKLSAGF* PLQFPQTSSARAPPFLCRLQVNTVG FLPSPHTSRPSHCLPACPLPSRTQPWVP VKPGPTACRGFLQHPPTPGSP*SFQG SSWWDTLRALCELLRILGRNCSEVFT TQQLSHEGMNKEFLITCAKKK
11566	25467	A	11666	3	401	CMERAVTVLLPGSATQSPVYAPRALAR LMLTAAMMISGFIADYEA*SSRCSACAP AGDSLSTYHSPADSFSIMGSPVGAQDFC ADLGVSRAINFITPTDDMTSPDLQMLVQ PALVYSVGGSETIAPHPGLVP
11567	25468	A	11667	1	446	LSCAKPQRPLRHIGIKIPFNVPFEETAN KHLGLVSKLPRGFPALFSLVSSPGQKK HYVQWLQSHSHSLIIVSLDFFFFFEK KPFPPFGGRERDQTFN*TPPDS*RE SPPFFSRGGGTQGWAPHCPPIIFRFPQK GVFPLRAR
11568	25469	A	11668	18	403	DPLQRFQYRGGLRVSVCGLQSPTRGFS GRWPNPAQARGPGEAQAWAPGGGPREA FSGQQRFPPLGLHPRHRKAGPGPPGMPG *HEGGGSC*GASCRGGACTAFPAASSP PIFGGLTPPNLNFPEE
11569	25470	A	11669	157	1	PRPQGFVVFVFFFEFGQRLCEGSAISA H*NLHFLGSSNSPASHVYAPLY
11570	25471	A	11670	396	7	ERKVGQARDKSACEGHSCADARSCLHLRV DQGGQHGSHGACPGRLRLGPDTHRQSCY QCRNRSFDRLPQGRAGTP*CAEAAAEF DAAVHPGQAPAPARLPALPGRGLPLPH PGGSQRVYCVRCIGSKLR
11571	25472	A	11671	209	3	DDLGTFRPGKQVRVTPREAGENPSAVL PCYLHLVPFV*EDEVKPEDIPDMPGNE YAREFLAHAPLY
11572	25473	A	11672	270	101	LSLNKRWILGAYIIFFTESHVSVAQAGVR *HNGLQLQLPPGSRRLPAFKVAFIFIG
11573	25474	A	11673	421	592	SSCTPGVIIKIPCVRSNHHMLKPGPMVA HTCNPSTLGGQGRITWSE*FKTRLGNM A
11574	25475	A	11674	176	6	LTFVYMPFCFALSSIMTYGLAM*FHFH SMTLFIIGVLSVALAIYQ*WLDVSRVS
11575	25476	A	11675	1	418	NTVCVCVCVCVCVCVERKAGHRLTDSFP IQGSPGAQARLCLRESTGALSSGLPA SYQPCGRALHPCVVFPPGRHNLNLY PPARSFREAUCYFROTLKWRSPRGGC GRILRVIRVTASTFRDTS*TESACLGARP CLDGK*VCESVPCFLSHRTHTRHTHT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
11576	25477	A	11676	305	698	HCI SFMGRSPRKIDQFCNSRNMVHGSVTFRD VAIDFSQEEWECLQPDQRTLYRDVMLEN YSHLISLGSSISKPDVITLLQEKEKEPVV VSKETSRSWYPGK*E+SRQGEALIVPDS PCAQRGVTPLRGLENFLO
11577	25478	A	11677	107	397	GGDRETLPAPADGCT*QERAEPLAY SCPRSSSTCRGRARRYDGCRTDRGHQLI QRGQQQESSRRTAQPGSSKLCRGGGHR PSLGTGVGHGCSL
11578	25479	A	11678	514	554	RAKPTTP*GGGEGQNGLLKPPVSGLPF LACPTTPKRWKPKPPPPAPPHLFF**K RGLIF*PGEVFNLRNWLPPSPQRRGGN NGRNQPPRGTFMF
11579	25480	A	11679	266	3	GPPLFLGLKN*TPFSPTKV*IPFSQVFS SPQGLKGGVREI*FFFFFF*DRLECNQT ISAHCNLRPLPGSSDSQASGTTGVCHVT RMY
11580	25481	A	11680	1	408	NTCALRHHDHFSFMSDQKTEGEERIVQ ENWLISWNNFSPFETLLTSLCPLGKEGM PGEDGTAGAGKVPGEDKIP*DGTAGED GTDEENGTTGEDTAGVGKTPGAGGTTG EDDTESEDGTTGEDETAGGGGTAG
11581	25482	A	11681	244	420	KDSESTKAYIRDNISTSKKKKSFWPAGA HPCNPSTLEGKG*IT*SQEFETSLANM VKL
11582	25483	A	11682	294	443	QMNTCTHIQPAYVH*ERYFRFSAMAHAL NPSTLGGRGWIT*SQEFQTRP
11583	25484	A	11683	346	1	VNTNQPTLRGTQASVYTCLTALIVLKL NQPYTLASVLLNAGNQPFHAFSPPSLH PDAFHSKIMSHIILLGFIPLPASQS LTLSPSLERSOTISAQCNLCPLGSSNSF ISA
11584	25485	A	11684	140	423	SSHQASSPPTTASHSMKISVAATPFLL ITITLGTCTESSSSRGYPHSECCFTYTT YKIPAQIRIMDYETNSQCCKPFGIVITK RGHSRWTFNK
11585	25486	A	11685	163	3	IKIFCNRLKFGPPSCGFFFLPLPPFF FFETLSRSVAQAGLQWRDLGSLAL
11586	25487	A	11686	179	1	PIVFLGMLFVAFAPRGFFSVTKPPNFF FFTEMESCSVAQAGVQWRDLGSLQARPP RST
11587	25488	A	11687	192	1	EGCFDGHSLASWISKDTAKWNGDELCS YQSCCTDYTAECKPQVTRGDVFTMPED EYTVYDDG
11588	25489	A	11688	89	3	SGGYCCCLCCRCSSYSCCCRLREGFTK
11589	25490	A	11689	168	2	QDRLOPHESKRKLGPAPQARRSESITPS VYNFSTESQLMSXGDENTDDSKETV
11590	25491	A	11690	301	397	HEVFSLVTMGNFLSPYLVDPRYLQVR LRFY
11591	25492	A	11691	18	421	TRALQITCYLHSTMSSESGKLTEDSL QLRCHPTWKLIEAPEIDLENRIWEEI OFLDTKYNVGIHNLAYVKHLKGQNBEA LVSLKKAEDLIQKEHANQADIRSLWTG NFAWVYTHMGLRAEAQTYLDEK
11592	25493	A	11692	188	3	PLQGGKGPAGKRGQKGFRLGGVRAERF RPPFGPSLFFFFFFETDSHSVAQDGQW CDLGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11593	25494	A	11693	24	391	AFRADAMGHFTTEEDMATITSLWGQGNVE DAGGETLGRLLDVYPWTQRFDSFGNLS SASAIMGNPKVKAHGKKGLTSLGDAIQH LDDLKGTFSQLSELHCDKLHVDPENFKP LGNGLQTAQG
11594	25495	A	11694	138	425	NSGVKAARQLNPGNDLGEKPGPGFKTH PGLOBETHFLKIHYSGLVGKPFWSQL LGNLNRNHNWTPERGGPRDLRHCIGIQ WATNGNFVLKKK
11595	25496	A	11695	158	838	CGTVHSCDAGQQRATAPSHHPCHDGNQ PILYRVLCCLFWILCFVFSHSIMSTKC PSVSPVSGMCKKRAITLMLKLIQAQ EGGKPVMAIARELGLNQSTISTILRDKK QISDAAKSSASVKSITVITKRRAGPDDM EKLVMWMDQIQKRIPSLMLIOAKAR SLFNMLKDRASDPITYTMFKASHGWFOR FKRRHNFHNVKITGEAARAGNEGAFAFK EQL
11596	25497	A	11696	834	1431	SSACQGGSGQGWPPRQPPWMMGWSSRRAPS VTHRTGERCTSGSAPLPLLLSLCSSL PRSWHSTLRQPPHPPLPPGCLPPGRE AQLSGAGHGPGPRPAAASYIPDTQADR KQQQHHPGPDQHVGHREGLAEDAATHL GLVAALSCWLLGRAEAGVQVPHGHDPK DQHPQADGGQRIVRAIGLGLGHVSGRR ARP
11597	25498	A	11697	143	1	ISKERGASRFSFGPWVFFFFLESRSVAQ AGVQWNCNLSLQAPP PGFT
11598	25499	A	11698	58	459	KGKEEKVKRKEAQNFSPYAADKQKERTK GNENDENKTKQKQKETTIDELFKGLDETG ENNDSTLTETPFLNRWKLIVLGLDG AGKTSVLHSLASNRVQHSVAPTLGFHAV CINTEYSHMEFLEIGGSKPFRS
11599	25500	A	11699	215	1	GTKKALWAGGGGFFPYLPMGPIGICG GVGKGSPLGCGCPIFFFFFETESCSVA RLDAQNPDLGSLQSP
11600	25501	A	11700	300	420	KPKILFGNVFAAPHMENLCKRGETVAKE ISEAMKVKAMC
11601	25502	A	11701	351	466	RTIKNADLSQAQWTPVPIPALWEAKVGRS LEVRSRPPW
11602	25503	A	11702	172	400	SNRLNKIKQGVFLNDSSTSPFFLRKQST GQAWNLTPVPIPALWKAASGSPMDSTT LLPSSSQVPSLVKMEKLNYS
11603	25504	A	11703	284	408	ASVFSSFFVCLFVFEMESRSFAQAGVL WRDLGSLQAPPG
11604	25505	A	11704	20	447	LPGADYGGGGLSLRLFHLLASAAWVFD ESQVTLNSAICVLSTVLIMEFPDLGKHC SEKTCQKLDLFPVKCDACKQDFCKDHPF YAAHKCFFPAQKDVPVPCPLCNTPIPV KKGQIPDVVVGDDHIDRDCDSHPGKKKEK IFA
11605	25506	A	11705	1	455	HSCSLQFTPTAWDCTGSVSSEQGERPAA AMKICSLTLLSFLLLAAQVLVLVBGKKVK KNGLHSKVRSBQKDTLGNTQIKQSRPG NKGKFTVKDQANCRNAATROEEGSLKD ECTQLDHEFSCVFAGNPTSCPKAQDERV YWKQVAKLRS
11606	25507	A	11706	1	428	DAEADKMAAAVRGGRSGGSGGCSGAGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ASNCGTGSGRSGLLDKWKIDDKPKVKIDKWDGSAVKNSLDDSAKKVLEKYYKYYVNFGLIDGRLTICTISCFFAIVALIWDYMHFPBESKPVLCVSIYVVMGLITITYTSYRE
11607	25508	A	11707	1	422	RSQARSSAAAAARASVPLRSGPGPSAIMPMFIVNTNVPASVPDGLSELZQQLAQATGKPPQYIAEHVVPDQLMAFGGSSSEPSALCSLHSGIKIGGAQNRYSKLLSGLLAERLRISPDVYINYYDMNAANGWNST
11608	25509	A	11709	88	423	AADAKQAEAWGAFMRLAYQELQDRLKEDKMLNLEGNKREHAERLGMGLVSRSSVSHSVLSMELVIEHTVPAKSSRSQGLDLPDDVGTFCSGSPKYKTONFSLWESIG
11609	25510	A	11710	393	130	NFSATAQSFHLAKLSTLDRFGSOAPQKMPSPKPGVVLPASTNAVPTPLAEATPSKAHPAISLLSTEEGIFKAVPSPASSCSFLHV
11610	25511	A	11711	331	440	KIFFNLFISRAWNCAPLVLATWEAVEGSELYPRES
11611	25512	A	11712	122	478	SGLCPCQOPFRANSCPPSSMASCAPESPESAPLPAGVPPLEDFVLDGVDAQGEEDDEEEEEEDLSELPPLEDMGOPPAEEAEQPGALAREFLAAMEPEPGSPVPKEWLDILGNGL
11612	25513	A	11713	102	2	TNLGNPRRPPPPFFFPETVSLLAQAGVQWCDLGS
11613	25514	A	11714	126	2	FFAPFLKIFPPPPFFSEMSCSVLQAGVQWHDGLSLQNEGSQ
11614	25515	A	11715	178	449	LSGGNLFGTITILLYCAITGGKLLGLIKLPTLPPLPSLLGMLLAGILITNPVINDNVQIMHRWSYSLRSIALAIILVRAGLVLESKALEK
11615	25516	A	11716	48	417	GSNGNHSVCCDITMEGGGSGSDKTTGVLA GPFPGAGEAGYSHADLAGVPLTGMNPLSPYLVNDPRYLVDQTDDEFILPTGANKTWGRFELAPFTTIGGCCHTGAAGFAMNGRLRGLKETQNMWNSKF
11616	25517	A	11717	103	2	PKSPTQWLMAVIPALWEAKAGGSGRESRSRAL
11617	25518	A	11718	1	413	WFSQVVLVSCLSFSYLCWKSLSKKRNGFEVLKIFLKNHPRCHTNRMIOQTATPVSALADEPAHIRATGLIPQMVSPASLEDENGDMFYSQAHYRANFAEADLNHAASLGGDYLGLDALRLRLCTLEPVFPQSY
11618	25519	A	11720	116	462	AGMLPFAVGSVDEEDPAEEDCPLEVPTE TTQSEEEKSGLGAKI PVTIITGYLGAGKTTLLNYLTQHSKRVAVILNESGEGS ALEKSLAVSQGGELYEWLELRNGLCCSVK
11619	25520	A	11721	167	407	EIYSLTRFIEVRMSKKISGGTVVEMLGD EMTRIIRETLKEKLIFFPYVESHLSYDLGIENRDATNDQATKDALAEFNKPY
11620	25521	A	11722	254	423	NQLSSINAMFKIKISFEVVFNDPEKVVGSSEKAVAGRIVEVCEVTRVKAIRILACG
11621	25522	A	11723	3	424	VSCDMEGGGGSGDKTTGSLAGFFGAGGAGYSHADLAGVPLTGMNPLCPYLVNDPRYLEQDTEDEFILPTGANKTRGKFELALFT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IGKCCMTGAAGFAMNGLRVGLKETQNM WSKPRNPVILDMVTRQGLAWMTLGLA AFGTMKWNVLTVSVLFLFSSAYSRSRVFR DAHSEVAHRFKDLGEENFKALVMIFA QDLQCCPFEDDAPSTSEVSEFATTCDD DHFECDRCRRVHTLVVVQLCTPATLLETD Y
11622	25523	A	11724	2	343	HAFGTMKWNVTIVSLVLFNSAYSRSRVFR RDAHSEVAHRFKDLGEENFKALVLIAP AHYLVHQCPEFEDHVKLVNDVTEFAKTCD DESAENCDKSLHTLFGDKLCTVATLQET YGENADC
11623	25524	A	11725	1	359	GAMSDRKFSAAPRHSGSLGFLPKRSKIRHR GKAKSFPKDDPSKPGHLTGFLGKAGMT HIVREVYRPGSKANTNEVAEAVTIVETP PMEVADTAGYMETPRGLRTFNTAFAEHM SDEC
11625	25526	A	11727	81	349	TKGSVSVCCVCLCVCLTWSHLRLVLTW LPDMPDDVLWQWVTSQVFTRVLMCLLP ASRSQMPVSSQASPCPTPEQDWCWTPC SPEGC
11626	25527	A	11728	264	388	QADFKDIMKFFGPLENQRSLFLEKAIT REAQMKNVNVKRM
11627	25528	A	11729	2	471	PGCSASWSKRGSGFDMLSSMAAAGSVKA ALQVAEVLAEIVSCCVGPEGRQVLCTKP TGEVLLSRNGRRLLEALHLEHPIARMIV DCVSSHLKKTGDGAKFTTII FLCHLLRGL HAI TDREKPLMCENQTTHGRHWKNCSE WKFISQALLTFQTGL
11628	25529	A	11730	160	377	LQSGRSEVYHAAIVIFLEFPAGLLTT PMLTVSIAELGLCFVRERDKFLGTTHCV CLDCLQVALDSDLKQ
11629	25530	A	11731	45	438	KLGRKEATVTKSECKSCSRKVGSPDRF RSPQKRSKGRQDCFTLCFQKVLKDNME LISPTVII ILGLALFLLQRKMLRRPP CIKGWIPWIGVGFPGKAPLEFIEKARI KVCGRGRGLRRQRCFLF
11630	25531	A	11732	169	292	DSILLVNLACSAVISAHNRLPLGSSDS PASASRAAGGAHL
11631	25532	A	11733	473	600	KFEWEKTEGRGKSKSNSETFETVISA LSTTEVAMHTSTSS
11632	25533	A	11734	19	349	APSPDAMGHFTTEEDKATITSLWGTNVVB DAGGETLGRLLGDYPWTQRFFDSPNLT SASAIMGNPKVKAHGTVLTSLGDAIKH LDDLKGTFAQLSELHCDKLLVDPENF
11633	25534	A	11735	234	359	FVHLKSTFVSSVQSRWLPVLPALWEAB AGGSPSEVKSRRPAS
11634	25535	A	11736	15	372	KLPLKALTGEEKTHINIDIIGHVHVSRS TTTOHLIYKSRGIDERTIEIFEKEAEM GKGSFKYACILDKLKAERERGITIDISM RKFTSKYYVTI IDAPGHRDFIKDMTTG TSHADCA
11635	25536	A	11737	1	357	IKWKAASPAWSWARPFRPMREFQTLAM PTNAARDQKLKLERLMKSPDLAVTIPEK MSEWSPGPPPEFDRDVMGSRAGAAAGF HYVRLRRREYQRQDMDMAEKRLDA EFQRRLE
11636	25537	A	11738	24	335	AFNANAMGHYTEEDKATITTSFPGKGNVE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DAGGKTLGRLLDVYPTWTHFRDFRFGNLS SDSAIMGNPTDKAHGQKRVLTSLGDATKH LDDLKGTFAQLSELHCDKLH
11637	25538	A	11739	141	335	MQFLPCIPILKSLKESVASHSQTVHSDI ISVTFNHTGELLSTGDKGRVVI PQRE QESKQVHR
11638	25539	A	11740	7	337	APSPDAMGHFAEEDKATITSLWCKVNV DAGGETLGRLLAVYPTWTFDFSGNLT SDSAIMGNRKVNAGTKVLTSLGDAIKH LDDLKGTFAQLTELHCDKLHVDPENF
11639	25540	A	11741	182	360	SRHSISPFVNQIQLGASVTELTVTTKT ARVSRQAQLMPVIALWEAEAGESPEVR NSR
11640	25541	A	11742	174	1	HFSDBSLFVCVRQDLTLRLPESCSLIT AHCSLHLLGSGDPTAASVWVGNTGVHY HA
11641	25542	A	11743	75	218	KIILGRAQWLMTVIFALWEAKVGRSPVS ASQSAWDRYREPPCPCSTI
11642	25543	A	11744	168	2	LAPLNSLGFVLGGVGQSGPGGFFFFF FFFFETESCSVARLECSGFI LAHCSLR
11643	25544	A	11745	83	2	REORFLPLFPVQLCPAPRGVVRGRQAS
11644	25545	A	11746	156	3	PHSGSGRVENPFFFFPFETGSCSVTQD GECTGATLAHCDLFCFLSSNSS
11645	25546	A	11747	244	330	KDRAQWTVFVIFALWAAKAGSLEVRSS R
11646	25547	A	11748	201	1	TSQPLIRITLSTFFFFSRDGGLLMLPRL DPBLPGSSNPPSCASRVDTGMCHHT RLIFFSQTDKK
11647	25548	A	11749	262	3	VYTSLTPFPFISVNLTLQVSPRSVSYEON ILCLLFTVITYFTCTFFVCLFVCFCK MESCSVAQAGVRWRDLGLLQAPPGFTY TT
11648	25549	A	11750	225	3	PIINFSVPQFLHLYNGIITESTPPSCCI LKQSLGQAGWFTPVITLWEAEAGRS EAWTLKTLIANMAKHL
11649	25550	A	11751	185	2	VSTPFNSFPFPWLVLKGFVFFVFF FFETFPSCSRPLENGAPLAHCLRLPR SSNSP
11650	25551	A	11752	261	336	DRVSLWSRLECNQAISSHCLRLP
11651	25552	A	11753	282	381	TDLLYKKKCGLAQAVAHAYNFSALGGQGG RITCS
11652	25553	A	11754	202	45	NPRKVKLQWALILPLPFLGGQLKSRFQ KKKKKKKKKKKKKKKTLVVIC
11653	25554	A	11755	293	357	LTBVI PALWEAEVGGSPFVRS
11654	25555	A	11756	264	1	TLFINVCCDSTGTGFSLSLPLSLFYS LRHNNIEIRLINNPTTACKYCSLKSHK SLTLQKLEMIKLGEBGLKLAQIQKLG LLHQ
11655	25556	A	11757	126	1	TLPGFLKELKIELFPNAILPLGIYPKE KLLYQKDTCTHMF
11656	25557	A	11758	399	226	IEKGTGRVWMLTPMIPALSEAKAGGSPE VRSPRPACIGLLKFWYRCPEQHPARLS EI
11657	25558	A	11759	235	380	DTTVLKLGLTLTQWASKCSSEKSRSTS LTLTQKLEMLKSEQMSKGD
11658	25559	A	11760	249	357	NRASGQTCPTIPFALWEAEAGGSLEP RSLRLTWA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, °=possible nucleotide insertion)
11659	25560	A	11761	168	372	KLHCLCPYLSEFFVFCPLETRLSLSVAQ SKCSGTVTIHTCSLKLKCSSDPATSDSRV AETTTGTVHAGL
11660	25561	A	11762	303	377	QFAGCRNLMVPIPALWEAKADGSPF
11661	25562	A	11763	135	1	ATTPGLFFIFYFPETESHISIAQAGVQCM ISVHCNCLCPGSSDSPV
11662	25563	A	11764	219	2	KLRSSQLSEFEVRPDSITLSMLHARAHT HTHTHPHLFLPHPCSRPHSTPTCMPIV THSPIYLPKHSHTYIL
11663	25564	A	11765	102	1	NRFINNPTMASMCSSEKSHKSLTLNQK LEMIKL
11664	25565	A	11766	245	3	PGPEEDDLVKFRPSLLWFMFLFFLER SLALSPLRLESCGVCESGVISAHCNCLCT GFKQFSCLSLLSGWDYRHPVPCPS
11665	25566	A	11767	350	97	GSPVAPSQVTRPTLMTSLADKWSLCLT SLRVNFGVALISLGSHSVSDTDLDLLTL FSTHLGLPKCDYKRVPCSAQLVTFL
11666	25567	A	11768	188	391	LGSVAGDLLCFGGVIFPCSPMFMSLC YYLIYIWNVSCVLFKTEPHFVTHSGVH WCDGLLOPPPPN
11667	25568	A	11769	131	2	YTYLYPNKSPITENIQLSQAQWLVPVIPA LCGAETGELEPRSS
11668	25569	A	11770	165	1	VLPLIHLICIYIYIYIYIYIYIYIYIYIY HICIHITHYIHIYIYIYIYIYIYIYIYIY ILILFFFFFEAESCSVAQAGWCN
11669	25570	A	11771	72	1	ILILFFFFFEAESCSVAQAGWCN
11670	25571	A	11772	121	3	TSFVLFCFETEPSCCCPGLECNALLA HCNRLRPGSSD
11671	25572	A	11773	152	3	HVCLNLTLPFLFERNIFSLCVCVCVCVC VCVVLCKKKCKEKFYFERTF
11672	25573	A	11774	190	2	GFSPQRQGRVPPVPLAGFPFFIFFFFF FFEMMHSVAPAGVQMCNHSLSAALTSP DSGDPP
11673	25574	A	11775	287	1	GAHRKRLFITPGESLRDQIAGFEHRGG EKKKTLFYKKKKKRKKRKKKKKKKKKK LPKCNMTKNNHQVPSYIIRPTRECADLRV FFIKFQILKY
11674	25575	A	11776	121	3	KCASRDLCKFFFFFFLETSRSVAQAGV QWCDLGLQAL
11675	25576	A	11777	142	1	EKTLHVRNTHHSSEGLVLIKHGRGLGVV AHACNPSTLGGRGQITRS
11676	25577	A	11778	179	3	SHQPVFGTDLDRGPKQLQSTSEASEA SMSEASSEDLPVPLEGAAPTRSESEAA KK
11677	25578	A	11779	147	6	KTFGLKKNNSFFFFFPETRSHSIARA GVRGCDLSLQPPPLGLK
11678	25579	A	11780	184	3	GFGFYIIPNYRLFFFSLLIGFFFLIFF ETEPSCVARLECSGVISAHCNIRLLGSC DSPA
11679	25580	A	11781	120	319	VKSIAKFLVNYQLHROTSCGQAGRGALR QRFGPRQVDHLRPGVRDQPGQGETPS LLEVRKLSSG
11680	25581	A	11782	91	3	YICLSLIYTHIHTHTHTHTHTHTIYIYV V
11681	25582	A	11783	221	332	SRIGMVDHPRSGVKDHPGQGETFSLLK IQKLARRSG
11682	25583	A	11784	243	379	LKYSVPIKNCRFWGTWDHTNRPSTLGG QGGWITLDQKFETSLAN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11683	25584	A	11785	327	5	GRVDSQPIYPKPNPPGSPFKIYPGSKTL FPYLQSRHSFSIPRSKLARFHQAKPLFC SKPSQSLSPHSLEKKDLSQLRWLTFVI RALWESKAGRSPEVRSRPTWPT
11684	25585	A	11786	245	359	FKGMDRLRSGVRDQPGQHSKTFPSVLKIQ KLAGHGGMRL
11685	25586	A	11787	356	67	RDIASITARLRYDRGVGITRELVLSKSD EYTKGSLVDFPSRETEPIGYIYIYIYIYI YIYIYLSLPLNHNMEISLGHFPLSNKFF VQNFDSPKLSYH
11686	25587	A	11788	103	3	KYIIFVCIFFFFETESCSVTSQSGVQWCE LRRRG
11687	25588	A	11789	136	1	VHQFTIRILNYYYYYFFETESYSVTQAG VRWCMLGSLQPLPFGFK
11688	25589	A	11790	291	163	SLLLPLFLECNSPTISAHNRPLRLGSSDS PASGRSLEPRSSKLQ
11689	25590	A	11791	107	2	IFKVVYFETESRSVAQAGVQWRYLGSVQ APPSGFS
11690	25591	A	11792	329	3	KNPNRTIGKSRGFIITNFPDGKGNKSS PRGNDLSINKNWAQAPQPRGQKLFPPK KKKKKETQSRSIPLRELCNGPTIAQCNLK LLASSNPPTSASHSAATISMSHSG
11691	25592	A	11793	213	3	ISFPLDILLQATLFRSQYVGFPPFSSLS PYLFFFKQKLGSQGFFFFLFFFKTESRF LARLECSGIITAQ
11692	25593	A	11794	1	400	KRAAPQPAPEQDLKKKKKKFPLAFSSL FRFWEKLLPSQFRQPRGPFPLTRGVSF AFHRRRFRWQYGNMGKEQQTWGNPGSSNP PPGTAGSLSGNRGPGWGKIDARFWLYA RDSFGHSRGLKGSCCQAHLGK
11693	25594	A	11795	3	769	RKEQTRNARAEVLKQAKANFEKEERRKE LKLRLGEDTWMLPDVNERIEQFSQHSV KKKKKKDKHKKKAKKKKKSKQKYEK NNSSSDSSSSSEDEWEAVPSQTPDKEK AWKVKDEKSGKDDTQIIKRDEWMTVDFM SVKTVSSSLKAEKETMRKIEQENQAL EQSMETPQSKLEDAEKAASKEDYRRER WRKPTYSDKAQNCQESRESDLVKYGFCS RDRYATTDTAKNSNNEKFIGDEKDRPG SLE
11694	25595	A	11796	110	13	RHHTHTHTKATHTHTHTRDRSGKIKC VPTV
11695	25596	A	11797	184	2	SEIFGKHFHYILTVHFMPTQVYVERD VLGQEQLLTPVIALWEAKAGRSPEVRS SRPA
11696	25597	A	11798	83	387	GERRRRRRERLWAPLQKKKKKKKKKKK KKKKKKKKKKGGAPLKKPPGGPHPSGG RQKNIPLKGGELKRADAGDFKPNPGRGK IARGGFEKNLSSWGGEK
11697	25598	A	11799	153	2	IFWEDTTVYSQYPOPLFSHSFFYFFFE TGSCSLTQTGVQVQWCHGSLQPR
11698	25599	A	11800	93	3	VWGRANWLTVSIALWEAKVGSPEVRS S
11699	25600	A	11801	115	1	NPLFFFFFEMESCSVAQAGVQWNLG SLQPLPPRFK
11700	25601	A	11802	295	137	RCFTPIFLINKLYFVYLFIYFFEMESHT VAQAGVQWRDLGSLQAPPNNKLYF
11701	25602	A	11803	287	1	MOPHAPFGKTCGGFQDFRPNLETSAGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						THSPLLAQNFVRGAVPSPRSPRFGSKG QGQFFFFFFFFFFEESHVSAQAGVQWCD LGSLQALPPGF
11702	25603	A	11804	202	3	WSVCCFKQGLSLPRLCNGAPGPKQSF PLSLLSNWGYRGPPLNFFFFFFFEMES CSLAQAGVQR
11703	25604	A	11805	3	315	FMLLILTLPLLRNDLVQCDVRSSVUCL QFLLGWSVILYPLMAAMPTMTWIFLIL FSMLFFVYVFLFLPLFLFLYSPFLPCF FFCFLYRFFFFFFFLIPSSSP
11704	25605	A	11806	126	3	KRGFFFFFFFFFFEESHVSAQAGVQWCD DLGSLQALPPGV
11705	25606	A	11807	130	2	QSIKMTCSLSLYFFFKKNVAMWLTVPVPA LWEAGAGGSHEPKS
11706	25607	A	11808	149	1	GGKAYLFFFFSLPRLCNGAPGPKQSF LCLPFSRHSPPASAFRVVGTAG
11707	25608	A	11809	258	3	KYYVQGNRQIKFVNASKNKLPSYSOKA SWFSRNRIRMGQHPMLDNPTSFTRK LQGANWLRPVTPLWAEAGGSLERSL
11708	25609	A	11810	153	285	CASFIRSHQKLKNGKGVQWLMPIVPVPW EAETGGSLQLRSSRLA
11709	25610	A	11811	160	3	NHLFLLLNRYKSTIFIGRVQWLMVSSAF WEAKAGRSFEPSSRPAGQHKTL
11710	25611	A	11812	89	2	ANFFFFFETVSCSVAGGQVQLCHLSLQL
11711	25612	A	11813	254	336	LLQGPQWLTVPVLPALWEAAGRPSEVR
11712	25613	A	11814	108	2	CVGLGFFVCLPFETESCSVAQAGMQWH DLGSLH
11713	25614	A	11815	166	289	SHSGWNAVWRDGSGLPLTPGFKRFPCLR VPSSWDHHCAPP
11714	25615	A	11816	192	2	DRDEGKVTRPFLLLCIFYFLICYLFLRRT LAVSPRLFSGRGCSSEPSHRCTPSWVT EQDSCRK
11715	25616	A	11817	228	343	LLQYSIQNEDAGAWWLTVPVITLWEAK AGRSLEVRSL
11716	25617	A	11818	322	407	VLRMLLHCLRECKLVQPLWKTVPWQFLKD
11717	25618	A	11819	119	1	WEKIVRGKKCKRNTHTHTHTHTHTHTHT THTYRESKRLRV
11718	25619	A	11820	269	1	FVQVFYILWQTSFCPLTCCQWFLGYHLS SVSNRFRMRSGKSTFFMTSEFFFMES RCVTQARVLECSGSI SAHCKLHLPGRPH SPALV
11719	25620	A	11821	217	389	EHTETVYGLGISSEHNGKGLFKMKMLTI WKDYDQWQWLMPIPALWEAEGGSRV H
11720	25621	A	11822	188	1	GSHMPCRVSSVSHESNNEFPAPVTSYPA NPQPRERAWNRQREKDKKERSQSRVGR VOAGLV
11721	25622	A	11824	126	3	KLQGGVQWLTVPVLPALWEAAGRSPEVR SSRPASTWRNLV
11722	25623	A	11825	224	3	ALITKKEVSAMELEGNRIQAYGVQST GARDYHAASRPVPAIKGTHHARVIFVF LVETGFHHVQAGLDS
11723	25624	A	11826	3	364	HELPEPLRVLTARHVARMAPGSRSTLL AFALLCLPWLQAGAVQTDPLSLFDHA MLQAHRAHLAIDTYHEFEETYPKDKQ YSFLHDSQTYFCSDSIPTPCNMEETHQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
11724	25625	A	11827	2	376	KSNLELLR ARELPETITVLRTAHLKAMAPGSRITYLL LAFALLCLPWLQEGAAQDTDTLYMLFDH AMLQAHRAHQLAIDTYHEYDETIVPKDH KYSILHDYQTSFCFSNSITTPYNKEETQ QKSNLELLRISLL
11725	25626	A	11828	288	3	IHTKNPSVHHHHQRPRVDKTTKMGKKQS RKTGNSKKWSASPPPKHSSSPATEQSW TENDFDELREEGFRSNTSELQEEITQTK GKEVENFEKN
11726	25627	A	11829	107	1	KRSGVRLQRGLVRWLTPVITPLWEARVG GSFEVRC
11727	25628	A	11830	220	354	QGNKSFKNIIAPWLGTVAHACNPSTLGG QGGRITGHEITILANM
11728	25629	A	11831	273	352	ENLKTGGIQWLTPVIFALWEAKAGRS
11729	25630	A	11832	239	488	SQTHCSGKTENSHGTSNDRNQVPTALHK RPSSPARFLTTRAVPVPPVDYLQSVAAFA VSAVASQWERTQKFPNPLLGETYELIR
11730	25631	A	11833	189	294	DQTRWLTPVIFALWGAKASGSPVRSLSL HFPLLF
11731	25632	A	11834	1	332	GTSPEPLTVLMTGDLALAMAPGSRITSL AFALLCLPWLQEGAVQTDPLSLRFDHA MLQDHRRAHQLAIDTYHEFTVTPKDK YSFLHDGQTFCCSDIETPSANHET
11732	25633	A	11835	330	175	PRELAQGSFENVRSVRKPRGQFOMFFF FFWROGSCSVAQACGVQWHEPEQGE VFVETGSRSSVAQDGGQWDLSSLPQPP RPRA
11734	25635	A	11837	267	334	SNVQWLTPVIFALWEAEAGGSP
11735	25636	A	11838	180	2	SVLEKKEKNLYKNLFTYLLKKVQGTQ CEGRAQICSVCCVCVSVCTCHVCAYV SSC
11736	25637	A	11839	183	2	AAPLTSSAQAQAGKPHLAPNSFFKNFT GRGQAQWLMFVIPALNEAKVGRSPEVRS LSSC
11737	25638	A	11840	54	330	DPNQGLPEPLKGLWTAHLVAMAPGSRITS LLAFGLLCLPWLQEGAVQTVPLSLRLF DHAMLAHRAHQLAIDTYHEFEPEYIPQ DQKNSFLD
11738	25639	A	11841	117	344	IQYVRQINITEMRNNSYLNHTSLTITI HTCLMGSYLEHFQNGCKGRARLMPVI PALWEAKAGRSFVDRSSKPA
11739	25640	A	11842	750	968	RAQGRWILKIPFSSFFRLFPLPLVFL YNSPPLFPFPFRTNATNNSFPFPLPFP LPFSPPPPSPSRPPPS
11740	25641	A	11843	757	1000	VVELVWYCCLFSPFFFLSPLFPFPFPF SPHSPFPFPFPRPLPLAPTRPPPPPS LFQAPPLLPSCFSPFPFPLSLFL
11741	25642	A	11844	278	361	TLLFFFFFEMESHFVARAEVQWRDLGS
11742	25643	A	11845	260	2	GSCLLEGKLTNRKDIHTNPSVHHHHQR PKVDKTTKMGKKQSRKTGNSKKQTSPP PKERSSPATEQSWMENDFDELREGEFT RA
11743	25644	A	11846	194	2	TKFAKEPSPPFCWQEVFKTSPLGFFFCF RSFVNGFRLKGLFFHETESCSVAQA GVQWARA
11744	25645	A	11847	219	1	SLGHTLKQSESSLFSFGGTPLLEFKPS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
						VYDPSVPPFQVSKGGCVGFFFFQTESC SVAQAGVQWHDLSGSPA
11745	25646	A	11848	126	3	RFFFKGLFLHPPFFPPFCFETESHVSVA QAGVQWCDLGLV
11746	25647	A	11849	216	339	KCFKVGKVKRLNRETIFYLAQNFFDRNWA TQKVVVKTLLLELI
11747	25648	A	11850	190	334	VSYHIEMSFPEVYNEKIHDLVCKDENG QRKQPVRLKQF1ICFELFL
11748	25649	A	11851	198	352	SRGGTGWTHGLECFVCLPVLFETESH FVPRLECSGAISAHCTLHLPGEL
11749	25650	A	11852	371	1	PFKLGGVQVTFPFAFAFWPLVFKKKG FPQGNLVLPFFSKVSGVGFPCPKPF SGWGAFOIGFFINRGKFFFLGFFL KKVFLKFLAKFFPPFFFPETESHVSQA AGVQNRSLGLV
11750	25651	A	11853	176	3	KGGFPLDWSMVKN1IVKFGEDLQISK LHTFFFLTESRSVAQAGMWCDSLHS C
11751	25652	A	11854	281	375	QLTFKKYFLGWARWLTVPV1PALWEAKAG RSP
11752	25653	A	11855	146	356	KCGALIAETEVPLFSELRDFLLAYSMT ELCFKRCVPSLHRLDAVDDCLHSCS CTDYPINRSLMNAV
11753	25654	A	11856	136	1	LSLICEFNNWLEMEYRSVSQAQVQWCD LSSLKPPPPRLQOCHSC
11754	25655	A	11857	277	361	IVLRGAMWLTVPV1PTLWEAEGGSFEVR
11755	25656	A	11858	295	152	VVFGFGFFETESHFVAQPGVQWNLGSL CSLRLPGSSNSPASAFOVA
11756	25657	A	11859	1	342	GTRLPEPLTVLWTAHLGAMAPGSRSTLL LAFALLCLPWLOEAAVQTAHSVRLFDH AMLQAHRAHQLAIDTYQSEETIYIPKDH KYSLLHDSQTCFRFSDSIPTPNMEDTQ HK
11757	25658	A	11860	244	332	TIEMMLDIKIQIVIFLFEFKMRKRIART T
11758	25659	A	11861	1	339	GTRVVTICQVQLHAYAHFLYFFEMEARS VAQAGVRWCDLSGLQPPPPGSSSSSSS S
11759	25660	A	11862	311	394	GMLGAVAHACNPSTLGGLGWITCSQEF
11760	25661	A	11863	130	1	VPPSVRTFFFFFETESHRSVSQAQVQW YLGLLQAPPPGSTSC
11761	25662	A	11864	3	320	IMMYALFLLSVGLVMGFVGSPPSPPIY GGLVLIIVSGVVGCVIILNFGGGMGLIV FLIYLGGMVVFVGYTTAMAEIPEPANG SGVEVLVSVLGLAMESVGLVW
11762	25663	A	11866	165	309	GLILLPMLECDRISAHCSYLLGSYDP SDSGSHVAGTTGTCHYAWLR
11763	25664	A	11867	208	314	GSRNKLGGQAWLTVPV1PALWEAEVGS PEIRSR
11764	25665	A	11868	102	1	KKFFFFETESHVSQAQVQCNGLSLQA PPPRPT
11765	25666	A	11869	126	3	NNALQLHSSYCKPKFFFLKTESRSLTK AGVQWCDLGLLQ
11766	25667	A	11870	1	273	KQLPVNPLNWRLELHGLLCTLNLSKPC MIFILVIVKVPFLPCNFKPHIISQA QNPPTV1PALWEADMGSHGYWITIVD FMCATLT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H-Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
11767	25668	A	11871	126	2	FPKALLVVFFFFFFPFTESRSVAQARV QVHNPGSLQCPLR
11768	25669	A	11873	269	9	OVSGKFWPDIYFKTGEKGLQCPNFPQGH PPRGLKKKFSKKKKKKKKKIAVGQAQ WLIPIVIPALWEAKVGRSPEVKSSRPACP TL
11769	25670	A	11874	114	1	LEAKPGVFGSGVLLVLIFFFFPETESHVS QGVRWCDLG
11770	25671	A	11875	146	1	GNHLSRSRGVDQDPQRHQKTLISLQKIQK VAGPGGAHLQSQEVQVGGSL
11771	25672	A	11876	2	159	SLQFFFFFWRFSFVLVAQAGVQNHDLGS PQPPPPGFKHSPASASQVAGRGR
11772	25673	A	11877	124	240	FRFSSGQAWNLTPVIPALWEAETGGSL EARSRPDWR
11773	25674	A	11878	135	5	QVLPIYFFSDSFTLSPRLECSGVTLPHC NLCLPGSSDSCASAS
11774	25675	A	11879	170	2	GFFFEKPKWYKNSFLCFFFFFPEFEFC SVAQGVQNLHLGLSQPPPVFKVDAAP
11775	25676	A	11880	97	267	GHGHAHLRGLCVLSLGFHHIPAPSVGTS DAEECCLCVIVRLICGYISRNCILYSDH R
11776	25677	A	11881	1	292	LEPLRLVLTAHLQAWAPRSRTLLLAF ALLCLPWLQEGADQTPVLSRLFDHAML HAHRAQLAIDTYQFEQTYIPEDOKYS FLHDSQTYFCFS
11777	25678	A	11882	93	2	KYQGMWANHLPVILALWEAAGRSPT SC
11778	25679	A	11883	145	2	PPLGLRLQVQAPTGGFFFFFETESRSP RLCKKGAILAHCNVLLIV
11779	25680	A	11884	202	1	TWNRKGVTLVRLVMNCRPCDRHKASQ LIGRVQRQENGLNARVGGCSEPRSRHCTP VVWTSBNPSSC
11780	25681	A	11885	42	155	GERSGLSPGVQDEPFGHSGTSSILQKILK LAGHGTCF
11781	25682	A	11886	215	1	STMARHCPLSPMLFNSAMEVLVRAISQE KEIQGQIQGKEEVQLSFTDDMI FNLEK RDCSINLLQMLV
11782	25683	A	11887	214	1	GYFFGLNVLAKLEKPSLKVQPNPSPKR PFLGFFFFFETESRIARLECSGAISAH FNCLPGSSDSPVSC
11783	25684	A	11888	215	3	WGQFFFFFSSFFFLRLQGLAVLRKCSG TITAHCSNIFLGSSDPPASVSLVATTG HEPSITQPHSHSGC
11784	25685	A	11889	118	1	RFPIGENPTKFFFFFETESLLPRLECS GVISAICNLSC
11785	25686	A	11890	267	83	HCLRSVGQDPGQGHKNFSIQIKQKLTAF SFKSKSLIVIPPLPFKNDKDSKSSCS LSPHS
11786	25687	A	11891	134	2	DLAVLPRLECSGMFLPLPRLSRKFRFS CLSLPSNDYRGAPRA
11787	25688	A	11892	116	1	SKGVGHFLFFFFFETESRSVAKFTGVQW CDGLSLCLLV
11788	25689	A	11893	397	475	RFVCSSTIKVLRDLSSDRENPGRLST
11789	25690	A	11894	115	331	KNVCLFVFMKNHLNPGDEGCKSPRSR HCTPSWAAQDSISIKYICICYRVLIDY LSKLVVLRINQLPNS
11790	25691	A	11895	134	251	INPPIVSRKKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						KKKKKKGGGL
11791	25692	A	11896	186	402	PGKNLTLENVPRNKVGEKAPGQNEPVP LGGEGYQDPGNGVKGWGPFPAPGFKDG PKRLADTFDLIEGDDG
11792	25693	A	11897	100	2	KGPPPPPPPPPPPPPPPPPPPPGQSQVKLK SPKCK
11793	25694	A	11898	92	3	SVARIMPVALFLLSVGLMVGFGFSKFP S
11794	25695	A	11899	283	362	MTYTMTHVAHWASVCLLNHADDPLD
11795	25696	A	11900	248	1	VMSAQPLSVILRFMGKKSNNWGMQYTE SEVERYDRGRARETERQRDERERENP RNRKLFFYGRFKHSPODFMPQKVHF
11796	25697	A	11901	253	2	KLOENPFKLNFILNLCVSLNVPILN INIKPSFIAPKPCPSKFORNYIYIYPS IYLSIYLSIYLSIYLPITISKVLKDVE
11797	25698	A	11902	179	3	LAVTKNEIMGFSFTWMEGDNIFPPPPFP ETKSHPMVRLCSGVSAHCNLRILVSS SC
11798	25699	A	11903	1	403	GTSSQESFGGCVSGLIAMGTRAKGERK LLCLFILAILLCSIALGSVTVHSSEPEV IIPENNPKVLICAFYDLSFFSSSFSYFF HLGFFIYPPYLPVSCPTFYIIVLLSFI YSHLSSVSYYSVLLIYTFIL
11799	25700	A	11904	37	242	KGPTRDQLQHPKARLPAPLVLWTAHLA AMAGSRTSLLLAFALLCLPLWLIYDGAS HIVSLFMLFIIF
11800	25701	A	11905	1	298	GTSGHGRGRKDSRTGSHSSSDHPGAKLLS TEEKQAETMRPPSAPPGRGCIWQGLL LSSS
11801	25702	A	11906	225	30	ACYLQKDGAFALPDVLPDMFGHSSLY PCQHAECCHIKNINVCVCVCVCVCVC TVICKLV
11802	25703	A	11907	196	320	HSSESSTPSQDTHHTHTHTHTHTHTHT HKIPQRELLPSVPD
11803	25704	A	11908	130	3	NGPVFSPPPPPPPPPPPPPPPPPPPPP CDLGLSLQSLPPGFK
11804	25705	A	11909	381	2	ASICGQKLIFFQHKKIILVQGVQLQKK NSTLKRWEPLSFQPPAPPLGSLKGIN ILNKGAKLLKGTNPDPGIVFFSVLPP FFGLKKFKKKVPHQKSPPPPPPPFPETE SRSAQAGVQWHD
11805	25706	A	11910	138	2	SVPLKEFTISQARKLTPILPALWEAEAG RSEPVRSRSPASTWRNP
11806	25707	A	11911	231	54	IRASFGIQIRICLTITTTTTFFFPETE AGVQWRDLGSLQPPPRQEQNSVSKQTK TN
11807	25708	A	11912	3	461	DAWGRVEGPPPLRPATSRRWAGFTLWRM EVTGDAGVPESGEIRTLKPCLLRRNYSR EQHGVAVSCLEDLRSKACDILADKSLT PVTLVLAEDGTIVDDDDYFLCLPNTKF VAMANEKWAYNNNGGTGWISQESFDV FEAYSGATLFFF
11808	25709	A	11913	318	407	LCGRLLWMLPVTIPALWEAEAGGLKLR MR
11809	25710	A	11914	340	5	DRVAKFSEARLFLPPPPPPPLKIFCFPR GFKIFRGVCPLLFPPEWGLFKQGPGRM LFFPPPLGGPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
11810	25711	A	11915	274	385	IKPQRNGETRAEKLKSLKIRVPLLQRN AAPHQQMNK
11811	25712	A	11916	259	441	DTKLPKVNIKLNFHALKKKKKKKKKKK KKKKKKKKSSSLRG
11812	25713	A	11917	254	402	LIVSVIDFLRWRLPLLKLECSGMISAH CRLRLPGSVHS PASGCQLLR
11813	25714	A	11918	223	1	NINSRKKFFFEVSSVPVFFGVFFPSP LKGSRAPLKLAWRPLPLPFFLEMSR SAQPEVQWCDLGLSQPP
11814	25715	A	11919	97	3	KPFFFFFFFETESRSVTQAGVQWRD LGS
11815	25716	A	11920	154	384	KEFFLMLEFELPPPPFFFFFFFLGKGLF FFPPGGGGGGQFTS IGPPPRGKKDPP SPPKMGCKRGTPPPPGYFFFP
11816	25717	A	11921	225	369	GTLNLLTYTKISWSGAVHYNPSTLGGW GKWNITSGQEFETSLANVVKP
11817	25718	A	11922	116	372	MEYTNKQWMSYNIHLYOTYKNSVIEHP TGVLPHSRVIMVNNIVLCISQKLELLR RLMWEEHLSPPGGGCSSEPRSRHCTPAWA T
11818	25719	A	11923	271	409	KKKKKKKKKKKKKKKKKKKKKKGGGA
11819	25720	A	11924	121	228	KKKKKKKKKKKKKKKKKKKKKKKKKKR GGGPKKKPWGGQK
11820	25721	A	11925	55	423	NKPKKKNFLKKKKKQNFPPFFYPLKEFFF PKSLNFFRRVVPKISPPKKKFFFKNSPS VFFFPPLKKKNFFFLTPLKFGPPKNFFK RPPPLFFFFFFFFFFFLGSGNCIEKL
11821	25722	A	11926	253	443	YQHQRPKVDKSMKMGNRQKKSSENSKNQ NTSSPPKDHNSSPARQONWMEFGLT EVGFRFN
11822	25723	A	11928	175	413	KKKKKKKKKKKKKKKKKKKKKKKAGG A
11823	25724	A	11929	490	182	RKQRIKGCKKPNPLAQGGVKKKGKGGP PNFFLKQKQDQLKNNWNLGKKKPIPP QVSLRQKGFPGRIFFFFFETESCS VAQAGVQTLSYKNNKIK
11824	25725	A	11930	110	2	KKIPKPPFFFFFFFYYFKAGSHLVAQAG VQWHDLAS
11825	25726	A	11931	169	987	YLEKTHSHSRNSNDQEELLDEEINEDI LANLSABELQSEMEVAPPSLPGV MIQDQTKPTQNTGNSLVDYMWKEK ASRRMLEEERVVPTVEKSEKTOREHE IEKRNKNMAQYLKEKLNEIVANKRESK GSSNIQETDEDEEEDDDDDDEGEDDG EESSETNREEEGKAKEQIRNENNNQQV TDKAFKEQDRDPAEQOSEKKISKLDK KLALDTSFLKVTRPSGNQTDLDGSLRR VRKNDPMKELNINNENIRK
11826	25727	A	11932	161	389	SVQTHPNLRSCSVLNAMHFFLLGYVIS GCTEPAKAIKPIDRKS VHQICSGPVLS LSTAVKIKVGNSLDAGATNI
11827	25728	A	11933	134	289	ASTQNNQMLRLNNSPTLLSLSLSHTHI HKHTRMTHTHHTHTHTYPTTKV
11828	25729	A	11934	128	1	IKKGEFFFFFFFETESHSPRLQCSGTI LAHCNHLGLSSNS
11829	25730	A	11935	131	19	MYIGWQWLTPIVLPALNPKVGASLEAR SLRPARTSE
11830	25731	A	11936	104	3	LRGQLIRAQNLMPVIPSLWEAMGRSFE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						VGSSR
11831	25732	A	11937	146	2	GGRLGIIYHAWNDEGFFFFEMESC SVG QAGVQWCHLSSLOPPHGGFK
11832	25733	A	11938	149	1	DKCFLCVCCLFIFIFILLIYVFFETESC SLAQAGVQCCNLGSPQPLPLA
11833	25734	A	11940	176	380	QSAVALPRLECGNMLAHCSLHLLGPKR FSCLSLSPSSWDYSLRLNYQGGRRWSKTH QAWCQSLTILWN
11834	25735	A	11941	133	415	KKKKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKGG
11835	25736	A	11942	222	420	QGDKFLDNNTTILYMEKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKYR
11836	25737	A	11943	163	425	KNPPKNSQLSPSTLKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKTG
11837	25738	A	11944	143	3	KMGKKQSRKTGNSKKQSAPFPKERSSS PAMEQSWTENDFDELREE
11838	25739	A	11945	200	3	QNSQVGYGAPHKETMALQARVNLGFPF RGPLKRPALFFFFETESPSVTQDGQVQW HDLGSMQPP
11839	25740	A	11946	221	3	RKIEGQPSSTRKSVRGVRCFQPLGLGFPF GGLFFFFFYETESCSVARLECSGVVSA HCLHLRSTNEGRGR
11840	25741	A	11947	68	177	ISSSPKNCCLCKKKKKKKKKKKKKKKKK KKKKKKKR
11841	25742	A	11948	210	329	RHHTHTHTHTHTLSLSLSTHTHTAHTL MYFLAFLDLRS
11842	25743	A	11949	183	20	LGTVAHSCNFVFLSRLGFLHVGKGLRL PTSDDPPTSASQSGTGMSPCTWPE
11843	25744	A	11950	232	329	VGIRKMSISSDEVNLFVYRYLQESGFSHS AFTF
11844	25745	A	11951	412	239	LFYEKGSRFVSQAGLELLELQKSPCFGL PKCWDRHEPPRQADLPFCVPSANASW L
11845	25746	A	11952	310	393	PHTDISGTPEIMHYVHVHVVTTQPRNKP LSSWPTLISGAPKAENAVENDDSRI LRGFFVLCFVLFRRQSLALSRLSCSGV ISAHGNL
11846	25747	A	11953	193	3	SVQTHPLRSCSVLKNAMHFLVLTGTEPA KATKIDRKSVMQICSGPVLISLSTAVK KTVGNSLDAGATNIDLKLDY
11848	25749	A	11955	100	1	AHLKRVFPIFFFFEMESHVSVTRLECSG TISAH
11849	25750	A	11956	35	521	KEKFFPHAGVYVGGPPRNLKRAPLFFFF FFFFFFFFSEFFFS
11850	25751	A	11957	214	1	KKKTFPFKEIFYPKLSRKKKNFPRGAK ILNLSIFPEKKKIPSPSPFFETESCTV AQAGVQWHLGSLQF
11851	25752	A	11958	114	1	RYFSGQQAQLTFVIFALWEAEAGRSPEV SSSRPALWTW
11852	25753	A	11959	188	12	SKCQCTFFSNFKTETEMESHYLAQAGLEL LGFSLHLPSTVSQTGVTGVSHCAQNAH LY
11853	25754	A	11960	241	556	SSIFPLFNKHLLSFSTLSSSLGREVS IQ DMCQGTQKQPPFPPLPHVFLHSIRDGE LCVGRDVHLTCQTDLAQVFCFLVGLV LSLPRAGVQWCHLSSLQPPPP
11854	25755	A	11962	362	462	KTGQALTFIIPLLWEAEAGASPEARSSR

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						SAWPT
11855	25756	A	11963	43	2	CCCYCCCCCYCC
11856	25757	A	11964	30	415	GLGFQKQIFFFFLGGQGNFDLLRAKKR PFLPPFPFKPKNGRVFLGSPGVKPK RPRQGDVFLKPRSLGVFLTSKKTPLGP WANFPFPFGDP
11857	25758	A	11965	149	2	SKTWLKAAYLNTYPCGWRMLIPVIPA LWQAGAGELHEPHILRPAAW
11858	25759	A	11966	179	3	KKNTFFFPBPKFGPFGFKPPPLFPFF FFFFFPPETESRSVAQGVQLSIGSLQ AP
11859	25760	A	11967	245	382	DVTDGSKMHPDFRSHVKKMLGVVAHACN PSTLGGSRGQEPKTSAN
11860	25761	A	11968	264	10	LSTLECKGVSPGVSPKGRKGLGYIFS PFLEKPHIPLGISMYFFFPFDGVSAQA AGVQGRDLGSLHLPSPGSSYSCASASLS S
11861	25762	A	11969	326	406	RLKKGWALNLTVPVITFLWEATVGRSPE
11862	25763	A	11970	120	1	KGYGFFFPFKPLGPPFFFFATESCSV AQDGVQWRDLGS
11863	25764	A	11971	84	370	RNGAELKTLAQTITINCRYSWVTLV LGDLESLCWHIFKKNLFCGPFSSFL LGAGRMKSHCVRLRCRGMISAHRNVCL LGSNDSPCSAF
11864	25765	A	11972	196	3	SRGKMGEYFPVFLKPNPSWAKAGNGKNP FFFFFEAESCSVAQAQVQCNLGSQAP PPRFTTPRA
11865	25766	A	11973	559	644	KYGCSAVGVAILLFLVFNKLAFTLWKK
11866	25767	A	11974	3	391	HEAQLPEPLMVLGTGHLAEMAGGSRTYL LLAFGLLCLPNLQEAQAQTVPLSRFLD HAMLQAHRAHLAIDTYQELBETYIPKD QKHSPLHDSQTSFCLSDSIPTPSNMEET QOKSNLELLRLSLLIE
11867	25768	A	11975	138	365	LKFECHSTLCANHGKQTFVFYFNKFL KYTFYSVLTYAINWYIKNLINVFKKKK KKKKKKKKKKKKKKKKKK
11868	25769	A	11976	275	433	MSILDLSKARNFLSFLBTGSCSITQAG VQWLNHSLSQPTPLGRDPASASQ
11869	25770	A	11977	108	3	RCGLFFETRASPCRFGWHLNLSLQPLP PFRKRP
11870	25771	A	11978	270	408	FENNVLGRLAQNLTVPVIALWEAQAGRS PCPENQNHDPYKGNWPBY
11871	25772	A	11979	228	441	QALKFVIEILSLSKCLDVSYFNHKKK IELLQKKKKKKKKKKKKKKPSQKKKD SSRGKDS
11872	25773	A	11980	2	447	GALALNKTADVNRNLFLVSGLHNKRNL QOTSLSKMWKIKCSILKKKKKKKKKK KKKKKKKKKK
11873	25774	A	11981	124	445	KYGEIMSONPARGGPKPSKNGYSEHLR HCCPPTFLISKKEIGDRKYSICKSGCF YQKKEEDWFCPCQKTKTSRRAKSLKRP KQKPVAPPVGGVAKAPKPSRLPRF
11874	25775	A	11982	48	429	KESNGSQDRLLPKIHS PDVSGGSGGMS QNPARGGPKLSKNQKSEHLRIHCQPLP PFLISKKEIGDRKYSFGKSGCFQKKKE DWICCPQKTKLGGKIRPPPKNGPGGS LNGRTTWVSLGFVHN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
11875	25776	A	11983	419	500	SLLVKVEKQWPGAVAHACNPSLTGGPG
11876	25777	A	11984	362	496	LWSEYRITLLLEKAWAHVTVTPATWEAEV GRLEPRSLCNMVRPIS
11877	25778	A	11985	142	433	RFVCSITIKVLRLDLSDESNPGRLSTGN SSLKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKGGGGGVIKKPLGGPIFGGGG KEKFFFFGGGFIN
11878	25779	A	11986	177	2	CQRNWTLSHHTHSITRFLQQLKKGNSP GAVAHTYNPSFLGGQGGVTVYVHRTGR TR
11879	25780	A	11987	178	443	DKKKKKKKKKKKKKKKKKKKKKKKKKKK KKI
11880	25781	A	11988	329	410	LIFFFIFFERESHSAQAIVQWHDLGS
11881	25782	A	11989	146	1	DRASALQPGQGRNPNVSKNNNNVIYII NTLTITIFLGTITYDALSPLE
11882	25783	A	11990	240	420	GVFAPLLGDVSGSGVTOFRDPLEBAVCL FLELECHAERTTALFRAVRQGLSLQNL SVAF
11883	25784	A	11991	239	410	GTFLFIYLGDLFIYFRNKSLTLFLPLEC GGVIVAHCSLDLGGSGYPSISALPSSWD C
11884	25785	A	11992	126	3	YTGEYKSPCHKDTCTHMTAALFTIAKT WNKPNGRVGGV
11885	25786	A	11993	300	22	SQLLGLRLQENHFNWGGRCSEPRSCHC IPAWATTRANSIFCGPQASSVEVRRSARK KLPSDILKRHTISMRVSGLLLVDSYFG RLATPVRAQ
11886	25787	A	11994	303	2	EGEIEFLSPSPPPFPGQENPGNSCPPLF PFGTFLDIRVAGSHKVGQAGVFKRPPS LHLFLIKRFFFFFETESRSVPQAGVQ WRDLGSLQTPPPGFKR
11887	25788	A	11995	171	457	SFSDHLLIGWIGFCNNLSKIALCSSPIK NKMDLQKKKKKKKKKKKKKKKKAKASS SYQDSS
11888	25789	A	11996	357	204	EKTGFPHVQAGVDLTSRSTRLSLPKC WYRHEPMRLAGHYIYYPOMK
11889	25790	A	11997	219	1	PRVFWAPPRIYFPGALFWAFREPGVSLG ARAPTAKGPKQKAGRTGTTTTFEMESH SLPRLCNGTIIWAHNCNL
11890	25791	A	11998	254	1	AHLRGNRLPKHTFFQYMTTLNKAQFSV GRQSYSPWRSFYTSLFFKYSCVFHTHT HHTHTHTHTLYFQIMVLLLSLRKKGS
11891	25792	A	11999	167	2	NFKSFFQGLSRGVLPKPNVFFLETES CSVSQAGMQWGLDLSLQPPPTRPPTPR
11892	25793	A	12000	104	3	RPWTFFFFSETESRSVAQAGVQWRDLCS LQPPP
11893	25794	A	12001	178	2	KIFQGAQNSPWGLFRFGGKNNKKGAPFC QKGFGRFFFFFETESRFITQGVQWCDL GP
11894	25795	A	12002	163	282	GIGGEWLSKYVIKIVKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKK
11895	25796	A	12003	195	2	KWGRITPLKGGGFCFTKKSGVAQTLLIKSP PPAFFVVFIFFFLETESRSVAQATVQWC DLGSLQAP
11896	25797	A	12004	152	1	CFVDVSAERLRPKDFMTTKTPKAMATRAK IDKWTALTKLSFCTAKETIIRV
11897	25798	A	12005	359	1	EVVPIWPPPKRRVLRSVKSGQFISAPIR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
						KKFPCCQVGLILAFPRVLLIGRPPFFFF GVLVVEIQRWISFLVVVVVRARIMYA LFLLSVGLVMGFVEFSSKHCPVYGALVL VSIGGRV
11898	25799	A	12006	189	12	DGRLPGSVCCYILI FLRQSFLLAQAGAQ WCHLGLSQSPPGFKRGREVRIRAVRG DQ
11899	25800	A	12007	131	3	KIFFFFFFFFEMESHSAQAQVQWRDLGS MQDPPPGFMPLLFY
11900	25801	A	12008	150	2	IILFLVPIEAVFFFTVAEAGVQWHNL SSLQPPPPGFKQSPASASRVA
11901	25802	A	12009	305	3	KFFSLKASTGRWNGFLFTTPPKGGLFP KIPIHQVFGGGLWEKQLGKAGLNGQPY KGFFKGAARFFFFFETESRSVAQAGVQ WRDLAHSVAHASAS
11902	25803	A	12010	263	517	DKGFLPPRCVCGQDLFFYGGIVFHGG YGPFFFFFFFKAESRVLVAQGVQWQDLR SLQPPPCRTGRSP
11903	25804	A	12011	107	374	WMGTWGLPVLITRSTCPPRSRLRLH TGATIWIFRLFETGTIVLPMLECESTVIN AHCRLQLPGSSSSPTIASQVAGTKAHL DCFVY
11904	25805	A	12012	144	261	FPKKNINPVFTFLQDPTGTFISLDRIGL GTYGRIVLVS
11905	25806	A	12013	371	3	IFHLRKIFTFLPGLFWFIRLLSEKKPK RFVWKIKKFKNGYPLKNPINKYKGRPF FFKGEKTPNGKVPVLPKKIKIPFSKALG FLQKKASKPPFFFFFTDCTVDQSGVQ WCDLGLSLQAP
11906	25807	A	12014	101	3	RGAFFFFFFFETRSKSVIQAQVQWCDLGS LQAP
11907	25808	A	12015	205	2	VFNPSGINVMYDAIILNKLRLATIQOH IKQRIILDQVGFHGMQGWFSIRKSINV IQHINRPDKKN
11908	25809	A	12016	168	1	GCVCQFQKRLGNGGLNGFFFLFFFFFF EMKRSRVVQAQVHWRYLSSLQTPPPEFK
11909	25810	A	12017	311	2	RGLRFGQWKTMENPNTFFSALRPGQLS SIRISGLLHTYPLGLDRSEPLSCSILSS KYVVWQAVTSALSSNKPASQGHWDKDF FLFFETESCSVTQAQVQWH
11910	25811	A	12018	383	247	LVEMGRHVHGQDGLDLTFSQSAHLGLPK WWDYRREPPRLATIEVL
11911	25812	A	12019	2	379	KVLVTAHLAAMAGSKRTSLLLAFALLCL FWLQAGAVQTVLSRLFKRAMLQAHRA HQLAIDTQYEFISWGMEAYITKEQKYS FLHDSQTSFCFSDSIPTSSNMEETQKQS NLELLHISLLIES
11912	25813	A	12020	3	389	PEPIRLVLTAREGAGAGSRTSLLGLFA LLCLPWLQAGAVQTVPLSLFDHAMLQ AHRALQALDITQYEFETIYIPEDQKYSF LHDSQTSFCFSDSIPTSSNMEETQQTNT LELLRIFLVLIELWLD
11913	25814	A	12021	247	386	PMLGHVSGSGGNGVRDPLEAVCPPLAKL KHCSGRSTALFRAGQRKR
11914	25815	A	12022	17	371	PLRDLTAHLAAMAPSFRFDLILAYALL CLPWLQAGAVQTVSLYRLSDHMLQAH RAHQLAIDTYHEIETIYLKDKQKYSFLH DSQTSFCFSDSIPTSSNKEETQKQFYLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						LLPISL
11915	25816	A	12023	3	359	LRALWTADLGAKAPGSRFTLLLASALLC LPWLEAGAGQTVPLSKLFDHAILQAH AHQLAIDTYQELERTYIPKQKHSPLLD SQTSPCFLDSTPSTNMEETRQKSNLEL FRTSLLL
11916	25817	A	12024	2	363	PEPLKGLWTDHLGALAPSSRTSLLLAYA LLCLPWLQAGAGGTVPPVTLFPHAMLQ AHRAHQLAIDTYHELDETYMPBDHKYSF LHDSQTCFCFSDSITTPYNMEETQHTSN VELLRISL
11917	25818	A	12025	314	393	GGAWWLTPVIPAFAWEAKGGRSLEARS
11918	25819	A	12026	80	392	PLIACSFLLFLFFFGFKILFLPPKRWK GGGIWVNGNPGFRQAFFLASSKKPGM GGPPLTPGKRFVFLKKGFSPGGPGGSK FSAAPTPTTGPFGWEIPAK
11919	25820	A	12027	165	2	WQKLLFHFGTESCSVARVGVQWRHFSFP KPPPPFQKLSAPASVADRRPPDAN
11920	25821	A	12028	1	338	VFVALKFLMCLSVCFISLENTYNSLPL QKNCLPLIFFFLPFEMEACSVTQAGVW GDLGSLQPPVSHNLGGGCGCEPRECHC TPCSRPGDRDFVFNKNTMIQDNLHMLT
11921	25822	A	12029	2	315	HEERERERERERERERERERERERER VGGETYKAEPLRVGGAAQKRAHFSARG LFMEICGDMCGEKGKPPHSLTEECLSR CGERFFDTSLAITRGCAQSV
11922	25823	A	12030	216	3	ERIIIFRGVRGNRLFSGRDITASPPLFYP PRQTHKRGVEDRHERGERERERER RERERERERARAP
11923	25824	A	12031	114	329	QTERNSININKDTHKTPSVGHQHQRP KVDKTTKMGGRNQSRKAENSKWKASSPP KEHNSPAREQNWMS
11924	25825	A	12032	177	1	TKKKTFFWQNTPLFSKKKTCRQKFFFFF FFETGSLPLRLVCSGAVLAHCSCLPGS AFL
11925	25826	A	12033	127	1	PSFFFFFPPNETESRVAQAGVQWRDL SLQAPPFGFITPSC
11926	25827	A	12034	47	314	GAPVASVSTSCFSCSATDGVVRNGKSTA GHQRYLCSHCRKTWLOFTYTAQPGTH QKIIDMAMVGVGCRTARIMVGLNLTIL RHLKN
11927	25828	A	12035	15	408	GAIFGAMGHFTEEDKATITSLWGMVNAE DAGGETLERLLVDYVPTQRFPSFGNLS SASAIMGNPKVMAGKKVLTSLGDATKH LDDLKGTFAQLSELHCDKLHVDPENFKL LGNVLVTGMAIHLGKEFTP
11928	25829	A	12036	122	2	KLVDVLPFGGGRVFFFFFPLETEHCS VAKAGVQWHDG
11929	25830	A	12037	154	1	GKPPFKLGFWGGPQRVRGRGPPFFFFF ETESPVAKAGVQNCDLGSLHL
11930	25831	A	12038	58	254	DPRVQRQRTTACHSLNPLGLQRPPLSL PSGWDYRHAPLCATQKILAYRVAQRERS AHGSYYQAS
11931	25832	A	12039	270	124	DGVLLLLPRLECNCAISAHGNLRLPGSS NSPASNKTKQNNKKTLSNKF
11932	25833	A	12040	63	355	LGRGTAAHRLWPKLSPASRVSYLSAAT NKRSPAPSRAPFMDNWERGGFFFT GSHRRRPGRMCSGATTAHCSLDFPGSE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11933	25834	A	12041	184	3	MGFTMFPSLVNS GVSRLLGGVSQLYGMYGVRDPLEEAVCLF SKLKHHPGRITLAFRAVRGCLSLQKFL LLFA
11934	25835	A	12042	118	3	DRVLLCYLGWECSGTISAYCNLHLPKSK RFSCLSLPSS
11935	25836	A	12043	40	436	LSEGLTKNRKDNHTKTPSVHHHHQPKVK DKTTRMGRIQSTKAENSKNESTSSPPKE HSTSPATEQSRMNFDELREDFRRSVI TNFSELKEDVFLCKEAKNLEKRLDEWR TRINSMEKTIINDLMELKMTA
11936	25837	A	12044	101	2	HLGQVRNLTVPVIFILWEAEVGGSPHRS SRDAW
11937	25838	A	12045	123	3	LTVTKLEPLGQARNLTVPVIALMEVKVG GSPFVRSRPA
11938	25839	A	12046	3	432	PIFGGGGRIFFFFFFFFGGGGVFPFKT KNKQFFPFLGPFKKILRNFFFLFFPFF FLNPFYFYGAPFFFFFGGGFFFLPFS RFFKFFNFPOGFFFGGGFFFLGFF FFFFFFL
11939	25840	A	12047	325	164	KNKRNRGGQARNLTVPVIALWEAEAGGS PEVRTTGVSHGTRPHLLNTVSYI
11940	25841	A	12048	187	381	LMDKRVSLWGDENILKVESNCGTITLYL LVCFEMESRSITQAGVQRDLSSLOPPP SRFKRFSCL
11941	25842	A	12049	84	464	SYRVFSPDITVLISRIQAEGEAGEKSPFC FPERVWCPRPFLSDLGRRLKLECGPDL DSTFLSFFFGGLTKGSHGALCEGSGVI RDHCGCLSGSGDPPISACLRVAGTGV SHHCIFCRQDLPGS
11942	25843	A	12050	232	20	LLQCSSRAKIHTSLTGCKLEMTKLSEE GMSKAEISQKLLHHGLVANAKORFL KVIRSATPEFRHAE
11943	25844	A	12051	401	518	FFETESCSVTQAGVQRNLSPLRA
11944	25845	A	12052	191	1	LFPLKKEIIFLPGPTNGAPPMFFFLKAP PLFFFFFFFFFFFVVNLFLL LSFLHILEP
11945	25846	A	12053	12	369	PLPTYSACIEVGSNPGQPGIDAKSVSHN NCYLKSKKKKSNQSNLLPKIHTFMG SQKTKGKIQNDPRGGPKLSKNQKYSKN LKKHCPCRLTFLISKREKGRNKRYTGKS GCFYQKK
11946	25847	A	12054	89	513	NFTVRSIPLNNIPMANLLLYLVPII AMAFNLTERKILGYIQLRGPNUVGY GLLOPPADAIPLFPKEPLTPAPSALFC FAAPALALPFALELCPPRPLGRP
11947	25848	A	12055	158	3	SQLTWPIMAQDSMCLNTVVFDDNIGWA WILMSVITPLWEAKVGGSLHSN
11948	25849	A	12056	113	1	KSHGGHGVVLVSVLVLAMEVGLVLVAV KEYDGAALA
11949	25850	A	12057	44	263	ARIARSAHEGKMPKRYTGARKNAENRPO RELQLKASRSTIDLAHAENALWYQLFL ISVGSWKNYILFYLYTT
11950	25851	A	12058	142	1	KKIFFRYKKGFSFFKFFRISLFFFFFFF ETESRSVAQAGVQWRDLGS
11951	25852	A	12059	12	347	QTERNSININKDTHETPSEGHQHRP IVDKSTMKRNQCKKAENSKNSASSPA KDHNCPLAKEQNWTEPHKLTVEGFRI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						ITNSVELKHEILTCCKEAGNLEQRLEEL
11952	25853	A	12060	245	3	MPEGSFLEITPETTRVFKKPKGFLGGV GPSLFLFFPPPPPPFFPMRQSLAVSRLEC NSAISAHCNCLCLGSSDSRSSSGSR
11953	25854	A	12061	94	3	KGGIFFFFFFFLRQSPSVAQGVQWCD LG
11954	25855	A	12062	108	5	NNLSGVRDQPGQHGETTSLKIQKLAR HGGRHL
11955	25856	A	12063	298	1	KKKKINTHAQKRGPPPPPPPPPEKGKAP PPQRTVKKGGEKDSFIPKREKKNPPL SFFFLVRVHVRERERARERERERERER ERERERERERERERAR
11956	25857	A	12064	122	1	VCEGCVGVGVDRERERERERERERERER ERERERERERAR
11957	25858	A	12065	126	1	ATCTKFRNDNRALLRVVFERERERERE RERERERERERESR
11958	25859	A	12066	48	351	FFFFFFFFFKGFKLVPPGGGGGGDIFL EDPPPLKKFKWGPPLGRGNKGGPPGW VNFGLFKKKGLPWPGGVKTPAFKGPS GPTPKGGNNRKNPPW
11959	25860	A	12067	1	365	GTRLTVLWTAHLVAMAPGSRSTSLDLFA LLCLPWLQAGAVQTVPLSRLFDHMLQ AHRHQGLIDITYQDEBETYPKDHEDSF LHDCQTSFCFSDSIPTPSMEETRQKYH LELLRLSLF
11960	25861	A	12068	174	1	PAWVMQHNVPVSLFFCFETESRSLTRLE CSGTISAHCNVRLPGSSDSFVPSRVAA RA
11961	25862	A	12069	270	375	TRIKRCNGGRAQWLTPVIPALWEAKAGE SPEVRSS
11962	25863	A	12070	197	350	KKIYIFLIINTIMDLIIPFLLDNILGFW LGAHAHACNPSTLGGRGWITRS
11963	25864	A	12071	3	378	HEQQLPEFLKGLWTAHLGNAPGSRSTSL LLAIDLCLPWLKRAVAVQTVPLSRLYD HAMLGAHRAHLADITYQIBETIYIPKD QKLSFLHEYQTSFCFSDSIPTPSMEET LHKSHLELLRIYL
11964	25865	A	12072	219	1	FSHPFPFGVFTPLVFPFRWEVLGSPGG GGGPPKKWAGVQKVVFPPPPFVEMESC SVAQAGVQWYDLGSPRA
11965	25866	A	12073	134	3	VFGPPPPPPPPFETESHVSVAQGVQWRD LCSLQAPPPGFMFSC
11966	25867	A	12074	175	357	MPINQPVKKMVCVCVCVYIYIHTPLY RVVMYMCYICVYIHYIWMCIYIHTV STYVW
11967	25868	A	12075	193	350	KIPIHLTSLYHTQNYLYKICGQAWNLTPV IPALWEABAGGSPEVRSRRPAPW
11968	25869	A	12076	252	1	GVEGFPFKGGGFVWKGFLGTPQIFWVG VFVKKKGGLWVKGLLGKPPPPPLFFFF FETESCSVARAGVQWRDSVKKKITARA
11969	25870	A	12077	273	366	IFIYLFYLFETESCSVSQAGVQWPNLG RLR
11970	25871	A	12078	127	2	KKKKTLLLLFFFFFEMESRSVTOAGVQW CDLSLQPPPLV
11971	25872	A	12079	206	334	HNRTVIVNNLIVHFRITKRCWTQWLTP VIPALWEAKAGSSSE
11972	25873	A	12080	135	2	KMKRFGEQDSQIPKTLQTQFFFLTESRV AQAGMQNCGLGSLHSC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
11973	25874	A	12081	147	3	ATTPGLPIFYFFPFTESHISIAQAGVQCM ISVHCNCLPGSSDSFVLV
11974	25875	A	12082	106	2	YFIPINEGYCFIYLFPEFTESRSVQAGV QWCDLV
11975	25876	A	12083	164	346	CPYKKRKNQAKWLTVPVIMLGRFRPRV DRPSSGVQDKPGQHGETPSLPKIQKKSQ AWWCA
11976	25877	A	12084	186	1	KSLSKGNFLFKGPPPPPPPPPPPPPPPP SRSVTQAGWAVIMAHCCNLNPGSPDP TPAPRA
11977	25878	A	12085	98	2	CPFFRVNFFPPFEMESRSVQAGVQRDL GSR
11978	25879	A	12086	154	2	SPTPEKGVWELSPFPSSQWPKINGCIFI FLYETSSGSAQAGVQWRDLS
11979	25880	A	12087	326	3	KTSVITTCGLPMWSSKGFPPKSPMWCKE CVCKFWANQTLKKNLAGRFQKPPSAA FLEMGGFFPFFPRFFQGSQPPPPPPPP BSCSVTQAGQCNLGLSLRPLPP
11980	25881	A	12088	154	3	KEFSFFAPGSKQRTSRSLRSPFPQVKP LFFFFFTETESRSVQAGVQWR
11981	25882	A	12089	174	2	SWKAILQYSLLEIILYLPFOPLCFPSHT HTHTHTHTHTLYSQINVLILLSLRKK GS
11982	25883	A	12090	265	30	WFIVYSEISQLWGLPFPNTLSTWQSLF IFVAEMRSCCVTQAGLELLASSDPPVSA SQSARIRAMSPSVANVIGRSR
11983	25884	A	12091	257	1	GSVMKHTTEBYENKVEQSSSGFIRPH LVYRVCFYLSVCLSVCLSIYLSIYLSI LSFFLSFFLLRKSILYLSIFLSFLLSP V
11984	25885	A	12092	311	404	LYHQNPWLYSVFFLESTESCSVAQAGVQ WCD
11985	25886	A	12093	331	83	GDDYKGARENSRDDKLFYVLIIMVVIOL HVFVKIHKTLQNGYILLCKLYLINLTK NNFQPKPTNSQKTLHIFHPDSTANI
11986	25887	A	12094	82	2	LREPNLLNPGGECNEARWCHCTPAL
11987	25888	A	12095	235	393	HGILFSSFVCLNQLQFSLQHWLMPVIAL WEAEVGSLSLEPRSTLAW
11988	25889	A	12096	80	3	PPPPPPPPFETESRSVARLECSGMI
11989	25890	A	12097	367	1	PKVDKPTKMGKKQGRKTGNSKKQSPSP PKRSSSPATQSWMENDFAKLREEGFR RSNYSLELQEEIQTKGKEVETFEKNLDEC ITRIPTIEKCLKELMELKPKAQELREEC RSLRSRCDQL
11990	25891	A	12098	94	236	MMADYFCMSPSIDGLKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK
11991	25892	A	12099	410	212	NSLHFSTSLFFSSHFHFKLISGQWQL TPIIIPVPEAKAGGLLETRSRSLAWAQ EDPISMPVCK
11992	25893	A	12100	140	324	NLGAQWMLPVIPARPEAEVGRSLAVR SSNSPASASQSGPTGPSHNWLMFLQ LLTRL
11993	25894	A	12101	247	357	KQICGRANWLTVPVSPLEAKAGESPEV RSLRPANPT
11994	25895	A	12102	245	2	DVLVGGGLCPAGTLLHLSIFLLSGCWC GSKDEAPCKQRISVQESQSRTRLRAGV SPKKAIPCMEGLILEDVLHFFDILQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, / = possible nucleotide insertion)
11995	25896	A	12103	230	379	KEASFFETESHSVQAGVQWRLNPLGS GNPDTSTSRVACTGMSHHVWL
11996	25897	A	12104	86	2	DGVSVLSFRLCENGLILAHCLRLPGSS
11997	25898	A	12105	116	2	SKQTFFFFFTVSVLLLPKLECNAGTSAH CNCLCLPGSSD
11998	25899	A	12106	271	416	QFTFSKAFNLVFTKPSFHISFYRTHYSQ AWLTPVPIPELWEAAGGSP
11999	25900	A	12107	194	3	HVLGTVLVAEATASNKRTLSQGLLLPL LPSVULVLAIRAIRQEKIKVIQIGREE VNRNRGR
12000	25901	A	12108	142	3	LCLLYWCKKHAHNRGQVRLTPVPILAL WEAAGGSPPEVRSRLPAW
12001	25902	A	12109	233	346	HQRSLIGWAGNLMFVPIALWEAAGVSP EVRSLKPAPW
12002	25903	A	12110	234	349	GFSPFFYDFCLFVFETESCCVQAGVRWH DLGSLQPPPP
12003	25904	A	12111	136	333	RLNFFYFFFFETASCSVAQAGVONHDLA HCIPAWETEQDSISKNTVQKRKKKVTIRA GISKTKNENF
12004	25905	A	12112	345	110	QDGLCLVMTLQETQPILAYSLWFPIVFP TTKACNVQGDGSKPLKKKYLQVQWLMF VPTLWAGDVEGSPELRSLEPA
12005	25906	A	12113	108	285	YNAMKNRFLKTLNNKNSIGWRNLMV IPALWEAKAGRSPEVKSRSRPGAVAQV DAA
12006	25907	A	12114	1	364	RVVAAEMGKFMKPGKALDLAGRYSGRK AVIVKNIDGTSRDRPYSHALVAGIDRYP RKETAAMGKKKIARSKIKSVKVNHYH QLMPTRYSDIPLDKTVNNDVFRDPAL KRKARREAK
12007	25908	A	12115	120	3	TQIWGAFLTLFFFFFPEAKSHSVAQAGV QWCSLGSLSQA
12008	25909	A	12116	120	3	TQIWGFPLTLFFFFFPEAKSHSVAQAGV QWCSLGSLSQA
12009	25910	A	12117	231	1	FLSPFSCYSAITKLLSLSYFLLOHILLLL LGSTPEAAAGVQVMSFADSDIVPPAST WVFTLQIMHNNKQATEAKK
12010	25911	A	12118	216	1	LIFPELLNFCYGVGLFGQGLALFFACN FFWRPSPKTPFFFFFYKEFHSAQAQGV QNCDLGSLQPLRGPX
12011	25912	A	12120	267	1	KKKKKAFSPFLGLGCTIRLQKHLGLTLV YRSHLISLLCLEGIIILSLFIATLITL NTHSLLANIVPIALVFAACEAAVGLAL LVYSIS
12012	25913	A	12121	167	372	ISGQDLLEKTKRVRFPQDDVFFNIF VPTPGAPRSLRQILELRGKTDPSPIIVG DFNTLSFALDRS
12013	25914	A	12122	124	2	GLLKNFIAPFFFFFSETESHSTVQAGV QWCDLGSLOPPP
12014	25915	A	12123	121	1	RFTAASANGSVAASAVGMDPGSEIIE SVPPAGPVSSVV
12015	25916	A	12124	176	2	RDLRGFSRFSNYKFWNFRGVGGIFKFFV GKGVKRFFFFFETESCSVAQAGGQWRD LG
12016	25917	A	12125	137	2	KLGFPGGGGGRIAPQKNFFFFFFFFFFE MESCSVAQAGVQWRDIG
12017	25918	A	12126	103	3	LEENLGNLTQDIGRGKDTSKTPKAMAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
12018	25919	A	12127	212	351	KAKID LITFETLNTCLGDNILDLGLARWLTPVI PALWEAKAGGSPVRSRLR
12019	25920	A	12129	187	3	RGSTMQQTNRTPGVRVLYIYLMIATMA IPYIPMANLLLVIPILIAMAFIMLTER KILGY
12020	25921	A	12130	13	329	ASRVITIRVMASNSTKSLFADAGYGEQEL DANSALMELDKGLRSGKLGEQCEAVRVF PRLPQKIPFPIILNSAFLLADVFRVGN NFLRLCLVKLVQTQSEKHELEKI
12021	25922	A	12131	231	330	MDTDETYLGRAPWLTTPVILPALWEAKAGS SPEVR
12022	25923	A	12132	95	2	KGKCFPPFFFFETESRSVAQGVWRDL SSL
12023	25924	A	12133	129	1	DLALLPRLWCSAMIMAHNCNSELMSDDP PISASQIPGTIGMCH
12024	25925	A	12134	196	361	TINEYYAAMKKKSGSPLLHFGGKKLNQD GGWAWNPVTPVILPALWAKTGGSLSPRS
12025	25926	A	12135	120	1	PPPPGLFFFFFETESYSVAQGVQWGN LGLSHPPPEFK
12026	25927	A	12136	235	3	KKGIRIERDLKQSVQCRFQLAKPPFP PSGVGKQNFPPFKKKKKKGRAQWLTPV IPALWEAAGGSEFVRSRPA
12027	25928	A	12137	185	1	IWCPPFCGPGQICSPFCHFFFFFF LEAETRSTFAQGVQWCDLGSLSQSSWTE LAAAS
12028	25929	A	12138	158	1	LRRGGVFSIFFCGGTMLVSPADKTINVA AWGKVGAAHAGEYGAELRMPLSF
12029	25930	A	12139	76	3	KVLARATROBEKTDQCTGKEEVK
12030	25931	A	12140	157	2	FFSSPRLKKRPGNGLGARENFFFFFS ETESPSIAQAGEQWRDLGSLQAP
12031	25932	A	12141	234	388	LSQLMSANLFFVLLFEAFHFSVNRLECS GMIWAHCNHLHLPSSSESFASTSQ
12032	25933	A	12142	112	453	LGRQAASMRREGISIHVGQAGVHGNAC WELCYLEHG IQPDGHMPSDKTIGGGDSS FNTFFNETGAGKHVPRAAFVDLEPTAID EVCTGTYRQLFHPQLITGKEDANNYAR G
12033	25934	A	12143	44	443	AKLGTRKLPLKAMGKEITLINIVVIGH VDWGKTTITGHLYKGGIDKRIEKL KEAAEMGKGSFKYAWLIDKLADRERGI TIDLSLWKDTSKNYVTIIDAPGHRDPI KNMTTGTSHADCAVLLDAGV
12034	25935	A	12144	3	386	REAAHRECTCTHVHAGVQNGACWEL CYLEHGIQPDGHMPSDKTIGGGDSSFT FFSETGAGKHVPRAAFVDLEPTGIDEVR TGTYRQLLHPQLITGKEDANNYARGH YTIKGEIIDLVLDIR
12035	25936	A	12145	3	386	AGATYIDRLRVALFETITPLWRFELS SGEATTMRECSIHVGQAGVQNGACWEL LYCLEHGVQPDGHMPSDKTIGGGDSSFT TFSETGAGKHVPRAAFVDLEPTGIDEVR TGTYRQLLHPQLITGKEDANNYARGH YTIKGEIIDLVLDIR
12036	25937	A	12146	3	385	GRATYIDRLRVALFETITPLWRFELS SREATTMREGICIHVGQAGVQNGACWEL LYCLEHGIQPDGHMPSDKTIGGGDSSFT TFSETGAGKHVPRAAFVDLEPTGIDEVR TGTYRQLLHPQLITGKEDANNYARGH YTIKGEIIDLVLDIR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12037	25938	A	12147	11	381	HTPEGRTRVFLVLAGVYVCEALRDWGR VTASSTGMAFLRSMGVLTALGRSGAK LCTGCGRLRSPFSFVFLRWVSSVLAR CPKKPVSSYLRFSEKQLPIPKAQNPDAK TTELIRRTAQR
12038	25939	A	12148	321	509	YSMDQYTFPFYQIMHLCFFLKTREVSLL PPWLCECSGATSAHCNPFLLSSNSPASA SRVTGIT
12039	25940	A	12149	51	400	AATMRECISIHVQAGVHIGNACNELYLC LEHGIQPDGQMPDKITGGDDSFNTFF NETGAGKHVPRAVFDLEPTVIDEVRTG TYRQLFHPDQLITGKEDAAANNYARGHYT IGKE
12040	25941	A	12150	25	399	EATTSTLGLRHQLGSRESTAMRECISIH VQAGVHIGNACNELYWLHGLHFDGQM PGDQITGGGDDSFDTFFSETGAGKHVPR AVLDLEPTVIDEVRTGTYYRLPHBQL ITGPEDAAANNYAR
12041	25942	A	12151	1	402	TKEEELCLACRRADGGWRSQMNAQSD PVGIVSAARTIIGSFNGALTAVPVQDLG STVIKKVLKRATVAPEDVSEVIFGHVLA AGCGQNPVRQAGGAGIPYVPAWSCHM ICGSSLKAVCLAVQSIGIGDST
12042	25943	A	12152	3	400	TDLRLVALKKTTTSSFCFPHHLSGRETA TMRECISIHVQAGDGHIGYACWELCYCLE HSLQPEQGMPGDKITGGDDYFNTFFSE TGAVKHVPRAVFDLEPTVIDEVRTGT RQLFPERLITSKEDAWNIY
12043	25944	A	12153	2	398	GRCALDNTETFAFPGCYLILASGHPOEK LMDMDMSPLRPQNYLFOCKLKAENDYHF IVANDEHQSILSTASLRAGANDMDNI VEEAMNYEGTPIKETLATLKMVSQATD SLGGSSEITPFSVLRLKCGSR
12044	25945	A	12154	203	405	FTCPSTRITCVISRRITSFCCAPDLNPMLS ANAMLDVFVTFDEPGWDSKNLQKKWSH YSFLTGRPKI
12045	25946	A	12155	229	397	TKLAHHKAGFALISKKITNKLKMFSLKF LPIHALNVITGSGMQPYPLVNGHYDLGK
12046	25947	A	12156	2	399	GGVPHCVWATAGMRPGLEGFTGLCAQT SSRGQKSVLKQKESCGIWLHYFLSRKQ EPRWEPCVSGSSGSGGAVADLADELGRY PALCCTLPVHSYRSWAGIRPQIMNGFLH PRPLVALLDGRDCTVEMPIL
12047	25948	A	12157	85	414	ALLPQSEALQGAVTMPHSYPALSAEQKK EVSDIALRIEAPGKSLAEDSVGSMAX RLSQIGVENTEENRLLYRQVLSADDRE KKCIGGVIFHHDTLYQKDDHGVFFVR
12048	25949	A	12158	85	407	GLLPHEPLQRAVTMPHSYPALSAEHKK DVSDIALRIEAPGKSLAEDSVGSMAX PLNQMGVENTKQNRRLYRQDLFRAEDRE KKSAGVIFHHDTLYKHDDNGVP
12049	25950	A	12159	85	406	VLLPHEALQGAVTMPHSYPALSGEHNK ELSDIALRIEAPGKSLAEDSVGSMAX RLSQIGVENTEENRLYRQDLFSAEDRG KKSIGDGLFHHDTLYQKDDNGVP
12050	25951	A	12160	275	146	EKTFTISFFFFETESHVSVAQTGVQWHD LQSLQAPPPWERRIA
12051	25952	A	12161	212	2	KRSRFFFFFKEHGSYCIAQVGNQWLFV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						GTITACYDPBELLGSKDPPTSASQVTGNT GTHHTQLIFVFLV
12052	25953	A	12162	253	2	GRVDSECLLANGNAEKSI FPCCLLVYLFI LSSRQSHSVAQAGVQWHDLSLQPPPPG FSLLSRVAGTGTARHHDWLI FVLGEBT
12053	25954	A	12163	228	1	LLGLWFQGLGRFTKI AKTKGERSQTQSG HSMHRVPAGLLGLLLLVFPGSRCDIQM TCSPPVAVASVGDRIITCR
12054	25955	A	12164	122	1	RLTFPEESRSVARLECSGAISAHCSLR LPGSGSPASAS
12055	25956	A	12165	239	350	GQRRLTFVT PALWEAKASKS LEVRSRLR LAWAGHGS
12056	25957	A	12166	235	359	TDKAISKRLSLVLR EYIFPEMESRSVAR MECSGVISARCNL
12057	25958	A	12167	209	396	QFSGIPPDQYKCGFKNYIYIYIYIYIYI YIYIYKRYTRAYTKRYMCVFSRATHNIV YLCAYI
12058	25959	A	12168	327	130	GGVGFGLGPGKEKPPRPSPPFFFFFEKES RSVPQARVQMPDFGSLPAPPFGTPTPLR ESFLFSSLM I
12059	25960	A	12169	317	422	RGEKPLFFFLQK KKKKKKKKNTKKG GRYKPS
12060	25961	A	12170	260	375	EKVTCSTWQWLT FVPVIALWEAKAGRSLE FRSLRSANAI
12061	25962	A	12171	304	3	KFFFFFKGFFFLGSGVPI FPPPKKFFFS KIPPGVFFFPPLKKKIFPPFPVILGPP RVFFKGAPLFFFPFFFPFFSETEFRSC CPGRLECSVAUSAHCK
12062	25963	A	12172	105	3	LIFLRQSSALLFRLECN GATSAHNCNLC TGSSD
12063	25964	A	12173	146	17	RIFFFFFLGSLAVAQAGVQQRDLGSLK APPPGVHAILLPQ EY
12064	25965	A	12174	234	2	LFPRKPSPSVLSLSLSLFRILKLS FMRHNNIEVRP INNPAMTSKCSERKSL VSFTLNLKPGMIRLSEGM LK
12065	25966	A	12175	292	380	VRGLGRVAHTCN PSTLGGQSGWITGGOE F
12066	25967	A	12176	109	1	GRIKKVIGQQAQWLPV IALWEAKVGG SEKVRSSR
12067	25968	A	12177	170	291	LINFYFFLRQSHSVTQIGVQWNCNLGSL QPPAARRRRRG
12068	25969	A	12178	260	380	LIFYALFIFLRSLTL LPRLECSGMISF HCNLCILGSSDS
12069	25970	A	12179	54	166	EKRGHRTVQGLNLLT LGSFRLGLPKG WDHQDPLP
12070	25971	A	12180	273	359	APAGHGGSCLOSQH FGLRLQADHLGSGV R
12071	25972	A	12181	27	225	IGQAQWLT FVILAEAKAGGS LEVRSR RPAPWIFVLVLLAS YLRFC LIQHSDL LYTSSTRGS
12072	25973	A	12182	1	155	VHRTFIAYKYSQFQVFRGAWMLT FVI PALWEAKANRS PEVRSSRSRGRG
12073	25974	A	12183	91	2	FNLEFFFFFETGSRSVARLECN GATSA C
12074	25975	A	12184	122	2	GQAQWLT FVIFPFEWEAKVGKS PEVRSSR RTRGRTRGRTRG
12075	25976	A	12185	389	20	TDGRREARRACFCGRVDPGELSFALKEIA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REMGKPFDRWAMLAGMSSTEYADWHRPYS THYFEDVLLDMFSGSLTYTVLSLFFSDP DMHPLDFSLNRRREADEPEDDVLMOQA AGLAGGVLLFI
12076	25977	A	12186	180	393	LNFGSGGCGEPRSRHCTFLAWTTERBSVS KNKIKIKINKQIEEGFLQFPFGQGFIVC YFPAKEPIALSKT
12077	25978	A	12187	37	443	PDFPIPFPPPKVQHLARFSPKTRAPAWT IRRLIPPPPKKRHPGLARGKFGPRELA KAGLAKCEPAGGPTPAVRFATPIRGGGG RVAGFQTPMGIPMGKARLGILLTFLGFAS GWIGAYRPRETLCGGELVDTLQF
12078	25979	A	12188	3	411	AFPERAATGTFODPVFASGKRAEAVGNM RLSVAAPISHGRVFRMRGLGPESRIHLL RNLLTGLVRHERIEAPWARVDEMRGYAE KLIYYGLGDTNQRAMRMADFWLTKDL IPKLQVLAPRYKDTGGFTRLMQ
12079	25980	A	12189	2	414	QEFGRTRKATFISLLFFSSSVYSRGVFR RDAKSEVAHRFKDLAETLRALTLLIAF AHYHLQCPFADHVKLGNRATEFAKTCVA DESAENCDSLHTLFGDKLCTDAPLRET YGEAMADCCAKQEPERNECLLQHKDD
12080	25981	A	12191	3	514	PRLLMEAGPHPRPDYHCCPKPGRLDNMHG FVHHIRRNQIARDYDKVKQAACEKVR RRHTFAPTRPKPDQLQVYLPHRDVSAH PRNPDIYESGESSSSGGSELEPSGHOLF CLEYEADEGEVTSVIVYGGDDPGKVSEK VSAHTPLDPPMREALKLRIQEEIAKKQS QH
12081	25982	A	12192	182	3	RGLFFIIPPPPIKTKINGPFWKVVFMFG PPLFFFFEMESRSVAQAGVQWHDLSLQ ALP
12082	25983	A	12193	53	400	PETPSWLGPVRRFFFIITKSVMWKKKKK KKKKKKKKKKGGGPFKTLGGDKFYW GVKKKIFFFLGGSKGHPMGFFKKLFFW GGKCGAPPPKDISCLNGKKNFLEGAIGBK TCCC
12083	25984	A	12194	182	3	KGIFITQIAPPKKKKNGPLWKVVFKGFG HPIFFFFEMESRSVAQAGVQWHDLSLQ ALP
12084	25985	A	12195	200	378	KSSKSQWLGYLFIGLLIYLFIFKFFLETR SCFVTQAGILAHNCNLLGSSDPPTSAS QAA
12085	25986	A	12196	341	54	SLSFHGGLSVLCIFSTYRKLSSQEQWLTP VISVLMEVKVRSRSPQVRSRPGDPAPSA SQSAGITGVSHHARPHLSLNPRLMIKL SEEGMLKRMGT
12086	25987	A	12197	1	462	GGPPRPFPRKAAVLTAVLFLTGSQARH FWHQDEPPQS PWDVRMDLATAYVDGLKD SGRDYASQFEGYALGKQLNMLLDNWD VTYTFSKLREQLPVTFQFWDNLDKETE GLTHEMSKDLEDVNAKVQTYLYDFQKTW KQELTFTESESPVP
12087	25988	A	12198	80	1	SNKVFFLETESCSVAQAGVQWCDLGS
12088	25989	A	12199	221	3	THGIMLDKKETQALFSFKRMGHAVEAT TCNINNTSGPTANKVTYQWFWFKFCRG DESLDEBEHGRLEY
12089	25990	A	12200	239	336	FGALFYTTCKFGKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12090	25991	A	12201	279	366	KKKKKKKKKK
12091	25992	A	12202	153	40	GFLPLI FFFETKRSSTIQGVQWCHLG CTLAWATETD
12092	25993	A	12203	317	406	LGKLCNGAVSGHNCNLLRPGSSDFSGSA S
12093	25994	A	12204	2	925	RSQPDHELTLDGSGKCTRSMPVPSAASE DRKLP I IVEDEGQPTRSRACSSPARGS RPPPSAIGCSVPVQASDSAGAPARTIAL QSLSSWLCYQIDRHSVPVTVKSPFBSV IMAPKKHSSDAQNLDRPKRSKVLPLSE KVKVLDLIRKDKKSYAEVAKIYKNESS IREIVKKEIRASFVSPPTAKVTATV RDCLVKMEQALHLWVEEMNRKRPVDS NMLRQKALSLYODFSKGCSETDTKPFTA SKGWLHRFRHRFSHHYKKKKKGMAQVA VSTLPVEESSSETRMVTVFLVSALESM
12094	25995	A	12205	272	1	KMARAGLLVIEGKWRTVYVFATREER EGMKSTNLMKLDITIGFNDKDLLISVG DLVDRGAENVECLRLITFPWFAVRGNH ERQPGQ
12095	25996	A	12206	166	478	ISAGLLPTSPLTGTSKLQDPNEHNLML MLNRVSLLLPRLECNDDTLAHYNLRLP SSNSPDSAFQVAGITESFTCEINALKDS SQVALWSFRCEMDHSSICNR
12096	25997	A	12207	102	497	PLLALLFGSQRTFLCLQLSLKPTRSSLL SPGSAGNPENBAPCOLNPEATSLKKKK KKKKKKKKKKKKKKKKKKKKARG
12097	25998	A	12208	131	2	FGFLGDKAKGGPGPPPPFFFTETSPS VAKAGVQWCDLGSIH
12098	25999	A	12209	221	499	QTRHKLNTSRSGRTGLQILIKEHQSSGR WOGTGDILWQSLDITCYSVPKSLDLFL LFIYFETESHVTRLECSGALSAHCNLR LGSSSDSPA
12099	26000	A	12210	297	398	HNFFFLKTESCSISQAGGHWDLSSPQ PPPQ
12100	26001	A	12211	341	452	NNSPQLQSSRLSLPKCNDYRREPPCLA GLLAYLPRR
12101	26002	A	12213	214	468	FFFFFHWGKVFFFFPPLEGRGGSVWV TPPPRGKNFPLGLGKGNPPPPPPR FFFFFFKKGVFFLPGGVKVTPLSRETTP
12102	26003	A	12214	223	477	CPTETQLQIFAREKKHFPSPVLLDLIDL GFFFEMESHVSVPLECSGPISAQSNLYL LGSHNSPA
12103	26004	A	12215	263	55	TPKRYGMQTATYLPKSKYIYISDLKK QDYIVYQSKKPEGAQWLPVPIPALNE AKAGRSPKVRSSR
12104	26005	A	12216	328	471	GVIHAQVLHAHTHTHTCTHTQVHAHS
12105	26006	A	12217	434	1	WDHSASPPTS VGTPLRADGPHRLTAPG HUVSSAMLSAPAAGRGSLGRWCDDRD KLSQRGPQPKWILWGNLPGGGLHRHI HKPLPTIPIPSTVRGEVLQQLLHSASF ILFIFILDRVSLCHPGWSAVARSRPTT TSTS
12106	26007	A	12218	304	43	EKPIGVAPSRVKRAGGKETECCLLKG PLQGFQGVLGKPLKNGPLFFFFPLRRS LALFRLECNGLTILACNLCILGSSSDSPA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						SET
12107	26008	A	12219	171	365	ALVOPRAGREAVTVPACSCSDVFLYET NKVARIQSIYNGTIFKPHVIVFSTVSK ELIKKLEK
12108	26009	A	12220	171	452	ARYKPLHPKFAFGLVPSSSQIGARHQL WILIKCSFYLLFLRQCLTLLPQLECSNM ITAPLQFPLGLKQSSHLTLPSSWDYRH EFP
12109	26010	A	12221	323	458	FVRQSLFLFIYFFFTESHVPUQAGVQW HDFGSLHRISP
12110	26011	A	12222	189	56	DRVSLVQPTLECSGTISVYCSLNLGLSS DPPTASPVASTTGGI
12111	26012	A	12223	246	494	FLCSSYAYDDHFLRFFFIHLILDTAF SQDITIISNLLFQDACSVPKKANLGOAQ WLAPVLPVLEAEVGRLLVRSRSPAW
12112	26013	A	12224	55	353	RIQGCSCWVKLCFKVEKVVQRTDAEQS QTKAEIQDMKQELSAVNMDKFAARSAL ERKINKMMNKLKTHVVKVQTAQSGMLKWV ISVAFYKLPGTVIRL
12113	26014	A	12225	199	23	LKLSSTIYYVPGTILKYFTGWARWLLPVI PALWEAEVGGSPVVRSSRPANSTSWIER HQ
12114	26015	A	12226	369	14	DCVRVGLSYPTVCPSCSVRKAPFSSR PHRGVLESQGPCKSRVRDIFFSMERER DRERERERERERERGQKRTTRVWGGER KLYSHAWGWRGGRLGSGMGCGIPPC TSVHQ
12115	26016	A	12227	206	2	QNGHMGGCPCEVSLSLFLETRSFPLFLA SLSMLECSGAILAHCNLRLPGSSNSPAS ASQVAGITGACH
12116	26017	A	12228	231	501	RSWEGGALHSGDFLASCRTTQSNMALQ RINQLEDEKLYRMQGHYEEKRALSHIEI VALNSHLLAEKVTIDKLSRDNVSAATW PMEDCR
12117	26018	A	12229	86	455	DLPTFFPPPHFGFSGPLLQSGSELPSNCQ TGGSHLSVSVLCPATLATTPLGLDFFTC GTSQPLGLQLLAHRSSELAGLSLPLGLST NCTSQRLPDRPHRHSADPHTHTHQTHT HTHTTTPATVT
12118	26019	A	12231	211	96	KSHFKAGGGGPPRYSPPFGGGGGGVPRV GGFPPPLTQ
12119	26020	A	12232	228	3	KRWFIKGLSKGLGPPFPKILKFLGFFFF FFFEQSFLVLAQAGVQLECSGTILVHFN LYLPGSSNYEASASHPRV
12120	26021	A	12234	137	3	VPLPGTLKNHSMVPCFLVCLFVCYETE SHSVAQAECSGAISAH
12121	26022	A	12235	139	1	FKLCFGQAWFKPTIPALWETDASRSL VRSSRPADAWADAWADAN
12122	26023	A	12236	80	1	VLLIFIFLEMGFHHVGGDGLDLTLT
12123	26024	A	12237	187	494	TERNSFNINKDIIHTKTPFVGYQHQRPK VDKTTKMGKNQSRKAENSKNSTSSPPK DRSSLPATEQSWTENDFDELTEVGFRRS AITNFSLEKHEVILTRTE
12124	26025	A	12238	252	503	CQGVGADDLSQASIQCELCASIDRF ILFFFFLGLGPPHNPPPTPKWKPKG APPLALWDIPRGAKGPGRQGRPAIHG
12125	26026	A	12239	2	471	RIALCPAVRIHREERERERERERETP GHTQLSPGARITPFLERERAFNDCFSLN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						YFNLCLPGDLIEFVSRYVQHCHALYLGDDG YFINITPVYGPAPFTTSKSVFSSRALE KTHLLKDVYGSSTYRINYICYETLPSLS VERIITRSFVIGQA
12126	26027	A	12240	14	149	FWTACRIRHEHGSGLLRGLPLHVLWT RIASTIPPHVQKSLPH
12127	26028	A	12241	588	671	RSRPSFQEQAFESSQYKEGKYITELNH
12128	26029	A	12242	384	464	RGQGVNWLKVVVPALWEAKGRLEAG
12129	26030	A	12243	325	459	TVLYFYLYFYFETESCSVAQAGVQRDL VSLQPLPNSPALPTN
12130	26031	A	12244	323	457	SLQRECGPADTFEMDSCSVAQAGVRWC DLGSLQNSP
12131	26032	A	12245	241	466	GALFFFFFFFFFFFPLSNKAVY F
12132	26033	A	12246	385	37	QARRRCLQTSRMEALGRWSYKVTFEFL QILPFPPIKLYKVI FGIKITPNEPHELE YEEGQRLGKSTVSQVFNEDTRLINWNR HITVNPRNTNSQNRMLKMAHESKYSQVFP PLQA
12133	26034	A	12247	318	456	LILKYFMYVCMYVHMVCMYKSCSVAQ DGVQWYDLGSLQPPPPGL
12134	26035	A	12248	362	473	SPCQNNNSAKTARTNTRFMALMWN GAILDALQK
12135	26036	A	12249	310	463	FSIKTRKNALGKLSLLRCHQFYLVVCV CVCVCVCVCVCTRTYALTICIAV
12136	26037	A	12250	169	54	EAKSGQARWLTLVIPALNKAAGGCPDEV RGSRLAWPIW
12137	26038	A	12251	49	449	GIPATSTSCVQVILLPQPPLLLGLQDSF LPQEI I I KVEGEDTGSITPSQEGVNFK IVTVDFTRFEEGTCNPAQRTILDRDVFLE NHRDLVSWDLATAVGKDKDSTSQRIFDE EPANGVKIERFTRDDPWLSSC
12138	26039	A	12252	130	428	RWGLAMLPRVLNLSWSQVILPQPQVGA TFGGFPNP GHMKLLGGISGGEAGVEE AEEGQALGLFGQPPSSPQLLLQTSWGL RTTRTCRWSSLLWKAH
12139	26040	A	12253	204	54	PGMKTKQSDLGQGVQWLTPIVLGLWETE AGDSPESRSRPAWAKHKIVR
12140	26041	A	12254	375	470	SLCLFFSFFFTQTEPRCAQAGVQWRHLS SLQP
12141	26042	A	12255	432	512	GGVRLWLTPIVDPALWEABGGRSPEARSS
12142	26043	A	12256	232	1	RGALSCKTQSFWGGQKFFPRPGVFKGVF FWGGSCFPFGCGFTFFFTETESCSV AQAGVQWCSLQSLQPLPRFK
12143	26044	A	12257	22	123	RFVCSITKVLRLDSSDRNPGFRLSTSN SSSTRP
12144	26045	A	12258	71	362	QTERNSISINKKVITETPSKGHQHQRF KVDKSTKMRKKQKKAENSKQNASSPP KDHNSLPAREQNTWNEFDELTEIDPRR WVITNSSELKEHV
12145	26046	A	12259	375	3	SPNIEAPPAKFFFFNQRFVFFCFSSCRA ENTHEIVWVKVYFSGNSKAKLFFSFFV QRDRSSPDSYLPLQMLWMTAGQERFR SIAQSYRSANALILAYGITCEESFRCL PEWLRIQIQA
12146	26047	A	12260	98	1	KYQIDLGGRGSSNSPASASRVAGITGTH HHTQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
12147	26048	A	12261	125	3	LPLIQYITGQERWLTPTVIPAPWEAEAG RSPKVRSSSPA
12148	26049	A	12262	228	385	SCLYLQMI PSSTEKSQMYKKTATGRAR WLTPVIPALWEAGAGRSPEVRSR
12149	26050	A	12263	227	369	MLKHKSNNQLQLGQMGLTPVNPVLWE AKVGGSPVKNSRPAWPTW
12150	26051	A	12264	102	487	QONRFFGTERTGRGTGRGVSSFPQLSPGS LELASSPSVGRGLGSAASQRSRGQER PKAQLRRPPRPSSSPRLRGRENCAHAR TPGGILDRPPTLTGTNLKGGRPAMMAG NPPEAHKTANGPGEQA
12151	26052	A	12265	391	476	PRSYRVCSGSSSAHCNMLGLGSSNFS
12152	26053	A	12266	378	476	MSSRLGLEVLGRAWMLTPVIPALWE AKEGG
12153	26054	A	12267	166	58	NPPFFFFETDSCSVAQAGVQWHDLSHCN LCLPASSN
12154	26055	A	12268	209	49	TPPNFYIKISRSQGAQWLTPVIPALWEA EAORSPEVRSRSPATRRNSISNS
12155	26056	A	12269	127	1	SSSFPLKTFGLFFFLCFESESRSVA QAGVQWCHLGLSLQA
12156	26057	A	12270	154	27	IQTGKKEFFFFETKSCLVQAQAGARL CPKKGKENSNFVL
12157	26058	A	12271	180	22	VLKHNIGRAQVTSVIPELWEVKAGGS QALRSRAARTRWDCNFEKTOVY
12158	26059	A	12272	207	422	GDSSRTGADEKPKGKVTNDNNINLKV MGQDCSMEQFKIKSHI PAGYGGSHRESQ HFVMPRWADHLRSV
12159	26060	A	12273	59	479	NSLGGGGVYSGSRFRFTPPGCRALSPWRV RVQRRCMSMTMFADTLIVFISVCTAL LAEGITWVLYRTDKKRLKAEVEKQSK KLEKKKETTIESAGROQKKEQEKI KNNRDLISMVRNKSMEAFIGFCTALMG
12160	26061	A	12274	354	439	VKTGECIAKTWNGPKCPTTIDNRYKKW
12161	26062	A	12275	366	499	TRAQYFVVVVVIGSQCVTLSCGMIMAH CSLDLGSSDPTTSAS
12162	26063	A	12276	136	37	KFGQGVHLKVPVIPALWEVKAGGSPEVR SSRPA
12163	26064	A	12277	419	48	DGKLVNLSFLTIVSSSGCFLLFLLIVRPVY FLRYNNSERPINNPWTCKCKSKRKSR ICLTFNQKLEIIKLSBEGMSKIRTQNL GILCHVSQVDEQKFKVATKATSATAKIN LSIKSYIMSGA
12164	26065	A	12278	190	1	RKGVSFPQMGPIKSGKSPFLAKLNFPF KKTFFFFETGSCFVQAQGMQLDPSFP DAWADAW
12165	26066	A	12279	276	389	WPNLSFFCFCLFLETETESCVARLECSG AISAHCNLT
12166	26067	A	12280	425	1	PPHPFGKPPPPPPPELFFPKTKNKKER VLFFSPPKKINFFSLTTPRFFSPPKKK KKKLNPPQKGGPPVPDIKPPPLFFFF FFFFFFFF FFFFFFFF FFFFFFFF FFFFFFFF FFFFFFFF FGLTVRVIMTCMLIVDGLL I
12167	26068	A	12281	253	90	IWPPQGSFKTAAPFFFFVFLVEMGFCH VVQAGVKLITSSPPASQTAELFI
12168	26069	A	12282	61	387	PKSSSSAPQISWSSFLPASTASMTSI RVTQQPYKVFNSGPAFSSSSYSRPSA HISSLIVSRVSSSTSPGQGLAAGMLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
12169	26070	A	12283	186	305	LHSSLANRKARLSQKKKKRGRSKEP LHSTVQVREEHKSLEHTQVHTHTHT HPHLVIMSSHS
12170	26071	A	12284	2	190	PRVRFDRVNNRSLNPLISRTMRTEPIPE NPKFSVKKKKKKKKKKKKKKKKKKKK KKKKKKKKGGGA
12171	26072	A	12285	17	197	SLGVGGGQGGGVHFPCKFFVLSFVS LSKHCSYLPKKKKKKKKKKKKKKKK KKKKKKKKKK
12172	26073	A	12286	158	405	GVASYAEQRKYFLEMSEYFPGGEAISIVE MTTEDLHYSINLDDKAPTGFERYVSHFE RTCTDDKMSYCYTCYRIFCERNKI
12173	26074	A	12287	364	142	GCAFFLGSPLEKERRRRVPPFFPNFF FETESCSVTQAGVQMCNLSLQPLLDW WQOPTVAHACHPOTLGG
12174	26075	A	12288	171	380	VFEAGHAWLQENLTSRDFWGSFFPPTDI GMLEKKKKKKKKKKKKKKKKKKR
12175	26076	A	12289	194	2	GPRGFWQFWTKGFFPKGFKVFPAPG GWFFFFPKRGFPFSPSLFFFDRLVLC GWSIVARS
12176	26077	A	12290	179	416	LIFLFTFACAVCFQIARPHFKHITETAL RCLIIILSCPPTPIRYKMYREGQARMLTP VIPALWEAEVGGSGSEVRSRLRAC
12177	26078	A	12291	3	408	LAYGFHDIRTYDTSALMVLVLDLIT GNKNGSGEAPYLPEDDFRDGEDDAAVLT EKQEDLTTLVTLPTVTEGHEQRQRTOLE AKLLKKRLELGSLLDLVEDLELIQLKK KKKKKSLPWGAPFKOFLGAPI
12178	26079	A	12292	119	278	PKSTEAGVKSVDLHPLPKNKAKTHLSCKK LKKKKKKKKKKKKKKKKKKKKKKKK KKKK
12179	26080	A	12293	119	3	MLFTGFHTKMSLNSITGWAWWPTFVIP ALWBAEVGKS
12180	26081	A	12294	205	1	ILHFPYSTETKQPKGLFLALFYSDCEQEK RKGGKLLKILFKAQGQARWLTPVIPAFW EAKVGRSPEVGS
12181	26082	A	12295	215	1	AFKIKLTMHIFSSPLCLQDEPHFPFTEA LLPHVRAIAYTFNQLQARKRYPKKHEK RMSKEPHGARLEGNO
12182	26083	A	12296	185	411	DVPLMFHMLHSDRFRIISTEIGVETVG KRVLHRIKILLLLLFFEMESCSVTHAG VQWCDLSLQAPPFGHTFF
12183	26084	A	12297	281	388	RIIEFFFEETKFCSPVQAGVQGRDLNSL QPPPPGFM
12184	26085	A	12298	178	3	TLLSVTGVPILFGSASSLLFSRKDIKI PTSVFFSPQTEPASFVQAGVSWCDLSL QP
12185	26086	A	12299	199	450	TLIRHMICNYFLLSHRHSFSSVDYPLCY REIYSILKTLNKLGGGFFLNIIKVMYD KPAASIRSEKQKAPLRSQTRIRCPD
12186	26087	A	12300	3	407	EFKDHSSTAMDETNPNGTSSSVTTTSTST TTTTTSSSRMQQOISVYSGSDRHAVQ VIOQALHRPPSSAAQYILQMYAAQQOHL MLHTAALQQOHLSSSLQSLAAVQASLS SGRPSTSPGTSVTQSSMVQTSI
12187	26088	A	12301	227	3	KRGTEGQTLFFPAPRAKSPFPKMPKK VEKEPPKGGFFFFFETESAPSPRLCS GAISAHCSLNPHASAHAS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12188	26089	A	12302	292	380	KCYRWARWLMPIYPALWEAKAGGSLEPRN
12189	26090	A	12303	13	186	VDERHTRLSENMAWVALLSLLMATAGTSTOTQSSCCCYDVFPRRSCKQLPWGRGCDL
12190	26091	A	12304	253	409	YTAVIAAAAAVGVGTITMTNFRSLPRLECNCAISAHRNLLLLGSSDSPASAS
12191	26092	A	12305	153	64	GRAQWLMPIYPALWEAKAGGPLOVRSSRPA
12192	26093	A	12306	265	420	GTINSRNTKLQLCRMKSKRTLGQFWLTPVPTLWEAKAGGSLEARCSRPAW
12193	26094	A	12307	295	1	RFLCKNKKTSPIHWKKKFPANPLFGKAPVFDLKKPKPKPHYRESRPRLKKKNGPKGFFFFFTETESCSVTQAEVQWRDLGSLQAPPDGSYHSPSKLIIN
12194	26095	A	12308	247	421	SWCCLKKKKKKKKKKKKKKKKKKKKKKPGGALKKKKIFS
12195	26096	A	12309	168	3	GQALLLLCLTAVAFSKTITVCHAPILGWAWWLTPVLPALWEAEVGRSPVRRSRP
12196	26097	A	12310	117	3	VAYNTAVFRGGVSLLLRLECSGVYSAHCNLRPLCSS
12197	26098	A	12311	256	101	BPPTFFFFFETGSCSITQAGQRDDHSPQCSPTPGLSNTAPASRACESGR
12198	26099	A	12312	146	3	FVALCIQLQPLVNVICFHKKKHKTGRARWLMPVLPALWEAKAGGSPEV
12199	26100	A	12313	207	3	VRVRTGVIMALRGLCSVESMTKDELIALRLSLGQLNRDVSITGTKEALALRV AELKQELDDSR
12200	26101	A	12314	282	2	NCLAEVKFMVSAISLQFOGISILFLSFFEKESCSVPQARVQWPNFSSLOQPPPGFKLFFCLSPGGGCSPEKSCRCIPGWQNETPSQKKK
12201	26102	A	12315	298	84	KTPQPPVVALSKNFGPPKTAIPFFFFFFFETKYSVQAQGVQWRDLGSLHSSLGHRARLHKKKKKKINL
12202	26103	A	12316	124	1	SKGHFFFFSETESCSVAQAGVQWHLGSLQVPPPRPTFF
12203	26104	A	12317	132	398	VVTNAVSIVTSPSPVSCHEVALAAKWLVCYLLRETYQKLHQEIKPTLSPVKKKKKKKKKKKKKKKKKKKK
12204	26105	A	12318	262	392	PHYCQNGOPARRSGSHQHQQRREDHL SLGVDRDPQGYSETP
12205	26106	A	12319	168	3	EAPKAIKNTTALQPLQGNLSONKEGQVQCLTPVLPALWEAKVGGSPVRRSRP
12206	26107	A	12320	48	385	DLGLSGHSTLASSFISLLLSYKCKLSPSTMIMRLPLPCGSPKIPFFLEKKKKKKKKKKKKKKKKKKKKKTGG
12207	26108	A	12321	218	83	NLSPIPFEGNFFFFFEMESKRSVAQATVQWRDLGSLQAPPPIRRKF
12208	26109	A	12322	197	1	KETWFPFKKEGGLFSFFKKRIFFFFFSK KIPSPPIFFFFFETESCSVAQAGVQWHLGSLQAPP
12209	26110	A	12323	128	36	RGLPFFPFEMGVSLPLRLECSGTTSAHCNLP
12210	26111	A	12324	140	3	ILNSNLKPIKNTTFFETESRSIAQAGVQWHDPSKQPPPLGFKR
12211	26112	A	12325	273	369	RKEWFLKKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12212	26113	A	12326	140	415	KKK RTGLLGPRGLQGPYPYGSREYKSGLLDL NASLLDPEVWAPSLSGPPTKPPAHSPSD PGVHSSCSAQSGSGGPPLTPSSRIHEP KPPGPFKK
12213	26114	A	12327	2	506	FVPLESEAPGCSGSRPPELEPERSLGR FGRFEDKQLEEEELLLLLLLLLLLLL MSHFLSLRQGRQSDDEERLNLSEL TPYLCLSCICKGYLIDATTITCGLHTTCK SCIVRHFPYNSNRCPKNIVVHQTPLYN IRLDRLQDQIVYKLVINLEEREKKQMD
12214	26115	A	12328	1	419	FRVPSRCARCOYLPLLRGASQIGYSGVRD PVEEAVCPFSLDKLCAGRTTLPFKAVRQ GHLSLQRFLFPVWLCPAPRSYGYVRGR ASLSCGGLHPVGASWPRCLPTOASAMAG TPFPFASLPCLSLSDCCASNERGSGMV
12215	26116	A	12329	259	414	NMENSRLCVWPKLAFVLFGLASLLSAHL QVIGFQIKAFTRFLSEPSDAVT
12216	26117	A	12330	302	404	SCYRVSVISQARWLTPVIPALWEAEVGR IPEVGS
12217	26118	A	12331	94	375	SRDMSPGLLTTRKEALMAFRDVAFAFTQ KEWKLSSAQRTLRVVMLENYSHLVSL GIAFSKPKLIEQLQGDPEWRENEHLL DLCPGWSAMA
12218	26119	A	12332	7	246	NPVIDFSPCGGIRVRRTPAGRGGPALRRV PETWEEAGEKMPSESLCLAAQRLDSKW LKTIDIONCFITRKISLLPLFCHIL
12219	26120	A	12333	150	1	YIYFFHLVRGLPGSGGYDEYFVVVVVNT SPSVTQAGVQWCHVSVQHKPP
12220	26121	A	12334	34	426	EPGFLFVFFFLIRGKTKPLFPFWGTRKNP KSGKPLFTPPGKSPSEPPKSRGGPLFPQ TRSLRTQSWFGGAPKPLPGGEPKFW AGLGGDPPTPRAPRADQTLQEP IQAPT RIONEGWATKFPQMPGQ
12221	26122	A	12335	185	3	TVITPLHFSILGHARLMSRVAPPFAENR SMBCGLGRAVCLLTGASRGFRGLAPLL ASHE
12222	26123	A	12336	60	316	GNGPISPTDVTLSPOKPTLLQGHERRAT TQIKYNREODLLFTVAKDPVSVGWRGSG RGKILLPGRWDTPLVLPLAGNQASHCE K
12223	26124	A	12337	3	167	SFRIOVGNGHTSKHYPKIQYSDQAGWLT SVIPALWEAKTGRSLVERSLAPRAP RPLSVMCGRLTISRVEDSGARCWFLFI YETEFRSVAQGVRRDLGSLQTPPSG
12225	26126	A	12339	354	433	GWAQWFMVPIPALWEAKGVSPEVRS
12226	26127	A	12340	238	382	LLIVYNMMLLPDAVFTCNSSLTGGQGR RITRGQEFETSLAMVKEHL
12227	26128	A	12341	101	1	KTQTNKTRKTSVGTWTFPIIPAYWEA QAGEL
12228	26129	A	12342	276	23	GSCLLEGLKTRNRDHTKTPSVRHHCOR PKIDKTTMGRNQSRKAENSKNQSSSP SKECSLAATEQSMHDFDELRREGFR
12229	26130	A	12343	122	1	YMGVNERGCGGTFKSSSLSSOLWNAWPI IPATQEAEEAGW
12230	26131	A	12344	180	360	LKVYFFSVGDLFPFPFPPLDSSALPS ISGNFPFPPPLDEEAFKQVRAEVKML GKS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, /=-Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
12231	26132	A	12345	35	411	TMTIVDKASESSDPSAYQNQPGSSSEAVS PGDMADGASWGAWSVSLNDVSNHTLSLG PVPGRVYSSSSVDPKSKPSQKQDALG DGIAPPQKVLFPSEKTKLKWQOQTRVGA GLQNLGNTCFANA
12232	26133	A	12346	278	386	ITVCYKQTIIGQARWLTTILPISLWEAKV GGSPEVRS
12233	26134	A	12347	111	2	KSQTQGVQWLTVPVLPALWEAEVGGLEL RSSRLAWA
12234	26135	A	12348	215	316	LNKRLMISFIIKKKKKKKKKKKKKKKKKK KKKKKKKKGGPL
12235	26136	A	12349	265	404	SNISYFLNNNFSKALSINIKYMSQARW LTPVLPALWEAKVGGLE
12236	26137	A	12350	372	1	PVFPLFPFKLGEQLFPALRFLAVSFLP KAAHEQEIKERVLAVHKNPIDPVYGFPK KGPTNFPFLPQVRVIFLGAQGVSWGF FVYKGLSLAPKLGPPPPFFFFETESRSV AQDGVQWCDLGS
12237	26138	A	12351	318	416	QGRQWLTVPVILTWEAKAGSSSEVRSS RPAPP
12238	26139	A	12352	144	1	NGYAIIVECVULFCFVPLRQSLVSAQAG VQWNLGSMQPPSTSLVQAI
12239	26140	A	12353	116	1	SGRYSFKMKQCGERWLASVLPALWEAE VGRSPEVRS
12240	26141	A	12354	102	2	ETRYKKQPGGWRWLTPPII PVLWEAEV GSPEV
12241	26142	A	12355	112	294	LISPSFCMWPSPHSGPTWLSRLISQHSFS NLKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKGGGAP
12242	26143	A	12356	138	2	SFFLKVFVFFFFFESESRSAQAGVQWCHN LGSQAPPPGSRHCPVD
12243	26144	A	12357	148	394	FGEPGEKGEAGKKKFGORGWCEPPCR GQFKEKFPCKEKAAPLKNSENRLGWG TKPIPLGKKKKPPPOEOMILGPPQF
12244	26145	A	12358	97	3	EKFSFCFVRARHTHTHTHTHTLTLSLFL GFH
12245	26146	A	12359	204	2	KHYTPAACFAPCLDEAPIIAAKPATT TSEQKMAVPPKYANLGKSARNVFNKQYG YGLINLLKTKS
12246	26147	A	12360	156	391	NRGLFKVESFSIPCSVRCSLHPSALVS PTPPTTDTTNWALFFETESCSIHQTMGR WRDLNLQLPLPGFKFRFCLNL
12247	26148	A	12361	179	1	ALKKLLIIDNSHKTNI VGHFSRNFPT LFLLETESRSIARLECSANPTCHNL SGP
12248	26149	A	12362	218	391	TILKDCFTKMICLSQAQWHIVVVPATWE AESRGLEPTS
12249	26150	A	12363	2	356	TNSHVDNSITQKPEFCIPRCGGYIVCOL QLVERAFIFNFFFLKRSFVLLPRLEG RGAIFRVTOEGSNLLTLGAPLGLPKGW NYRGDHPGPAYFYFLMGKRLQLIQGGRG LKKNNLL
12250	26151	A	12364	94	1	KNPFLFFFFFSESESCYVAQTAVQWHD LGL
12251	26152	A	12365	237	2	YSSLLFKPAESARGILRHHTVPKSTSAI SKILFCFLFVTEFLSPGLKCSGAIKV HCSLNLGSSNSPTASQVPGS
12252	26153	A	12366	340	442	GLFVCFVWFLETESCSVTQAGVHWCOL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
12253	26154	A	12367	208	45	SSLQPS EGGEFFFFFSVFFVFRAGVLPCCPGWS ETPGSSDPPALASQAGITGATVNST
12254	26155	A	12368	60	443	CSSCVSSKPGQSPHLKKQGD RMGAHLISG GCTEATAGKGMKRLCLVAWSTCAGARPPS RNRGSGQHSARPGQPRLPVVRLLPPPPP QAQPKFCKKMWLGGPISIEPKQHPGPGG KKKWAGKAAPRLVPT
12255	26156	A	12370	341	421	SGWVRWLTPTVTPALWEAEAGGSPEVGR
12256	26157	A	12371	280	393	NTIDHYVTQWLTPVIRTLWEAEAGRSPE VRSSRSAMPT
12257	26158	A	12372	268	399	TLCSSLSAESIHSYPEFSCDKNYLMTH NEAYKACMKRAFHLPL
12258	26159	A	12373	209	468	EAVPDETSHPSPADSFSTSSNLACGTHH LRRLKLYVEELEYYPKRIQCFFHSFF FFBSRLLLLPRLECSGSGSIHACNLCLL GS
12259	26160	A	12374	381	488	TIITCLFQKQGRGARWLTVPVLPALWEAE AGGSQGOE
12260	26161	A	12375	276	395	GHVVTKKKLLTFVFFEMESCSVAQAGV QWHDGLSLQPPP
12261	26162	A	12376	295	472	VYSSVALNTFTLLCNHHPQSPSEVLTFP NKKCRGAILAHNCNHLHLLGSSDPTSASR VAG
12262	26163	A	12377	390	511	PGAVAHACNPSTLGGRGQGITRIPSL
12263	26164	A	12378	417	511	AHRSFFEMESCSVTQAGVQWRRLGSLQF SPP
12264	26165	A	12379	133	406	KLSLNKRDKYKQVCKETKKKKKKKKKK KKKKKKKPAQKKKSGSPR
12265	26166	A	12380	247	345	HMWSQNLNGLINKKKKKKKKKKKKKKK KKKKKKKKG
12266	26167	A	12381	156	15	NFFFFFETSCSSVTQTRVQWFDLGLSLQF GKQEQNYVSKNQKELIH
12267	26168	A	12382	275	1	KIVFLKGPPLFFFFKKKVFVFLKVGFKG GLNFIKTFPPGGKPKISKRQIFFFFFFF ETEPHSVARLECSGTTISPHCNLHLPSSN DSLASTS
12268	26169	A	12383	43	379	LLGYDESRLSWICLCLSCGLQLLSFLN LLVYVFCQTCVCFHYFFQYFSTLELLT FWDSNVNLIRHFGIVPQVLDLDFVFSFN KEIFLGQLQWLMFVIPAWEPEAGRSPE
12269	26170	A	12384	303	1	KGPPFFFLGLSPFFFLKCVFFPPFFFLRT PPFFFFPPFFKNNFFPPPKKNNFFPPFP PPFFFFPPFFETRSRSVAQARMGWD HGSQQQPPGSSDPTKP
12270	26171	A	12385	141	1	KKEPLRAPFPQLFCFFYFETTPCSVTQ ARVQWNLSSLQPPPLRYK
12271	26172	A	12386	31	417	CLADSSSNLTQSDSRGRAGIKHPIPL KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKSGGA
12272	26173	A	12387	291	412	LSSEMLLFCFVYFLRWSETTPVAQAGVQW CDLGLLQPLPG
12273	26174	A	12388	310	1	MTPCPLFFCFKKRKGAGGGIKKALFPN PQKEVFLGPPPKGPFPLGQFTPPWGKK IPRLNPLFRSSIFFFFLLDGVSRLLP LECNVISAHCNRLRLGSS
12274	26175	A	12389	117	2	KRNPRQGGPLFFFFFFFETRSRVQAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12275	26176	A	12390	117	319	AFQWDLGSLQ SFLKKPKDSTKNLLKLINEFSKSGSGPKI TIQKSVAFIYPNGEHSEKKIREVITFTI AAKTIKCPQQA
12276	26177	A	12391	95	2	EKSWTSLEKRLTGLWAKRLTPVPALWEA KAG
12277	26178	A	12393	127	395	IPGSGGFCILKQSAHLHLNKSFSFLSF IETQSLSVTQAGVQVCYLSLQPPFP KLROKNRLNSGGRCNKLRAHHYTPGWV TERDS
12278	26179	A	12394	252	391	FFCFPCVLLCFEMESCSVAQAGLQWPG LGLSLRQGFAMLARLVSS
12279	26180	A	12395	275	3	TFFRLVILKSKSETVEINCLETQKSHVAR AGVQVCSQDWEEKAGFNWRPSKARCP TSVLKCHLQWAGLQWMPVPALWEAKAGG SPEVRS
12280	26181	A	12396	111	3	GNNVIRGLRIRPLKQWACWFTVPVIFAF WEAEAGG
12281	26182	A	12397	124	1	VSRGRTVHQEKPTERAASPRLECNGTIS AHNINCLPGSSNS
12282	26183	A	12398	259	387	YQGESFCLFIFIFLFFIFDYTESRSVA QAGMQWHDGLSLKPP
12283	26184	A	12399	103	1	KGRFFFFFVFETESRSVAQAGVQWRDL SLQAPP
12284	26185	A	12400	308	416	CGNNFERAGRVRLTVPVIALWEAKAGG SLEVRSLR
12285	26186	A	12401	92	1	HTWGLTQWLMVPVIALQEAQVGLFEPR SS
12286	26187	A	12402	265	388	GLSWLFRFRPGHLFYFIPFETMSVSITQA GVGCCDGLSLQPP
12287	26188	A	12403	279	1	SLSSKMESGSLTFSTIDIWGIYITLSCC PGHCMPFSSIRGLYPLDASSTTSSCNV QNSPDMGTCSLWQQLRLRWEDCLNTG GRCCSEPGS
12288	26189	A	12404	387	152	NPPPGFNFGGPLKNFFSPRAGEKFVFL KRPPPPPPPPPPFETESRSVAQAGVHW RDLGSLQALKSPCDLVSAFKGF
12289	26190	A	12405	262	464	ITFWLACILVIHSSDFDGHGLFLPLAVA DSAAVKHSCSTICLNIEYIPNGIAGSC GISVLNPLRNC
12290	26191	A	12406	204	67	KCFGQAWLMPVIALWEAAGRSQELR SSRPANAKELNNRTRAS
12291	26192	A	12407	134	1	IQRPCIQLFSTFFILIFYPFTEIDSCS VAQAEVQWHDPGSLQ
12292	26193	A	12408	145	403	TYMYSLLINYKANSHTVKNKNTARFL ESLLCAHPNPPIKLIISLLREKKKKKK KKKKKKKKKKKKQK
12293	26194	A	12409	65	415	RNRRIISQSWNGPSRKPOSSALLCGLGH LTSQVRAVRSVPQCLVRIKGGSGPSKP KKKKKKKKKKKKKKKKKKKKKQKGG ALKKK
12294	26195	A	12410	124	404	PWWFELHRRNCQWPGTVAHTCNPGTLG KKKKKKKKKKKKKKKKKKKSSSSS
12295	26196	A	12411	164	2	TGAGLTIMDMVGVPDILQRFCLVFLC FLVFFETESDSVAQAGVQWCPNSSL
12296	26197	A	12412	114	3	PGMVAHACNFSTLGGQGGWITRGQVYRT GLAKTVKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12297	26198	A	12413	583	391	LADTGFHHVGGADLKLPLTSCSTRLSLPK CWDYRCEPPHPLAVPDTVLSTRGLISEKS FLPLCTFR
12298	26199	A	12414	280	2	KVSSMNAQTSVLFSITMIGISETLKYRGR KKRREREGREGREGREKDECRKVRSE IEGKKRKRKEYREGRKRRIEVSANEET PRDHPANK
12299	26200	A	12415	264	352	RLVHGCDIYICINITYTHTHTHSHSTH T
12300	26201	A	12416	359	485	TDARMDWCYQEGTGSQAWLTPVIPAFW EABAGGSFEVRLS
12301	26202	A	12417	171	1	PLFRNWFGLFELPPPEYQKKKGYPFFFF ETEPCCVTQAGMQNYDLRSLQPPPPPEFK R
12302	26203	A	12418	265	1	WHKSNELAAEASAPVKARASNTILGPH THGKRRCPVSLRNVLDEGVKSTNFFPSF ETDSSHVTOAECSSAISHCNLHLMQSR DSGA
12303	26204	A	12419	278	388	SSLTGFPIRRRNEPQGHGETPCLLKIQ KLAGCGGV
12304	26205	A	12420	205	413	WNLFVYLYQTHYKRVVSYNTILFTNKK RAIGQAEWFTPIIPAVWEAKVSLPEVR SVRLSLPKWRITS
12305	26206	A	12421	103	2	RSLSKRTETITLGLPAVLIILFPPLIT PTSKY
12306	26207	A	12422	372	478	NIFVFLKETPCQSQWLMSVIPTLWEAEA GGSLRPR
12307	26208	A	12423	174	416	KMHYCVLSAFLILHLDTVALILSTCSTL DMDQFMKRKRIEIRGOILSKLKLTPPK NYSEPEEVPPEVISIYNSTRDLQ
12308	26209	A	12424	572	733	RFSCLSLPGSDWYENCLNSGSRGYSEPR SHHCIPAWVTEQDSVSKONKTQSA GYIFIFIYFFETGSCSVAQAGVQWNLG SLQLPPPPSSDS
12309	26210	A	12425	123	2	TADFYGVNYISIKLLPKKKKKRGPFKE SKFTAAGLQKNIFFLSAPNFIALAVLKL RRDWETPG
12310	26211	A	12426	224	417	FFETGSHPTVTQGMQWNCNLSQLPTNR LKQSSHLSL
12311	26212	A	12427	115	3	PWAGHLTSLGLSLPIFNIGIAGQACWLM PVIPALWEAEGRSLEVRSSK
12312	26213	A	12428	250	398	KKGLVWVGANKLWVTFPQKFFLNQPSGW ALTFRGSWFSKRRAPAPFFFFFWETE SHSVAEAGMQKHDL
12313	26214	A	12429	215	3	FSHHBAKFGGGLPYRQPLGLEKETEPR LNDRFMAGPSFFAQQLRWFFLOKEWER EGCSFVQCVEGFAMWPYPLGSPPOPL FFFFFPEAGSPSVTOAECSSGISTANC SL EL
12314	26215	A	12430	345	2	LYSSLGDRVKLRLEKTKNKWCLHSYIS TCKIINLHDYILPCTKTNSWIKYLVNR TNSIKLLEEDISVNLHELGSNDNSFLMT PKAEIIEKIIYKLHFIKKIFHVEDII EK
12315	26216	A	12431	348	3	NTAIGHPHQAIYLSYLSIYLSIYLSIY LSIYLSIY
12316	26217	A	12432	160	52	GRSKLHICREHSICATEHVCGCDTENNT NLCOVQWLMPSVILAIWEAEAWSPSVRS
12317	26218	A	12433	180	2	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12318	26219	A	12434	193	3	LRA PGAENPPPKGGPPPPFFPPRGFPFGVFF LKKRGFPFFPPFFFDTESSVAQAGVQW HDLGSLQ
12319	26220	A	12435	321	422	NVEGDFLQRIKNIRYWPQAVAHTCGPST LGGRGG
12320	26221	A	12436	116	2	HDRFCLFVYDRVSTLSPLRCESSAISAH CNLRPLGSSN
12321	26222	A	12437	302	400	THTHHTHTHTHTHSGLLYLFPKGKQSH EFCW
12322	26223	A	12438	329	399	LALQARLECNGTISAHCSCLCIFY
12323	26224	A	12439	310	2	KPTLSRGLFCARPCFFRRSNMRSNPNQS YQVGKDTFGFTVKYTKLKVLGPRSGPKG ARQGVHKGKCLLTLPKMLRFLFPFETES CSVTRLECSGAILAHCNL
12324	26225	A	12440	151	401	EGMPHLPGSHSSSNITLKGRRSGREARR KGRKERRKGRRRRERKEEKGRRGKIRR RKDRGENEEEEENNRSSKVSLEISTCP
12325	26226	A	12441	276	1	FHPFGRPSVSPRVQPKIGIITHTCVARI EKGGCKALSLCPQYVGSNFFFFETRS FSVAQAGVQRCDLQSMQPPHPPGSSDDP APASRVAG
12326	26227	A	12442	140	1	NSHFPKNLGSPSSFFFFYLETESRVA QAGVQWLDLRLSLQPPPPG
12327	26228	A	12443	310	3	LPFCSWGLYGAFARCPPLMDKQLSQVPL WACPLSTAGRTRLCVACIKAAQAGQGF FFFTESHVSVTQAGVQWHDGLSLQPPHT AKPKHTHTHTQTHTIPDT
12328	26229	A	12444	337	2	GFFAIVPKKGQKMFSPFPKEGIFSGPC FISSTPTLLGVKKILPPNTEIRPVLSS IINTSVHIREQKKTYYGIFTGKSRFFF FETDSRSIAQGVVWRHLGSLQAPPPG
12329	26230	A	12445	112	9	GRVRWLTIPALWEAKAGRSPEVRNSR PAWPTIR
12330	26231	A	12446	172	3	IPGELLIGRAKFAKNWPAWPRGIPGLGR QKSFPPFFFTETESRVAQAGQWNLGGS
12331	26232	A	12447	221	418	RKAERLEVFRRRLCQARLRFPPHCLAA PMPLVLVKKPILGRANWLTVPVIALWEA EAGWLEERS
12332	26233	A	12448	280	392	PLGRVRWLTVPVIAHWEALAGGSPPEFRN LRPAWPDMA
12333	26234	A	12449	410	129	PSQETFFYPGPPGKTFPPLKKKKKNNRG GGGLPFPFPQKVKKKKFFYPCGRGFKQK KFNPLPPRGEKNPKPPPPKKKKKKKX KRKEKLV
12334	26235	A	12450	159	1	KKRGGLGLFTIKKTGDDPFFFFETE SRVAQAGVQWYDLGSLQADPPGLM
12335	26236	A	12451	270	1	NPLKFFFSFLFONPLKKDPAIFNPPFFF FPRIFFWFFGGVSKAGINFFFFPPFF FFFFFETESRVAQAGVQWDLGSLRT RGRTRG
12336	26237	A	12452	249	33	DKLVKLFLLKLLNSFFFFETESRVA QTGVQWNLGSLHPPPGFKFNAYAW AHAWVVLPAQNL
12337	26238	A	12453	190	86	TNDLGTQWLTVPVIALWDAEGRSLEL RSTRKA
12338	26239	A	12454	318	2	PPTFPLKTLFFVFPLKLFSTLSPKKK FSNPLVASPPFFFLTIGNSQVLLKGGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFETESRCSVQGVQWRDLEKK EKKKCNSSNGGRHYISTHLKYYK
12339	26240	A	12455	204	288	IQLNTHTHTHTHTHTHTHTHTHNETGKMW 1
12340	26241	A	12456	409	13	QGGAPPPIPIMLSLPEAGLLHVAQPGVK LLTSGDPPSPPSKSAWQKQETRLNLGG RGRSSQRPPPRPAMATQODSVSKTNKG TKNNKKIRKSLCKTLKEMLAMVNIITK YLLCTDVPSTVLCTHLYLT
12341	26242	A	12457	204	3	KKKSPFQSAKFFLGGGVFFFLVGNRS PFVAQAGKPLGSSDPPIIASQSTAITG MNHHTSSGAPH
12342	26243	A	12458	289	3	KAREKKKVGATKNIIRIVDLKSGRTSLCK KTEMPVPGNRRKQKQPNBNLRISTRPE TESRSVTRLECSGSAISAOVILPGSSDSP ASNWRQSETLS
12343	26244	A	12459	261	388	SWHFGRSKQVYCLSLGVRNQGPGNVST KTTIKSQAWHAPW
12344	26245	A	12460	313	391	RVGVRVHMLKPVIPALWEAVAGGSPEV
12345	26246	A	12461	112	7	HICIFYFETESRSVAQAGVQWHDLSLQ PPPAFGK
12346	26247	A	12462	389	3	ALHEGAARGSPFPPGGKKKRGSPFPMGN QAPQVPGKLGSGGPGFWFFKSLPLPQGG KPGVFYFKKVPPTPKDPPPTLWGGWGT TGGPPGPLFFFFFETESRSVTQAGVQ WRHLGLQPQPAHAS
12347	26248	A	12463	26	349	CIMIDSTGTGIFHCWCEMAHPFWKAV WQPLFFFFKRGVYFFPGGIGKPGFGLR EPLPGIKGVPRPNPLGGDLRPPPPPP INLGFPGKGVFMVWPGVGNFLI
12348	26249	A	12465	187	54	GYKNKPGQAQWLTVPVIALWEAKAGGSP EVRSSRPAMPWIRTRG
12349	26250	A	12466	199	55	IIQLRQNSFLPFCFDIIESCSVAQAGVQ WHNLSLSQLREVPGKHAPSH
12350	26251	A	12467	107	3	FAHCLIGNSFFSFFFFFEVGSCSVAQA GVQWSD
12351	26252	A	12468	120	1	GNWCRAQWLTVPVIALWEAEVGRSPEVG SSTRIGLPTHRP
12352	26253	A	12469	105	2	VYLYYIFLFFLETGSCSVTQAGVQWQD LRSVTS
12353	26254	A	12470	238	405	FHIICLIFILNQVSKWTHTVCSLLBII YCLLQWLTVPVIALWEAKAGGSP
12354	26255	A	12471	425	1	LNDAPIFEGGKKKKNFESPERGDKFFP FKRADPFFFFFFFFFPQKKKKPPFA QKKGGRGPPGRLSQWPLAGPLKITQPP WSRVFSPILLFFFDMEPSVAGAGVLW HDLHLPGSSDPPTPASRVAGITGVCHH A
12355	26256	A	12472	122	2	QNKYSLEKMNFTFGRPQWFTVPVIALWEA EAGGSPVRSR
12356	26257	A	12473	144	420	GAPRFISRPRGKTPGGGGRGKFNKGL GENPFFPKGVGKNPPIFFPFLQNGPT PLVLGSANMGFYLYLKRKGPGKREALR AEPQGPFFY
12357	26258	A	12474	80	1	KGGQVQWLTVPVIAFWAEAGGSPPEV
12358	26259	A	12475	54	294	LKSWQHRQRYVSLMSFIFPFCWYQS QRSPTGTQIILEISDTGKNKYPNCTGSH RKHTHTHTHTHTHTHTHTHTL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown. *Stop codon, /=possible nucleotide deletion, /-possible nucleotide insertion)
12359	26260	A	12476	364	234	EEKGPHHVSDDLNLNLSWSACGLGPKCWDYRSETSRSLASLPF
12360	26261	A	12477	288	450	PGTVAHACNPSTLGGPGWSRTPGLKRYICLGLPKCNDRELLPELPLCLIFL
12361	26262	A	12478	271	396	TISFLSYFFFLFFLFFFFFWKRSQGRESRF
12362	26263	A	12479	289	2	SGCLLERLKYRKDLHTKNFSVPHHHORPKVDKTPKTKGKQGRKTKNSKNQASPPKKECSSSPATEQKWMENDPAKLRKGFR
12363	26264	A	12480	323	1	YSMVYPYVFLTAKKQLOVNNNTQLTKCSYQLYCHINHSTLQTHNISTLMILGHIPLCIPVNLSEAWAATPALHFVKLLLTETLHHVCRALDIIILAIVSLVALITS
12364	26265	A	12481	279	429	MNGQRKCVVYTYLTLYTTEYTSITLKRKKWGTMAHACKPNTLGGHGGWTA
12365	26266	A	12482	308	423	LTFEKNITGFFFFFETEFCEPVPQAGAQGDLSLKLAP
12366	26267	A	12483	272	474	MVSWGLSRAKIPVWLSFFFFEKKSHFFPQGGGRGDLSEWQPLPPRSKGFSCFTLPSTRDYRPAGP
12367	26268	A	12484	84	229	LPKSVCHLLFLSSCSHVQACLPFTFC
12368	26269	A	12485	392	3	HDCKCSASPAMLPVQPAELTGKRRFPFPFKKRIFNSKQFQSWRKKL
12369	26270	A	12486	76	1	LFIKIPSPGGAPFPVGVQKKITFFFFFPFSPRTPFPFIFPPGKGPFGGGLGPPFFPQKRGGGFNSKWTWEKFPPLFFFFFETESHSAQAGVQVHNDL
12370	26271	A	12487	204	8	KLISWVHMPVVPATWRAEAGDFSFFIFFFFFFFFCCFKTGSHSAQAQAEQBWHDHGSLQPPQPSFHLSLCATMPGLFFLFLFLFI
12371	26272	A	12488	96	3	KKPLGQAMFFFFFETESCSVAQAGVQWCDL
12372	26273	A	12489	126	1	KPBHPLPFFFFFFETESHSAQAGVQWCVLGLQAPPPGFTP
12373	26274	A	12490	107	2	IAGRAWLMLAIPTLNEAAGGSLPRSSQPTCAT
12374	26275	A	12491	302	2	GGGFFFFPFRKGGVFGTVLFGVDFGFSPPVFKTGPVFLGAQKKKIFPPPGGKINFFLGRGLPFFFFFFFEMTSCSV
12375	26276	A	12492	248	398	AQAGLQWCDLGLQHPPTQVTLGITAQSYSRVHINNRYDLAV
12376	26277	A	12493	341	1	SGSHPDGAAIKGSFVORLSKYKTSHFREIYPLEHASSISKYETGALPCSQELLNSQENSVMNFKPCLNQLFPQDVMSCIIIRFQTKDTLKHATIQEAKTSLPCTHHTHTHTHTNHSIFELLCMQCDYIN
12377	26278	A	12494	95	3	PLFFFEKSCSVAQAGVQWQNLGSLQPPPP
12378	26279	A	12495	62	420	CAAKLCTEAHTAASADHTSPHGSVSGLPCHFPPPHRRQSRPGRKPGAHLRAGRALSQKPVGSGATPHNLHHQIRQTQNGLIQLLGDROAPWVTVPLVPLWEAAGGSLARSRLPA
12379	26280	A	12496	58	492	NSPPFPAPSQRTPSPAAAAAFTTGSSSAPCPASSSWPRSSIALITYFPDQPCGLSP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NNLAWKQNVLCFKERLEKMFRRIRQVLG LLVWTLIAGTYEYFRVPAGGWMFVAVFY WVLTVFLLIIYITMTYTRIPQVFWITVC LCFKR
12380	26281	A	12497	2	198	RQGGILSAGFLVPGDTSVSSPRPRAAGS QSSSTRVLWKLSGAMLRLLVLMGVSAF TLQPAHITG
12381	26282	A	12498	71	346	GMEFSSKSTETHYQPGNSDPAHTATGP GGLSAAKAPANTPLMLDTSSRKLVAWDGT TDGAAGVILAAVAADQSTTLTFKSGTFF RYEDVLNP
12382	26283	A	12499	122	59	HQIYIYIHTHTHTHTIYIYIYI
12383	26284	A	12500	220	3	PKKBSVRCVANKWILLILCOTLSHWSL PQSSLAATPCCCLNIGTVDVLQGLGVAH AMNPSTLGGRDGWITS
12384	26285	A	12501	125	1	HVLVLSHFLVFLFFETESKRSVTRPKR SSAVSAHRNIRLS
12385	26286	A	12502	373	476	ILTRDGVSLPLRLECSGTSIAHNLCLL GSGDYP
12386	26287	A	12503	440	573	STWEDHLSLGNRGCSPEPLHLCTFTWT E
12387	26288	A	12504	146	5	HPHLQTHNGAFIPQELTFLLEKRDGLR CRGNRSVPVGPFPWNRSLD
12388	26289	A	12505	140	44	AQGLTPVPIPALWEDEVGRSEPEVRSRSD WPTR
12389	26290	A	12506	247	420	LEISVTFSCSPGCLPKKHITHTHTHTH THTHTHTHTHYIRTYITTLARPLSALH NF
12390	26291	A	12507	346	473	KAYIIGLNCFYETKSSVAQAGVQRDL NSLYS
12391	26292	A	12508	87	414	RTGVYRVGKDRSRSDDLICPPLGLPK CWDYRREPPRACPLPLSHSPSPPHFSF LSPLFSLPSPCSPLFYIFFPPLPLPISL RWRLIPEGFRMAPLCIQMPLGHD
12392	26293	A	12509	386	467	LLLFFEMESHSTIRLECSGAILAHNCL
12393	26294	A	12510	344	472	KFLPFDPVAVSLGITYPKSKSYQKDT TRMFIALIFTIANTW
12394	26295	A	12511	424	132	RGEPPRSRGSILSPVGPFGGETPFPFLKKQK ITRGGGGGPLFPPLKRVKNGSPFPFGGK SPHGAKFFCPDPAWATKRNVSXKKKKQK TKGSRILLYNE
12395	26296	A	12512	351	510	GGTFCKQSKIQSLQPAVEIFIPORVQW LTPVISALWEAAGGSPEVRSRPA
12396	26297	A	12513	362	463	NTTWLGAHACNPHTLGPGGRITWG QEFETS
12397	26298	A	12514	137	1	ETISLLPLRLECNAGTAHNNHLPLCSR NRRPQKAVHVRQAYSFO
12398	26299	A	12515	251	592	GAFTGLAFTMAGGRPHLKRFSFIIPCV FVESVLGIVILLAYRLEFTDTFVPHITQ GFFCYDSTYAKPYGPPEASRVPPALVY ALVITAGPTLTILLGELARAFFAPPLLAG PV
12399	26300	A	12516	3	413	SWGSRKFLCPFRSLSGSRELHPAQGDRP GPLSSSGKRETGTHRETLGKKVSSAPE AQQAGLRSLQALGGLCYDLSPLTEPRPL LAATAFPRPCPALPHQPQRTMGVSSSL ISGHSFHSKCRASQNLKRKSSHLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
12400	26301	A	12517	115	2	KSHGGHGEVLVSVLVGLAMEVGLVLVW KEYDGAALA
12401	26302	A	12519	444	34	YCLRQKHTEYRRRSNLEMASCSLGRKT CTFFTLYQNLKMIKLSSEGTWQAEWLKS RPLAPNSKVVEAKEKFLKKIKSVTSLNT YILRKPNSLIADMENILVIHIEYQTSYN IPSSORLIQSKALCLFNYLEMECRI
12402	26303	A	12520	1088	935	ILIIIFINRCEFLRSKSSSEETIYQIQS YKGFVDRTVMYNSNFFLKLFDLYL
12403	26304	A	12521	2	347	AMAAGSRFSLLLAFALLCLPWLQEAGAV QTVPLSRFLDHAMLQAHRAQLAIDTYQ EFBETIYIPKQKYSFLHDSQTSFCFSDS IPTPSNMEETQOKSNLELRLISLLIES WLE
12404	26305	A	12522	50	205	VVGESDRQSSGFNASSAHACNPTNEVET GGSLEARSRLQCTMFASVKSTRP
12405	26306	A	12523	105	2	RFVCTSTIKVRLDLSRRSNPGFRLTSN SSLYER
12406	26307	A	12524	279	455	KTKNWLALGGPPCFPGQYGETPFLSKNE KLGHGGAPLYSRLRLRRRNSLTPGD RGC
12407	26308	A	12526	305	454	LYFLFLPPQIINRMVLFFVCFPFETES HSPVQAGVQRDLGSLQAPPPG
12408	26309	A	12527	363	459	CTILGQAWLTFVILALWAEAGRSPEV RGR
12409	26310	A	12528	182	36	QHIVVFHKEHGGVRLTFPISALWKAEA CRSPVRRSSNAWAHACINSA
12410	26311	A	12529	388	530	KSLNFFFRDGLNCVQAGLELSSDP PAGAFRVACTTSMVHHSQI
12411	26312	A	12530	134	1	GHKKGVLFFFKTESRSVQAGVQNCIT GSLQPLPAHATPRPV
12412	26313	A	12531	230	1	KKFGFFPQAGFGGGLHLFTTLAPWQAI SQKREKPPFFFFETEPHVSARLECSGT ISPCHNLPLSSNDSQASTS
12413	26314	A	12532	145	3	KLKLELSAIPPKPRKEITLFFPFETES CSVAQAGVQRDLGSLQAP
12414	26315	A	12533	365	2	LIFFFTSLIWTITLGLTILNCPCIPGVC YIQFANTFRFALETFNEIAYNLIILPL TKQDTNLIKLIKHSFFSNFLKQLLFV FCFVFLFAMESCSVAQARVQWNLGT LQPPPPRFK
12415	26316	A	12534	313	475	FFWSSCSFQGGGGITITIIILRWILA LSPLRLKWRDLGSLQSPSGFKRPF
12416	26317	A	12535	124	3	MGSLINGAELSVYRQVCDCKPGVCVCL CVCVCVCACTCM
12417	26318	A	12536	333	58	ACNPSKVRSCRPANSMVKSCLSKNAKI TKEWNNANFFVFVFLVEMMFHHVQQLS LKLLTSSDLAASASQSYGITGVNHYAQP ARTRGFR
12418	26319	A	12537	214	3	SDPRRACRCPKEAPEQQRRLPGGSVPAL SIPFFFKTESCSVPLSPRLSCSVISAH CKLRLPGSCVPPAS
12419	26320	A	12538	146	1	MNPLAFTNPRPPQILKPLFILRRRES HSAVQAGVQWCDLSSLLPPA
12420	26321	A	12539	195	1	IFTFPPQAKRGDPFLSFFFFETRSFSPR LECSDAITAHCSLNLPGGPEPTTPIPK SWDHSVPP
12421	26322	A	12540	151	334	LLGRLRHKNLNLPGGGCGGTIMALCNI

[illegible]

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						NLRIPGSSDSPAS
12444	26345	A	12563	277	370	WSPTLVFQAQAQWCDLGLSQPALSRFKR PSR
12445	26346	A	12564	55	251	AMVITPTVFNNITINSKPLGHISFQLFAD KPKKTGENFHTLNKKDKGPGSCPHRIIP EFIQQGDDF
12446	26347	A	12565	129	3	KYSVLRPGTVAHTCNPNITLGGRGQQITW GWFEFETSLANVAK
12447	26348	A	12566	172	1	PPFKKKKPRPPKKNNPFFFGAISAHCN LCVPGSSDSPASPSRVAEITGSRCHAEP Y
12448	26349	A	12567	257	380	GICRPLLGQVLGSGATGVRDPLEEAVCP LAELKHCAGRSTA
12449	26350	A	12568	120	1	GVFLFCFVLFETESCSVARLECSGMISA HCNRLRLGSSNS
12450	26351	A	12569	250	2	IGKPKTPQVWFLKTRGGGNAAFSFKFK FFQLKPPRPVFLKIFSCQKKIFFFFFFE TESRSVPQARVQWHDLSLQAPPPGF
12451	26352	A	12570	338	3	VSTPEKNFVHTRGFSKSSSKYKVCNPF FQKLGSPFSLKGVFGPKPYSCSGSR VSTAPYFLNPGPSKILPFFGFLGFE KFLSFFFFEMECRSVIAQGVQWCDLG
12452	26353	A	12571	5	556	ICCCCLKFKINTFQLGHFNKINFFCVTRSG PVTQAGVQWCVNLGSGQPOPLSSQS
12453	26354	A	12572	115	2	DRVSLVLVLAHCNLCRLGSSDSPASASRV AGITGARHD
12454	26355	A	12573	279	377	GQVQNLMPVVPFADWBAEGLLPQSSSR PAWAT
12455	26356	A	12574	117	1	KTLPLFFFFFEMESRSVAQAGVQWYDL GSLQAPPNGFT
12456	26357	A	12575	253	374	SLPGMVVHACNPSPLGGRGRRITWGRKF GTSLANMAKPCIL
12457	26358	A	12576	130	2	KFGPFLLGGFFFFFEMESRSFAQAEVQW RDLGPPQAPPFRFT
12458	26359	A	12577	132	3	RVGPFPLLEFFFFFEMESRSFAQAEVQW RDLGPPQAPPFRFT
12459	26360	A	12578	3	370	LKNCMLGRCRCSLRSNHCITDAMVTE RDSVSKKTLVLMKQWNPFLRLPLALC RKKFPGRPFQVTHLVKEVSLTKPCA EGADLDYDERTSPLFAKSWERNFPFV HPGPVEGCPK
12460	26361	A	12579	131	2	FIVFLPYFLFLETLSLSVAQGVQWHDV GSLQTPPDRPTTRA
12461	26362	A	12580	202	2	RMKKNQHKRAENSIGNQTSPPFKDHNSS QTRQNMWNEFDELTEVGFRWVITNS SNLKEHVFC
12462	26363	A	12581	109	2	KIFFFFFFFETESRSVPQARVQWHDLSL QAPPPGF
12463	26364	A	12582	105	375	LIMILLPLQILVHSGTFCLPFGFETEF HSTPRLECNVMSAHNCNLPVKTSPAS TSQIS
12464	26365	A	12583	106	3	RPITFFFFFQTESRTVARAGEQWCDLGS IQPPPP
12465	26366	A	12584	484	700	SSSNWRAFSRKDKTWMHTPEALSKHFI PYNAKFLGSTEVBPKGTEVVRDVRKL KFARP1KKSEGGKKKK
12466	26367	A	12585	301	1	TOPKRVTKMKNNIPEHAFLSSTFPWPLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NLPADFYATSQTKPDILQSMQAFKNS GIGQAWNLIIPAALWKAIEVGGLLEPR NLRPAWVYGKTLSQLK
12467	26368	A	12586	76	379	PLHPPASCAPASLSCLIGPSDPLFSD SARPGWGRGWGRAPQLPPSPFLYNLIK KWSRFCHQKKKKKKKKKKKKKKKKKK KGFFWRAPPPFFPGGGFFS
12468	26369	A	12587	109	376	LEFFKMSGVVPTAEPOFAGEMENQTKPP DERPDAPPEYNHSLPGPPGTAVPPPTG YPGGLPMGYSPQGPSTFFLYQVVGIIH PVRYQ
12469	26370	A	12588	323	1	KKFCPPFFPFLFQFKQKTNPLSPFSG GFKMNLGGFNPPFRPPWSPQIGFFLGRS KELILGLFPTRIGIGGFFSFFFCETKS HPVMRLCSGVISAHCNRLRLVS
12470	26371	A	12589	262	1	GDPFTTSGPCTNQKHELMNFKSDSLV EDTLAGRSVLINKLTPOTLQPRNTGPVL VIYSTPTAVRLQDPPIHVVHRSRKLKCP EKK
12471	26372	A	12590	284	374	TESRNWGWQWLTPVILPALWEAEGGS PE
12472	26373	A	12591	297	387	GQAWNLTSVIPAPWEAKSGGSPDVRSG LA
12473	26374	A	12592	206	407	VKPPQNPRKAQKLKGLVYIHYVYVYV YIYIYIYIMYICRYISLTVVYVNSKEG LDTAHTCNRS
12474	26375	A	12593	222	379	LTGTSIMGNFSLILVYTRVMGVSQWL TAVIPLLWEAEGGSLGSRSSRPA
12475	26376	A	12595	301	189	KKIQSQAWLFPITIPALLEAEAGRSLEL KNSRSASAS
12476	26377	A	12596	209	3	SVKPLFFINYQSQVVLFLFFRGLRKS TI SAHCNHLPLGSRFSCLGLPKCWYRC APPTLKIDLTGD
12477	26378	A	12597	306	3	NGKRGFYMAPEPPFFFFHFFSPLPFL FFFFIFPLPFCFALSFLVGSSLSRLL CFMQHIFYCDAWNTFDALIVGSIVDIAI TEVNVSTWRLSLTVR
12478	26379	A	12598	1	249	WFGQCPLEFSIQELQLFLGGGDEGVS LLLRLECNRAISHCNRLRFPSSGDPFA SASRVAGITGACRDHTCEPRVPFSS
12479	26380	A	12599	228	404	RLSSLSFVTFEGCLSPDILLKCPDFO TVTHTCNPSTLGGRGWNIIRGQEFKTS VNM
12480	26381	A	12600	101	380	LSLTKNCALLSEETMMQENTRLHRRVS EVEAVLSQKVELKASTQSRPLEQDLA TVITCSSLKRSLEQARMEVSQEDDKAL QLLHDIREQSRKLOEIKQEQYQAVQVE MLMMNQLIEDLVSAARRSDLYESLRES RLAAEFKRRKATECOHLLK
12481	26382	A	12601	464	3	CAIQOTLYEHFMKSSRLGPTOLKIFTC YCNKVFKHSLQAHRLIHTNEKPYKCP QCSYASAIKANLVHLRKHGTGEKACDY CSPTCLSKGHLKVHIERVHKIKQHC CKKYSYDVKNLKHIRDADHPQDMYCG SRGSARMSRALPS
12482	26383	A	12602	140	1	WIGSFLSSEEDGTVVQKISGVQSRSL VYIHTHTHTHTHTHTV
12483	26384	A	12603	112	2	ESLRPGAVATHNPSTLGGRDGWINKDK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=/possible nucleotide insertion)
12484	26385	A	12604	139	1	EFKWCERY KKRVKRGPPGGFKLGGKFFFSPTKFF FFETESCSVAQGVQWR
12485	26386	A	12605	204	460	SGQNGEYCHPRFCTLCRAISLLIAR VCLKHENKVASLSTQANGCFEGFSET ESRSVIQAGQGDDPGSLQPPPPGSCLS L
12486	26387	A	12606	317	1	KRPLFKNIQKPPFKNGAPRKKGPRCTF GPNQKNLPFFPAFLSPFPFMTCKAGVF FWGFPFPPTKIIGGQKVPFPPTFPFPF FFETESLSTSLSCSGAISAH
12487	26388	A	12607	248	367	TQILSSGSVQSLHHPICFIHTHTHTH THKHKHPS
12488	26389	A	12608	2	387	QKQQQRAGRETSTCSLRIISAPMTATFV ELSTKAKMPIVGLTWKSLGKVKAEVK VAIDAGYRHIDCAYVYQNEHEVGEATQE KIQEKAVKREDFIVSKVQWCILAFNT IVPKSQWQSLQTPQRC
12489	26390	A	12609	258	23	MWERTGIRPQTQTLTGEPEGLDHGRSIS PNSVMNGIVPHISILTLNGLNAPLKR PGIAEWIRIYQTMCCLOETGR
12490	26391	A	12610	176	433	DALSSAMGTVLGTQTFSPHTTEILMLSPF AWGSSSLTQTLFYVPSGAKRTGSYVLAR VGQKYKTLWLGAVAHANCNPSLGGGRWN IT
12491	26392	A	12611	312	410	AHMYRTCSRGWSWLTGIPALWEAEAG GSLEP
12492	26393	A	12612	3	289	VFEFLSRKLSYILRMFWTFKFWFLERF WLPPTIKWSDLEDHDLGVFKPSHLVYT IPYAFLLIIIRRVFEKVPASPLAKSPGI KETVRKVTFNT
12493	26394	A	12613	294	432	FMKLEFFFFFERRSCFVAQSGMGQGIN ASLQPLFPSSNPFSLPL
12494	26395	A	12614	138	375	SNATCSHADPLFLCCHICQALKRTIR QTFFEGKPYGLILLYAVFFFLRLSCS VAQAGVQPNLSLETPPPSA
12495	26396	A	12615	232	1	GVFORAKLRAGLCPFOAMDTFSTKSIAL CAQKKLSKMAKAVAVLVDDTSSEVL DELYRATREFTSRKKEAQKML
12496	26397	A	12616	236	419	LEMENGVWVFFPFPNPTLWETEGVRDOP GQHEETLSLKIIFKISRHHGMRGQSLL RRLRQ
12497	26398	A	12617	197	1	LCHSEGSFLSRVSALLFTLLLLVMESP PSVSQPGVQWPHFSSQLPLPRFKQFCN TLPSGWDYK
12498	26399	A	12618	132	3	NSFMHFLTFTYFEMESCSVAQGVQWRDP GPLQAPPERVGGVR
12499	26400	A	12619	255	2	MNSLNSFTDIAVPLPHYNRILPHFKIIL SYFLKSFQVKGIGRQKWLTPVIPTLWE AEVGRSLERNCPAHQPGQYKILLYKK
12500	26401	A	12620	141	2	FHPTYYIISCVCVCVTSRFFARLECSG AISAHCNHRPGSSNSPA
12501	26402	A	12621	274	421	TYVMEVCCTYYFLAQVLSLAPFNFYIIR PDPRTPRDPDRPDRPRPDRP
12502	26403	A	12622	132	2	NQSIKKKIELQGFQSGRGKGVQVWL HIIIPARWEAKVGRSP
12503	26404	A	12623	390	86	IFPFFYQNTNGMAPGNQIPQGFSSRFF FLRQVLAALNPSELTGTEITDQCRKCSS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SLSLCSSWDNRCAHPPVLNLFYVETGS HYVVHIGLKLHLSRYPG
12504	26405	A	12624	297	396	IIRVRGQAQWLTPVTPALWEAKAGGSPG VRKSR
12505	26406	A	12625	303	381	KFHLVPSINTMSGSQELQWMPVPHFL
12506	26407	A	12626	318	152	GDKRRVLVSKKKKNLWNFGRIQWVPPVIP ILLEGRAAGSGPEVRSFRPTGQQSMTFP
12507	26408	A	12627	48	388	QLGNGKVRLLYQRHSSSSFFFWGEGFPF GPQGGGGGPNLGPRESPPPGVKGTPPPS LLEGGEPPGPPPPPGFNFGWKKGLPL YPGGFTSGPKGEAPTTPPGGGGKGLP
12508	26409	A	12628	116	3	KVATNQAWLMPVLPALWEAKAGGSSSE RSSRTADAW
12509	26410	A	12629	227	400	VLVFLPFCKEHWVFTLLPVSYKKKK KKKKKKKKKKKKKKKKKKKK
12510	26411	A	12630	182	3	TNNLFPFPKFGVPLFFFPFPFPFPFP GSHTVAQAGVCSGAILAHCNLRPGSSN TPA
12511	26412	A	12631	134	473	ASTIMDLFGRRKTPKELLRQNRQALNR AMRELDRELRKLETOEKKIADIKIMAK QGQMDAVRIMAKDLVTRRYVRKFLMR ANIQAVSLKIOTLKSNNMAQKMGVTK A
12512	26413	A	12632	100	462	QLLLCCCCCROWTAFNVASPAFPFPAWA HMAPSLLEPPSLVTOICKLSAFSGPSI NAFLLSKKKKKKKKKKKKDRGAPLKK KK
12513	26414	A	12633	313	441	CWELLKWLVCFLCHITKNNCWAQWLTP VIPTLWEAEVGGSL
12514	26415	A	12634	129	400	VSQQCWPTFPALYSISRQALASPPQGRF WDLQPTMPSEPLFPAPWPKPLRLRAL PPAPRCLGPSTAQGLRSAGAWCGTGRHL HLRQC
12515	26416	A	12635	308	399	EIRGWTQHWVTPVLPALWEAEAGGLEPVG SS
12516	26417	A	12636	285	390	IFGVNLINSPIYFETESRSVVRAGVQWRD LGSLLQP
12517	26418	A	12637	260	2	GQGFPPFGGSGSGPKKKPLKGFVLVGG KQGFPPFRPKKGFPGVFFFPFQTASRS VTRLECSGMILAHCNLRPGSSDSFASA SR
12518	26419	A	12638	76	3	ALQVQWLMVLPVLPALWEAKAGGSSLE
12519	26420	A	12639	219	484	LZLQEPDLDPKLEPLPLAELAQQLQTE ELSLSEILCSYLKQALKVHQEVNCLMIF LGECEBELALKLKKSERGLLYGVPM LKDT
12520	26421	A	12640	33	462	EGLSWGYREHNGPIHWKEFFFLADSDQ SPIRIKTKEVKYDSSLRPLSIKYDPSSA KIISNGSHSFNVDFDDETENKSLRGGPL TGSYRLRQVHLHWGSDADHGSQHIWGV SYAAELHVHWNDSKYPSFVEAAHEPDG LAG
12521	26422	A	12641	2	414	SGPAAPATPMSIFPELVFNVDNGVLEGL VRGLKAGVLQADYLNLEQGETLEDLKL HLQSTDYGNFLANEASPLTVSVIDDRKL EKMAVEFRMRNRHAYQPLASFLDPITYS YMINDVILLITGTLHQRSIAELVPK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
12522	26423	A	12642	161	463	KEKARSGKPELLEPTTSATAMGLTIS SLPSRLFGKKQWRILMAGLDAAGKTTIL YKLKLGIEIVTTIPTIVNVETVEYNNIC FTVWDDGGQERIRPLWN
12523	26424	A	12643	124	2	TVFEGGQAQWLMPTIPALWEAAGRSPEV TSLRPAWPRTRG
12524	26425	A	12644	258	454	NRELCDYQGLREDSKRGKGEINQTAQCF LWPRQKMSQTKFKKDKKELIAEYEAQIK EIRTQLVEQ
12525	26426	A	12645	636	182	APLERPSMIFPFCRGGQFDDLRSSPAPQ TPRPALGDRKGTPRIAEFGGAGRAEAP PRGSRQRFGPQRQNTAHTKVRVTRLSA APARHSPAFIACRQVGRPRLSARRSGKK PHLTVWCFFSPQDP IQDTTLQILLLSLL GGDTFSDFFCS
12526	26427	A	12646	199	414	IYHTSRSLDRKLAQRYDELPHYGGMD GUGVPSMVGDPHAPGP IPPVHLNHPG PFHAKQNYGAHAPHN
12527	26428	A	12647	130	3	DRGFLCVHTPLKKNKNTHTHTHTHTHT TNHTHTSHHTHTK
12528	26429	A	12648	192	443	LLLCWAQESLGLGTENIASSHTAGLEWE SLFLACWFPWFGCLFVWLFVWFPSPKSGS VLTELCSSVITAHCSLDLPGSRDPPASA
12529	26430	A	12649	393	179	LHSRVRSGSCFCSCVSNPVTGGMHFTS SPQSNQEQADQARWLTPVILAMEAKAG GLPELKSSRPAAWTF
12530	26431	A	12650	263	2	KAPLLVYKMEPNPFGGNGFSPGMGTNPTF GVRPGGETKELFFFFFETGSHSVIQAGV QLCNLDSLQPPPPSVKPSQYSWDRHKQS NTK
12531	26432	A	12651	355	111	QDCPFIRLHLPLSFLSVFLECTKISLSD WRMLPFLGDPHPLALSSLSVSPINTWNY SPQOLMMFRDVAVDFSOEWECLDL
12532	26433	A	12652	271	3	RQLKNTLYFFSHKMLSTKHITYNYTLF LKSAPIFNLETDHNLNCFPGSISAKSVYI LFYFFETEPHSVAQAGVQWRDLSTLQPP PRPFT
12533	26434	A	12653	333	2	PPSPGVGNFPSPGQDPLGKTFFFFRGP PRFWGGGFFILAPFPFGGLFPFPLPP SQGPFFFPFFFPFFFPFEMESRSVSQAGV QWRDLSSLQPPRARFSDSPLYFLEGR
12534	26435	A	12654	310	444	TYLSNIFYFIFLFLVETESFSVAQDQWRV CGLSGLGPPPPFGGRFS
12535	26436	A	12655	336	411	DQFGHGGETFSLKIKLQKLVCEGGAH
12536	26437	A	12656	114	2	GYFFFFFGLESRSVAQAGVQCLNLSLQ SPPPGFKQF
12537	26438	A	12657	191	1	KNFILTFSFRGAKNGDVFFPPPGYIQTG ENFFFFFLKWSFTLVAQAGVQCNLNS LQFPFPPR
12538	26439	A	12658	1	445	LRTGSEFSGRDSKGLAAAEPTANFGLLL ASIEDQGAGGGGCGSRDQVRRCLRANL LVLLTEAGVAGVALGLGVSEAGGALAL GPERLSAFFPGECLLLRLRLMIILPLVG CSLIGGANSLDPALGRIGAWALLFFLG TTLASAL
12539	26440	A	12659	2	224	ESTASRIAEAWQPETLPKGLNYSGASP VVLNAVLPKKKKKKKKKKKKKKKKKKK KKKGGGVFKKKKIKGGGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12540	26441	A	12660	96	1	GLKDGRRGVQLTVPVISAPWEAKVGGSP EVMS
12541	26442	A	12661	1	457	CWVHLQKGCCHFTLGRHLSGQAEALLTSQ TGRPGRGAPHIPDGAARQRSSHPRRGG QAEALLTSQTQGGPGRGAPHLPDGAAGQR RSSPFRRAAGQGGSSPPRRWAAGQRLS SLPRGQGRAEALLTFTQGRPGRGAPHIP DEAAGQGGAG
12542	26443	A	12662	175	351	KGVFFFPSSWKAGGAINFKGTTFAPRGKG NPPFPNPSGGGGPKKKKPGQIPRPGFLG PPV
12543	26444	A	12663	247	401	SSNQEPGCKGPCVLTIFYFTLGRAWWLM PVIPIAEWAGTGSGPEVRSWRPT
12544	26445	A	12664	152	251	RENSCCPIKKKKKKKKKKKKKKKKKKK KRGAP
12545	26446	A	12665	2	365	APTRSRCLRHASCTACTRTVSTDTSSLRR ADPKGRSALLADIQQGTRLRKVTQINDR SAPQIESSKGTNKEGGGSANRGASTPP TLGDLFAGGFFVLRPASQORDVAGKEEPI LAPLWTVSP
12546	26447	A	12666	179	1	LELSKSGSHWMHFLRSFYSLSLPOLN TTVWPTIITPILLTLFLITQLKILNINY HLP
12547	26448	A	12667	279	35	NQAPFKARFFTFKNVFLKEIKKKRCWS GAPPIIPPPWGGGGGPPWGGNLSPPGP PVSTPFNGAQKKKKKKDRYGGACL
12548	26449	A	12668	299	399	TSIKKQKRGVPVQMLMPVIALWEAKVAG SPEVR
12549	26450	A	12669	1	385	KMONRGFFFLTFLLALGLTSGAAKKKNK GKKAQPGSKSPNWPWGCPSPSSXDCGGV FRKGTWGAQTHGIRGRGPCNWKFEAN CKSKFKNWAGDGGPGTKVRQGLTKKAP SIAGQETIRVTRPCT
12550	26451	A	12670	357	1	AGKIATKICPVSSMQAPTCGPPVGGNDNQ GQAPDGGQFPPLQNGQTSSPDFSNENSP ATFPNQGQGDAPPQLEDEEPAFPHITDL AKLDMINRPVRVVPVLPKGELEVLKKK GLDFSKK
12551	26452	A	12671	107	373	TGNVTPLEDCACQEMRLAQVHLLETR KQQQVKIKOLLCENEVFLDKGDENTVV DLGSKROYADCSTFNDGYKLGPFYKIK PLLN
12552	26453	A	12672	196	45	YLYPHGSRKRLAKKYVYDKLFKECCIAD LSKYKENKVCFFPHIYGRFLFK
12553	26454	A	12673	33	448	KEGAERAGAAAPVWSPLIDRRDSARTES GTSLSGADMGDMKTDPDFDILAAFDIPD IDANEALHSGPEENDVPVGGDGKPPQCVG SESEHTASASAGDGGVGPVPAHASDHGLFP PDISVLSVIVKNTGLSRAGWRPWVVDV
12554	26455	A	12674	250	29	KKQTNMQSPYEDYRIFTYSSSLYHLS IYPPYILSIYLSIYLSVLPHTLSIITD YVSILEHLRPLWRIQP
12555	26456	A	12675	377	442	SDRQWCMFIVPATAWEAAGES
12556	26457	A	12676	1	553	RIFPGRRFRVKLSPCDPAMGRTRLLFVW AFCLLGADHTAGVQSQSPSNKVTKEGKD VELRCDPISGHTALYWRQSLGQGLEPL IYFQGNAPDKSLPDRFSAERTGGSV STLTIORQQRDSAVLYLCASSLATWHS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, ° = possible nucleotide insertion)
						ELLFAKHPHLSLQLLDTLNKGFSLLL PPHKGQVLDLDSFG
12557	26458	A	12677	232	3	GWSSDCQQRARVIEBKHSRQKGHIAENP SVHRHHQRPVKDXTTKMGKKQNRKTGNS KTQASPPPKERSSSPATCI
12558	26459	A	12678	134	3	IFIVEFGGKPFSCSTISLSQWLWCLFIG IGELLWQGVSTGTLV
12559	26460	A	12679	212	47	NGTHPHGYTLTHTKHTHSICATHHTHTHS LLLVRSFPLPKNTTISFRSCCKLGGP
12560	26461	A	12680	224	2	MKMASFLAFLLLNFRVCLLLQLLPHPS AQSVFLGPSGLANVMGSDADLPLHFP PMSAETMELKWVSSQCI
12561	26462	A	12681	35	397	KPLISQNKIHSVSSSOTGFFFFFPPGE KKPPFAPRGGGKGPFPPLPPGGGNRAPP RGEKKKGKPPPKNGAFPPQKEKTPG GGGGKKKTPAPPTPKVVDQPLPRREQRG PGRLPFRGA
12562	26463	A	12682	188	514	HTHLVVVLSMAAFFFFFPEKNFLFAPR VEKRGKDLGSLKLPFGFRHFSGLTLQG SGNNGAPPSPSVI FLVFFKEKGFPLVGR BGLILPPLQAPFPCISFRGAINGPS
12563	26464	A	12683	366	3	ISQTQTQTDWVLSLELGGCELARHDTVA IPQTRSPFPPLMISCMTLFSLQMDRAF PPFPQTPTITIQQISTSPATWPLTHLH STPLGSVEYSSNTHKSSLSPTSQWIRVD PMLASPTV
12564	26465	A	12684	99	1	SSCIRFFLEQAYGQSYGTYGQPTDVSY TQACI
12565	26466	A	12685	247	31	FLKEKRNQYFLIFQRWLDPNKPIRKQL KRSSPYSLNFRVKFVSDPTKLQEEYTR WVGYIFLENI VKTLI
12566	26467	A	12686	416	253	ESDMTTPVTGAPRDADLWSSHAKMLAQP LKDSQVEVRFLGSGQIFLCWRPSNLI
12567	26468	A	12687	116	3	CLLGRNWLMPVTPALREKAGRSLEVR SLRPARPNY
12568	26469	A	12688	380	1	SPESKSLGLNSKRVSPLLCYGVCPFPVS MAELRQVPVGGRTPOGELRPEVVEDEVP RSPVAEEPPGGGSSSSRAKLSPREEDLL DPRIQEELEHLNQASSEEINQVELQLDEA RTTYRRILOESASV
12569	26470	A	12689	157	488	REFVSGGSHLKAQVRLEALLLTGTGPV WAHLISILHMTAMGQRENKREAASSRIQV LLNHSQAIKQESIILFEMESGVWPRLO YSRMISASCTFLFSGSNPSVSAPI
12570	26471	A	12690	514	3	PSTRAGLLCGSAENATPFLCGITMAAGP LYTYPENWRAPKALIAAQYSGAQVRVLS APPHFHQGTQNRTPFLRKFPAGKVPAF EGDDGFCVFESIAIAYVSNELRGSTP EAAAQVQVQVSYADSDIVFPASTWVSTP LGMIRHNKQATENAKECNRPLRVSSSLV GP
12571	26472	A	12691	304	4	AESLRVAHERLDRSTSSDINFPQTQS NLEMMNSEILES WANYQSSTSYINTELS LPSKVNKGKSTEFQRMKTLQVKDQAITT RVQVRNLVYTVKINPL
12572	26473	A	12692	221	2	VGPATRDLCFADEPVVGRQKQKQWVVL CLSPNRGLAGRPDTLHITCASAHMRTHT CMHTHRHAHAHVHTHCI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, =possible nucleotide insertion)
12573	26474	A	12693	3	205	YMLCSILSTQEAFCISLGERKFIYFLTYL FRDGVSLLLPRLECNVLAHCNLRIGD RARLHLSKKQK
12574	26475	A	12694	233	3	IMGPAHLFGNHNWGGWGLMYKAFFFLF FFRTGSHSVAQAGTIPVHCNLRPGSSD SPAPASRVAGNTNVPHHTLY
12575	26476	A	12695	408	3	FAREMERFVCRVKRPLGMREVRGEIN IITVEDKETLLVHEKKAVDLTQYILQH VFYFDEVFGEACTNQDVYKMTHTPLIQH IFHGNGATCFAYGQTGAGKTYTMIGTHE NPGLYALAAIDIFRQLEVSQPV
12576	26477	A	12696	123	631	REAVCGGKGSGGGFGSRSSGAVSAA VQDMGDPGSEILIEBVPAPGASSTTD ENEDDIQFVSEGPSRPFLEYIDLCCDD ENPSAYSDILFPKMPKRGDFLHFLAV KKVKTDTENNEVSKNHCRLSKAKEPHFE YIEQPIIEEKPSLSKKKIDNLGASDCN D
12577	26478	A	12697	429	629	LALLYPLKVGWKPVPFMEEDILGPLFP LNEEEEEAEEEEEEEENPVHKIPDS HEITLKHGTTK
12578	26479	A	12698	158	404	LPILLSVERLVEIYATFIQDLFSASNIP YSSSVFRIEMDQPRTHSGPTTANPAPS STNSSAPSATNSKQERSSSLSKPS
12579	26480	A	12699	185	3	HRRFISTPSSVTHPAMVRLGLQVSGQLV SGSNARCIALLRALQVQCPILLSLMIQP HLVY
12580	26481	A	12701	181	3	TVWASMFLSAALRARAAGLAHWGTHVR HLHKPDMQNGAGGALFVHRDPRENNRDT PCI
12581	26482	A	12702	373	1	ILVQERDSQVRVIRMDIKLVSSRDVRGGR VEKQMTDHRVIYSVRKLQKRIPEPFI SRTTPKLLFLVLPSGKTPGHPVSSRTI PEPPLPTEPLERIPEHPVPSGTIPKPP PPLPIEPHETMY
12582	26483	A	12703	272	508	TKLGKQKQNRKTGNSKQSSASPPPKERSS SPATEQSWENDFDLREBGRFRNSYSE LREDITQKKEVCENCDLBE
12583	26484	A	12704	341	1	VPOHFHRLPAPSLGQPSWPLMSGSRPR SSLSLASSASTISSLSLSLSPKPTTRAVN KIHAFGKRGNALRRDPNLFVHRIGLWHLK QDSSGLRLWKRRNVLPSGHCLFFYKDSH V
12584	26485	A	12705	187	365	WEPSCRGPSAFKPTRCQSYDWCACGAE GRSAMEQPOERSPEVREEEETEEMAHAE GTP
12585	26486	A	12707	238	596	LWLVRVKYSIMSAAALGLEIVFVFFLAL FLHRYGDFKKQHLRLVIGITLAWYLCF LIVFILELDVSTTYNCRCKHAANSSPP ENSNTGLYATANFVPSGHCFCFKPWSYI PDGIMPI
12586	26487	A	12709	131	2	DRVSLSPRLCSGTILAQPSRLKQSSHL SLTGSWDYTHAAPCI
12587	26488	A	12710	151	2	VROGLILLPRELCRVIMINALCNFESPL SDPLTSASRVASTTATCHTC
12588	26489	A	12711	151	1	NFPBFDHFTVGLCRAGSSLIHWWECKL VQSLWKAVWRFIKDKLIDPLLY
12589	26490	A	12712	28	411	RVVPARPAGEPREPHSVWVKLNQQAP

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						LYGDCVTVTLAEEDKAEDDVVVVLVFL GSTLRHCTSTRKVSDDLETAPGHDC ETMKVQLCAFKEGLEFVDFTEKYFLLPR MYRYRYCLVTYPSAAV
12590	26491	A	12713	351	675	ENRHTFIYSLPLGLQKHQVLTVDIGFG GTAIMTVGKSSKMLQHIDYRKRWLQDL RIFIGTFKAFDKHNNLLCDDCEFRKIK PKNAQPEREEKRVLGLVLLRGEN
12591	26492	A	12714	326	457	ACSHHQKRSQAPPAHLWDFCDPFGSLP LLNPSVCNPGREVSPT
12592	26493	A	12715	200	1	TITKVCVPTTRTCGLKGLMAKALFDQK DRESETECQVWLTVPVPALEAEVGG LEPRSSRPV
12593	26494	A	12716	208	405	KKERENKHTNKGRKKMWHICQWSSSL HRKFQGIYRKTTGTGWAQWLTVPVPA LEAEVGGPPEV
12594	26495	A	12717	157	3	AKETPTHKSGCKRKFPPFETESRVA QAGVQWRLGSLQAPPQPTPCI
12595	26496	A	12718	1	472	SPAILPRLAILEPPLPDWSGTGRADAH LWYNFTIIHLPRHQGWCEVQSVQDKN FLSYDCGSDKVLMSHLEQLYATDAWG KQLEMLREVQQLRLLELADTELEDFPS GPLTLQVRMSCEADGYYRGSSWQFSFD GRKFLLLFDSNNKKWTVV
12596	26497	A	12719	537	1	LHTMNGNESSGADRAGGPVATSVFIGW QRCVREGAVLYISPSGTELSSELTQTSY LLSDGTCCKGCECLPNVPKVFNFDP LAPVTGGAGVGPASEEDMTKLCNHRK AVAMATLYRSMETTCSSHSPGEGASQ PMFHTVSPGPSPARPPCRVPPTPLMG GPGSLPPEPSPVSQACI
12597	26498	A	12720	369	3	NAKIIPATRKKALELELFPSSPDSTGG TPKATISDNDALQKNSNPYITPNNRYS HONGASYAWHFARKSQILKMECGSSHD TLQELTAHMMVTGHFKVTNSAMKKGK PIVEPTVTPV
12598	26499	A	12721	230	3	KFFFWLAGLTGKNDSASASLNQVHIS PFLSRHHPFSLGLPSSPVLLQSGRRQL ATLRALESASLSQHPHPV
12599	26500	A	12722	26	110	REQYAEGNMRGPAFGKKTSLGQLQK NVEV
12600	26501	A	12723	224	1	WQNDQDASDPKPYSTSCCLSFARLAR RYGDVFQIRLGSCP IIVLNGERAILQAM VQQGSFAFADRPAPAFASRV
12601	26502	A	12724	120	530	KKVARGRSRERSRRRSRPFKAITNR T*GTRCTPRRWRSTVLGMRSCTRAR* QRSGLSRGHTRSAGLCDHGSVRAGSD GADGTGGDRLRLGLGRDILLSSSSQSA FSSSASGSSFFSATQPLRMLLEYFWL
12602	26503	A	12725	434	222	KEEKSREGEVKEQD*EKDREBEVEK SRE/RRRSRRRRRSEV*YRKGRRRR REDILVAERSHRSFRNSIPSTL
12603	26504	A	12726	268	370	SNILLHMSMFFFGDIPSV*KNLPA* KTPGPDGFIIDKLYITFRGELTTFP HILLH*FTBEGAVLFNSFSKAASTIL TPKPNYDMMKEMYSPISSITWNCQSF FLEQIFP
12604	26505	A	12727	103	636	VCFLSKQPHGSRFPFCS/PPRPGS* VCQQSRPLQSPAFSAQQLA*HRRGL LLOLQG

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						PRSPMQPVPHGGRVSGQTLPGKPTKRP PGAPRRGGHSHLLK*LVCAQPPPRP*S *ASQAVFTLQVPGKPQWITP CPVVPVAP TP\PLSNGGLGVSRH*DGH*QAPTSP* PRCQGGACGEPQ
12605	26506	A	12728	1193	1638	GLGFAMFLPLALNSWPGQDPSVPASRAA GTRGVHRIHTOLQVSPNYKVLAMHSQ L*SQHFRKPRRSDHLRSQVDRQSGHGE TPSL/LKNTRISWAWHTPLVPATRAEA ARELPE\PGROKIASERPVKPICTASLG NTCETPPQKK
12606	26507	A	12729	304	101	RHLHWPCPSPLAPT\PDISHCEPEPKSQ SP/CPGT*CLGFLKCPSSCHFA*K/PLH PSEPARKSLAPDTC
12607	26508	A	12730	91	264	SORSISGLRVKENL\FVMIMFPPIYSSQ TFWSQTFLMLKIVFMGISISICYIL/NT EKNLGQGWNLAPIIPALWEAEAGLL*L RVKENL\FVMIMFPPIYSSQTTFWSQTL MLKIVFMGISISICYILKRI
12608	26509	A	12731	1026	406	LAHFRSQIFSFSHILVHFPERMVLNRY LACVRVVRFLHVLAYFGRIVLKRYF LVHFRREVRFRHMLACFRRMVLYCYFL VLRKILLIYVTFITYRKVFLRHNFLRG GY*RYKPGYAPRLSFFLYRCQCFLHYF LFYLWLRHLQF/CCFVVSFCLDFLFL FSAACVFSVLQIATVMFPFHALQLEFF* VVLCSNSRFQ
12609	26510	A	12732	1508	157	QDVGGSGFVDTHPGRMASIFSKLTLTG RNASLLFAHWGTSVLTGYLLNKRQVCA EVREOPRELPSPADYFDLIRKHNCAEC LTPA\YAKLRNKVTPNGVYTLQDCIQTGV DNPGHPPFIKTVMGVADGESEYVTFADL DPVIKLRHNGY*PQG*LKHTDLDASKI T\QQGFDEHYVLSRVRTGRSIRGLSLP PACTRAERREVENVAITALEGFKGD\LA GRY\YK\LSEMTEDQOORLIDDFLFD KPVSPLLTCAGMARDWP\DAIGI\WHNY DKT\PLIWINED\HTRVISMEKG\NM KRVLISR\FCRG\LKEVERLI\QERGWE F\MWK*AP*EYILT\CPNSLGT\GLRA\ GVHVRDPQSFSQDPTAFLKILEKPRTPR KRGHKVVWDIAA\VADV\ISNIDRIG RSEGEL\QVIDGVNYLVDCEKLERG QDIK\VPPLPQFGKK
12610	26511	A	12733	261	487	TGSETDCAKQASFLPREVPTVAEMKME LLKNKQFW\RGVVWAHCNPSTLGGQGW IT*QGEFETSLANMAKPHLY
12611	26512	A	12734	382	668	YKRITD\FVDSETHILINKRQSCRIPG FIQLVOLISHQLAAPRDYTVSHSVAQAG VOW/RNLGSLLEPLPGFKRFLCLS*HAL KNLSGCTPPQV
12612	26513	A	12735	401	27	QDRAEESAEPRAWSHSDNSHRYTTLFIC LHTHTVHNPVHS\HTHTHTHTHTHTHT TVSHRHTETPLLLKOTGLKF*NSRDD TPRSRFGSSGLQRLSSSPFPVPGTGV ASADFCGHDLTT
12613	26514	A	12736	202	182	KYLFIFINLTWNILFFFTSHCSVQQA EVH*S*LKPMPG\SSDSPASAFQVSGI

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						TGSPSSSWLTL*FPLKIGFTKKG
12614	26515	A	12738	319	2	QNTFFPHIYEVIPRDVAFLLFLEMSYSVY VVAVLSPLYVFNKLA/LTHCLRALSFL HKIQEPS\LGSGS\PLSCNTII*RLCL RSLHLVFRSLWILPICDSSVF
12615	26516	A	12739	1363	2000	DRVFVIPGWKCSGTIKVHCSDLDLPGSSN PSTSAF*VAC\ATGTYPYPCPOLNLYF* MEERGFTQVA\QAGSQNSWGSKNPTSE ASPKVLGMNKP*NLNPNRSLN*DGSI RYKDNYP/WEPPKRSYKCLRQKSI*L SAGPRDYASQPRKNYPISLLTFCTSS LHFNPTLTCSSQLQKSIRKLSBESC PPLPACSLKHTQAIKIITF*RLHRTA/L FYLLK*NCFRN*S*KYFLLSVSNLKI/ QWVRSSILHPGAPGYTPTV*RPKHKSNVL I*IQS\ITRCLFYILVYMRITFPLQLFL SKHPSTYKEDFA*VLPLSFFFFEMESRS AARRSLSSLQPLPRLKFRSLGSSW DYRCAPPGLASPLSS*GSCCSIQFIL RMSTISHAINVLVKNTYLVLSASEHS LTKKFC
12616	26517	A	12740	1696	743	GGQIRSGVHDOPDQHGFTLLSKIKQS AGPQGMHL*SQILRLROENL\NRGCS EPR\SRHCTPAWATEDQSDVSKKIK*KK *NHLESKQOQPALEPPQAGGQLRTE QLQDGRRELAADMTL*PHSKRLGALPR PLLSAYFYNKVHAARQAVLETPTPTTS YQREEGEQALILGVEAQASSPTVFHRR RQSQALCSHRKSQAPVRPAHPRRVPG LGKPSQGLSAHLGQDRAPAPRRASWDQ RSQAPISVTFPSVLDKEESVPCGPGFP HAPAPRGIHGATWEGASRGYPGHFLAL PQHNSDEQRPN
12617	26518	A	12742	2473	445	RGARRRRRRRRRRRRHQSRPVRAAPRQ PEQGRRRGAPTHQGPLIMMLELPPFGL PSQQMDLIDLWRQDIDLGVSRVDFD SQRRKEYELEKQKLEKERQEQKQEQE KAPFAQLQDDEETGEFLPIQPAQHIQSE TSGSANYSQVAH\PKSDALYFDDCMQL AQTFPF\VDNNEVSATPQSLVWPYSPG HIESPVFIA\TNQA\QSPSTVAQVAPV DLDDGMQDIEQVWEELLSIPELQCLNIE \MDKLVTETMVSPSEAKLTVEVDNYHF\Y SSIPSMKEVNGCS\PHFLNAPDSFSK HPLKNDPNQLTVGLNSRM/PTVYIDP G*KNPILVF\MAEPSIRQQAQPSPATLS HSLS\ELLNGAHGCFLDLFTL/CKAFNQ NHPEGTA\EFHGF\DSGISLNTSP\SVA SP\BHS\VESSSYGDTLLGLSDSEVEBL DSAPG\SVKQNGS\NTMYSSSGDM\VO LSPSQGAEHFTCMDAQCEHTRGKDLFV \SPG\HRKNPISQDKHSSPLGLISQR DEL\RAKAL\HIPICRKKSFNLPVG\D FNEMMSKEQFNEAQL\ALIR\DIRREG RNKS\AAASGICRKENWENIVEQDL DHLKDEK\EKLLK\ERGENDKSL\LLK KQLSTLYL\EVFPQAYRDEDEGKPYSPSE YSLQOTRDGNVLPKSKKPDVKKI

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12618	26519	A	12743	6	457	RPRNRPGLRVDPVRGRVGHAPHEGLVP ERMYRSGPTACETQAAA*ERAFGPSSPT C\RLP\IPRMSTSVPGQHTWTQVRVKDD EEDPLDQLISRSGCCAASHFAVQECMAQH QDWRQCQPQVQAFKDCMSQQARRRQEL QRRQEQAGAH
12619	26520	A	12745	297	12	QERPVRLMLVHFGRLRLADHLKLGVRDQ PGQYGETPSLLKI\PKLSGM\WNA*IC
12620	26521	A	12746	98	428	YNISFSTVLLLTTPITILCLYTRKDAI APESACVCPCLSLGQVA*IPNVVIRLD LSKKHVTYAGGFWCAKCVLDRINRAFL IDEH\KIVPKV*KALSSSKAFCEHET
12621	26522	A	12747	3	638	LMLWSLCWMAVSLFLQFTLGSLEPCQ QASWREVDLLHSGQSEASSKPSGGSVFV GLLLDQEMVPTLLVCICGILLHDEMVP LLVYTRGILLHQEMVTPHPLGLYPWDSPP LDGHSPPGLF\RGAAAPS*GG/PLPVLV YTRGAAPPSSGDS\PPPGLYPWDT\PPS GDRHSPPGLYPWDTTPSGDGHSPPALYP WDSPPSGDSHSPGLFPFRG
12622	26523	A	12748	2	333	DMVLLCHPGWSAGSI*KTKKERERMNLL HR* *IDRERERERERQIQ*KE*KRINEF EGSKERFTQSVQKRN\LEKIRTLDTS ETIYLSIYRN*SLRRQQRRTEREEMRH
12623	26524	A	12749	30	333	KTSYLLPVQWKAQNDNERYSSTNTIMA LPLPLPVFPRSPSDAERKLDCAISAISAH CNLPA\DSPASACRVPAIAGARRHA*LV FGFFWRRRRFAVMAVLVS
12624	26525	A	12750	231	39	INDLL/CLF*FKKLINGRVW*LMPITPA RWEAKAGSGFEPRSLKQ\AMITPMYSS MGGREQDPVS
12625	26526	A	12751	49	273	HLQVTEVFVFWVVCVFFRRWGGSHCV/AQ AGV*MLPTGTIVVRCSPSLLGSRDPPAS AS*VAGTTGACLANCRGF
12626	26527	A	12752	505	897	SVLRVQVYSASFSLFPHFHEVLPCHTQWNA VV*SOLTATSN/CLGPNMLKAPHLAN* KKIF*RGQLSMLPRLVLANSWPHMILL* LPE*LGLQARATAPGSGGTFPCLTQDSL MCSPTVHKLSDSIALETHQ
12627	26528	A	12753	335	542	CCEFFLSQVWMLPVVPAVR/SASAAG LPGPGSORLR*ARKSPVNSHCSAGGRG IDPISIKQQKNNR
12628	26529	A	12754	356	72	WHEYLLMEHTKKCHLS*GLYNGLN*Q /WCTHPVVPATWEAKAGESLEPRSSRL* CTMITPANSHCPPAWATARSCLNQSINO SSNNWQMITGGK
12629	26530	A	12755	340	127	NYLFIYFRDLSLTLMLRLECSN*FTGSI VHITLKLGLSSLP/ASASQVAGTTGTRH HVQLSNFYKIKIKPKP
12630	26531	A	12756	290	511	KKNQPGT/CGRSL*SQRFGRRLQADHL /DLQGHGKAPSL/LKNTKISWALWRTPV FPSSQEAEMEELIETSSRLQ
12631	26532	A	12757	254	549	YPGAKQRPFGDSVGRTHLQSRNCVLL HNQC*PKSNTQTFF*PKNLE*NAT*KS TDL/WPGAHAHLCPSTLEG*GEWIT*G QEFETSLGNI\PRQIY
12632	26533	A	12758	617	451	NKRKREGLTLLSRLKCNQVILAHCSLYKP GSSEPPTSA*VAGTIY*GT*HHAWAY

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						TF*SLDSRRTCFLVAVSNFFYYTSLFLKL RQQVLLTG/PYHLFSARPSSCGSDKKAR ELNLSLSL/CFFFFGKRVSGTGQGVQ*H DHS LQLMPSRLKQCSHLSLSNDYRS TTPHLANE/CNPLSGWSRPGCLK
12648	26549	A	12774	315	98	FRCFNLNSINPLESPHVRKTCAGRAQWLA PVIPPWFEEAA\SQMPQVHISR*LEARS SRPAWPTWQPKCLKYKN
12649	26550	A	12775	275	59	NPSFPYTIQKISWAWYMPFVVLATR/LRQ *AEIAPLHSSVGDRAKCLPKKQKTNKQ TKTSGEFVLVQGPATVC
12650	26551	A	12776	73	381	SLNSELSSIPRPTNEPSTSDSAWPMQ NLASEPLPLP*TPPFPFALSA/PE/P LPFTSPRDTLPPLPSYKQAPVLSVH PPVMLKYVSPSSPLLSSFLYL
12651	26552	A	12777	274	342	LNCVIA*WLMPTIISALNKAEGVGSFFA/P /RSLRPAAWATW
12652	26553	A	12778	2	478	TIYYTKYITFRVNLGLQLLTAFPCVCV CVSLNGPKNAKDYGGSHLKYSVYITGFL LQFSLKFDCLPCVCVCFPP*MA*KMPKI M/RGSHLKYSVYMT*FLF*FSLKLKYFC DPILRKI/WPGAMAYTCNPSTLGG*GG QIT*AOEFETSLAKVVKPCLY
12653	26554	A	12779	680	453	SETDWRKNKFFPSNPNLRTNSWNSNC SKRTFKGH/RVGLGVLAHTCNPSLTGGR GWSNP*GOEFENSLTNMNVHFS
12654	26555	A	12780	59	487	SLKHHPERGLSQFSQCWTOEMLGGSHVQ QRAWELCAPENLTCPGYLSFFLRDQDAL LSKLECSGTIPAHNRNPSLPQKLVSSH LSPPSSWNSRCTTPHQLLLEFF*DRIRL FCPSWAVAQSOPTVT/SELSPQLKVS SHLSPPSSWNSRCTTPHQLLLEFFNL* RQVFTMLPRIVSNS*VQAILPPWPPKVL RLQA
12655	26556	A	12781	109	361	LSFWHHSRNYTLYPYTLNFMWSAFPTP KEEFFFSFPETRPHSVQAQAGAH/AIIA HCGSLDLLGS/SDPPTSAS*AGGTAIIP G
12656	26557	A	12782	3	204	LIDGSLALS*C/LFGCAITAHCSLELLG LGQ/SPVSATRVAAETGVCHQAQAPVN LHLRTSKHCHG
12657	26558	A	12783	2357	6366	LTGS\NSHTITLT/LNI/NMGLNAPT*RH RL/ANWIKSQDPSCCQIETHLT*CRDT HRLKIKGWRKIYPSPMGQKKKAGVAI\ LVSDKTDPNPTIKRDKEGHYIMVKS IQEBELTILNIYAP/NTGAPRFIKQVLS DQRLDLSHTLI/MGD/FNTPSTLDRST RQKVNKDTQELNSALHQADL/IDIYRTL HP/KSTEYTFP/SAPHHTYSQNWTTIVG SKALLSKCKRTEIIT/NYLSD/HS/A/IK LKLRIKNLTQNHST/WKLNLLNDNY\ VWHNEMKAEIKMFETNE/NKKTPTYQN FWDAPFAVCRGKFT/ALNAHKKQE/RSE KLDITTSOLKREKRSKQHSKASRRE ITKIBAAELKEIETQOKTLQ/LKIKSE SRSWFF/ERINKIS/RLARLIKKKREK NQDIT/IKNDKGDIT/DTDLTEIQTITREY YKHLA/NKLENLEBGMDFLDTVSLPR

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						LNQEEVESLNRP\ITG\SAIVAIINS\L PTKKSP\GPDGF\TAEF\YQRYKEELVP \PLKLFLIEKEGILENSFYASIIILI PKPGRDTIKKENFRPISLNMIDAKILNK ILAKRIOHHIKKLIHDDQVGIPIG\MQG WFNIRKINSINVIQHINRAKDKNNHIIISID AEKGFDKIQQPFMLKTIINKIGIDGT\YY FKIIIRAIYDKPTANIILNGQKLEAFPL KTGTRTGMPSLTSPLLFNIVFCPIVFWA R\AIRQEKELKGIQLGKEEVKLSLFADD MIVDLNPIVSAQNLLKLSINFSKVS KINAQKSAFLYTNRRQT\BEAKS*LMS ELMSELPTTASRIKIKYLGILTRDVKD LFKENYKL\PLIKEIKED\TNKWNIPFI PCLWVGRI\IMRMAIL\PKVIYRFNAI PIKLPMTFFTELEK\TLKFIWNQKRS\ RIAKSLSQKNRAGGITLSDPKLYYKAT VTKTAWHWYQNSMVLVPKORYIDQWNRT EPSLIIPIHYTIL\FA\DRPLLEKNKQW GK\DSL\FIKW\CH\ENWLA\ICRKLNL \DPF\LTPTKINSRIKKLAVRPKT IKTEBMLGITIQDGIQKDFMSKTKKA \NATKAKIDKWDILKLSFC/TICTAKE TTIIRVNRPTKWEKIFATYSSDKGLISR IYNELKQIVYKKKKKTPTSKKWTK\DMNR HFSKE\DIYAA\KDHMK\CSS\SLAIR EMQ\IKTT\MYHLTPVRMAIIK\SGN NRCWRGCGEIGTLLHCWWDCKLVQPLWK SLWRFLRDLELEIPVDVPIPLLGIYPED YESCCYKDTCTRMFIAALFTIAKTWNQF KCPTMIDWIKMMWHIYMEYAAIKNDE FMSFVGTWMKLETILSKLSQEQKTKPR IFSLIGGN
12658	26559	A	12784	787	926	PQAIRRFRPPKALG*HNSVDLGNWAWFT PAIPTLWDYTHEPLYLAKIS*CFKQVYK FVLNCIQNCPGPHAAHRS/SOKTS*V*S NYLFFSFCEFTKFCSVTQARLQWHDLS LQPPPPGGFKRFSCLSLPGGDWYRRHLTR SANFCIFSRNRVSPSNPGWSPPTDLRRS AVLGLPKRNDYREPPCPAKIYTIMAPQ KVNSHSSQVVSFLS
12659	26560	A	12785	248	285	CVVIF*CMVILYVLIVVEKITSIRLAVY VV/CITIRLFPVK*ICSCLLGC*FLFFNV C\YHIFLIFVFFFFFFFFFFFFFFFFFELN ILY
12660	26561	A	12786	243	37	RRSAGHGGSCL*SQYFGPRTADHVRVS N/RGTELSLVKIQKVSQAW*EPVVPAT RQAEAGADAWDR
12661	26562	A	12787	75	289	DYRHEPRFFLYTFEEMDSHVARAGEH WCDLGLS*PST*GSSDSASTSR\QRH HAWLIFGL*RRGFAC
12662	26563	A	12788	83	256	RRMVYVUGLFTQAN*PKYESTEE/YI K/RLWYHLMYESSAIKIEKLOTRAQNR LILY
12663	26564	A	12789	197	499	QSLKSVEETVFRNNKQ/SIPTFOVILMP WWLIPII*ATWEG*GRSPLNPGV\DDP GQHSKTPSLQKTKFS*AWNRVPVVPV\ IGEAEVSGILPSPEERSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
12664	26565	A	12790	394	91	FYNSTRFKWKNIQFLITRCRGDQIQVIR AHAVQLGFHVLYF/CLSQNLSIYLIYSI YVYTRYIHTHMCIII*VLYITYYIV KH*KEHWIKHCFTTERK
12665	26566	A	12791	735	75	FFFRQEGFLSPFKRGVPPPHTKKFFSP RGSFLWGWGTSRPPPRKCFSPPPPPVFL PPPKKKKII SFSP TKLAPPPEYFKSPFP PSAPPPSPSPSTTFFFKNFPSPSSP SSPPFPFSPFAMEDPFVQSRRIY*FLPP PF*IPELPRVULKKKQGGSGWGLFPP PKGPKRVRPLGPEPKTRLCHIKTKPEFK KKKKKKRFLISCLWMMHMPAIPSTLGG
12666	26567	A	12792	482	342	MGVFVFFFTGSHSSTVWAGVQ*CNLSL LQP/PASSDPPTSDSRVAGST
12667	26568	A	12793	405	169	FYKKKKTGSLSPRLKSCSTIYIAHCN LELLGSRSLRLSNHTPLAS*ARTVS VCHOTHLIF*FVFTGSCYVASA
12668	26569	A	12794	270	94	YVCYSYKQIKICSHVKRRE*NTFKYLL KYIALGLTGHFFPL*TFSKTVTLNPGAV AHACNLSPLLEGQGRWII/R/QEIKTL ANN*IPVFLHVNIFLVCVSYIHTLDY LFVYSYCILISL
12669	26570	A	12795	284	415	NFIKIIKKKVMGLFYGKTFLLNKKKKR KKK*WPGTVPHA*NPSTLGGLOGWITR GOEFETSTLATN*NPSTLSIRGF
12670	26571	A	12796	1387	32	APSSFAIRSFSSGPMNAFFSSMWKRPW PNLEVVMNLRISIFSRARRFVCTSKDLR RVSTRFLVHLTAFLGYKAGMTHIVREVD RPGSKVNKKEVVEAVTIVETPPMVVGI VGIVETPRGLRTPKTVFAEHSIDECKRR FYKNWHSKKKAPT KYCKKWQDEGKKQ LEKDFSSMKKYCQVIRVIAHTQMRLLPL RQKAHLMGDQVERGAPVPEKAD/WAPR EALSSKVLVTQVFWAGIK*SNFIGGDP AKGYKGGQPVCAWHPKRLPQRPHPRAL RKGSPVLGAWHP*ARVAV*ESVARWGR KGLPFHRTINKKIYKIQGLIKKDKL IKNNASTDYDLSKSNLPLGGFVHYGCV TNDPVMLEKCGVGTKKRVLRLKSLV TKRRALEKIDLKPIDTTSKFGHGRFQIM EEKKAFMGPLKKDRIAKEGA
12671	26572	A	12797	86	364	EQDNRIFFSFLSLFFFTGETFGFPAG GGQGAILGLPKPPRGL/SSPPT*GSQE VGTTGAPHDIFCFFNKGETPRLYKKNK NNRGGGATP
12672	26573	A	12798	101	440	HCSRYATGIFEWYSGLVLVILLRFGIYE PMNLNIGDPYDPSRSLYKMLRWERMAK SLIEVSLKNSHFWLGLAHACNPRTLGR IGGRIA*TWGF/KTSLGNIRPHLYLKK I
12673	26574	A	12799	364	195	NFPDGLGEETLLWGGEIMGTTFP*FPPF KEGFLQDPDGGGNSPPI/QGRSFSFP PGKFGPPQGFKRPFPFFFLNNQ
12674	26575	A	12800	86	489	PTAMAEGLAAGVMDINAAQLGLKTA LIHDGLAHGIRKATKALDKRAHLCLVLA SNGDETYYVKLVEALCAEHQINLIKVD /NKKLGWGLQCQIDREGKPRKVVGCSC IVVDYKESQAKHIRENF*CKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
12675	26576	A	12801	64	211	GNHKISNYSLAPHWYTTVPAT*EAEAG GSL/L*CAMITTPVNSHSLA
12676	26577	A	12802	300	3	NNUTTGSNIGFHSFFLLRKIDICVSYIKM DAMNYIKNSNPNGETQVQ*YSPFN*NL KIWLKGLVA\NPSTLGGHGRIA*A*KFK TSMGMIVTCLINKQK
12677	26578	A	12803	208	394	SOHFPRPRREDCLV\QEGGYSEIPSVQK NVKISWAN*CMFAIPATREAEAGGPLEP RRSRLE
12678	26579	A	12804	183	348	AFILGKGKVEFPNCLGWA*NCMPVVULA SWEAEAGG\SLPSSSEL*CAMLIGCLH
12679	26580	A	12805	397	238	ETEFFCCPGKWKWDGLSQQLPFGPKR FSCFSLSFK*WQ*SLAPVGGCK
12680	26581	A	12806	1	293	PTRPRTSYEQQLLYLLPFVFSIVLEVLA RAISQETELKSVQMGKEEVKLS\ FVCV YIYA*ENPVVESTKTVDANLFDTRDFHA IFPQTVEGVGMVLG
12681	26582	A	12807	297	281	AKNPRRQPREIPGGVFPTPGFFPYFKAK MPEGFPFGGFFFGKGVLMGTPTPPFFFF FFSETESRFVTR\ QCSCGAI SAHCKLRL PGSCHSPETC**R*G
12682	26583	A	12808	255	59	AGCGSGLFGRPRGVVDHLSPGV*QDSVQ HGEILSTNTKISVWVNSVPVQ\ EVGR SLEPOR*RL
12683	26584	A	12809	247	310	PLHSILGTPTTTPAPTGGKPLLIIRTSILY *KPLISQANWCAPLVPATQ\ EAEARGSL EPRDSRRS*AMIKPVNSHCTPSNALPRP LPQFLESHC
12684	26585	A	12810	101	477	IGKEEIKLLLFDPNLMETVNF*MYKPL ELIS*FSKVTEYQVNTK\ SNCIYT*QL QTENEIAKTI*FMIAKSKIKYLKISLTK CN\ KWRDILCICIGRLSIIKVLPLKLM CGSEKIPNPNTPGF
12685	26586	A	12811	1022	696	CFEVLFFKEMGSHYVAQAGVUKWDHGS LYPPTP\ GSSDPPTAS*VAGTIGANHHT WLIFKFPVETRSCPLIQAQKLKLASSYP SQPRTSPKCLGFTDVKSLHLAWLCP
12686	26587	A	12812	166	143	RKEERFGIINNLFHFHVEKLEKEQT\ NPK TNRKKKIIKTRV*INRIEYRTIK\ IN KNKSWFF*KINKIDKPLAMLDSGRGRDSN Y*NITKSIEEGRRKKEEAGKRKEEGRKR RRNRQRWR
12687	26588	A	12813	163	423	KAFWEFINHKKTGPF*RGPTGKVSPPGG NLASSI*KG\ DPFSPKLGPGQSSGGPF PKKPTPTFNLAFGGLRGRETGRGPFFLA GLLP
12688	26589	A	12814	2521	2842	INTMYFFP*EMLVGWAWWF\ RASNPQHF GRLRQADRLRSQVDRDQSGHGETPRLLK NTKISWANWRAPVIPATNEABAGESLEP GREGCEPRSCHRTPVWVTRMLY
12689	26590	A	12815	173	395	LDQPGQREITLSLLKKQTKNTKTKKKNG FKKFL*LDTWVHTY\ NPTPLGGRGGGFF *GQDFETLANMGKROFY
12690	26591	A	12816	43	346	CVYVS\ GVCVCVCVCVLASVCMYVCLH L*VLFGIIFY*DHNIKLRSPFCPLKNT FSHYIF*KIIWPGVEL*VTVFLFLSLL HTSCVYEKSYAILIFSL
12691	26592	A	12817	647	931	SOHFGRPRRDLHRSVGQDQPGHHGETP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleo- tide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, -possible nucleotide insertion
						PLLKT(VKLAGRGA)*L*SQLLGRKQSE NRLNPGIRSCSEPGSHRCTPAWATE*DS VLKKKIGADKY
12692	26593	A	12819	392	2	PLFFFFFLETESHSVTQAGVHNFPGP SKPPTSAP*AAGTGMHSAHAQ/LIFF L*TELPSCRPGCSAMAVHRDPTDQHG SASFLIWASSPLLRQTGDSLLGGHHVD AKFSVDTLQALCTCAQNS
12693	26594	A	12820	1183	870	DRVSLTLPRLGVAVARNLQAQWKLPPGF KRFSCLSLPSSWDYKHTPTPG*FH/RG *FVFLVETGFRHASQAGLNSLPQSDP PTLA/EPKCA/DYR/HDLAWPRKM
12694	26595	A	12821	172	298	YLSIYLYT/YLCHLSIHFSIYFYLYL SINPEYVWVSFSEL*LT*L*YLSIYLYP IYVSIYLSIHPSIHISYIPLHIGFLF LENFD
12695	26596	A	12822	51	254	YDFLKKHLLSYRAKDLSEFLHLHLHF SGN*SVSYICVCVCVCVCVCVCVYICL IKSWCS*S/CGVL*AIACGVGC*LIFG VL
12696	26597	A	12823	199	668	OPLPAPSPSAQKRAHPTTSPARQAE/ SLPSQSLGTRTRPPLGRPP*SPWGWQD LWGWLPSPPTLPAPESLSPASLSTEVVL CGTRYLVWGRSGAQA
12697	26598	A	12824	33	442	GRGLKKSKQKRNALLKYDSKTRVGT LFHWTSVPVTRPLL*INIRLIKLDVIK CSIHKIFHSEFLFFKQHSL/CI*LSK* LCS*KIHQSGLTVAHVNCNPSALGGQDR RIT*GQEFETN*VMWVGPCLYPLFP
12698	26599	A	12826	363	75	HWEPRPAGPTLPSAFGSPSGRCPHPT SG/PPPNTHTPMSRSPSWEGSDORPQ PPHTDTGSPFN*GSRLRHERPPMGRERQ RPPFTTLVRPLHSH
12699	26600	A	12827	76	486	CTVNLFIYFEMESCSVVQTVQWCDLSS LQPLIWFSCVPTQISS*IPMCGRDLVE GP*MMGAINSLCCSYDSK*VS/ARSLD FFFFF
12700	26601	A	12828	345	672	KKCTADLSLEKDT*YKLEENR*QERI MLRAEVEIENKIENIKTGSSSEKGY KIDNPLTRSIRRKVNKITSIRNEKGV TNPTEIKRTVKYIMKNFMINLT
12701	26602	A	12829	208	1	PSNPTPIFRNENICFKDPTLMLAA FLVMKK*KQLKSSNDE/KLWYIHMME *YIAIKRNKLLI
12702	26603	A	12830	649	172	FFLKYSLSTTSVNAPSFSTCGGSOQVLL APLSRLAWPNV/HPPPOPRHPAPHSFL SPRSPFNYS*SSQGPLLPQSKHVRP LPQANARLPSAKNPARGPPGAAQAPRDR PFA/VCPLPPHSPLRHERAPRFLFLP ATEPALHAVHGRQERVT
12703	26604	A	12831	1068	567	KLWFFCSRLRLHFGSIFKVPFL/PVEK LLPLIPSLCPSLPLQLQPAQVPFNTAT WLCEC*/P*RV*PAPGVQRVGHFNFFPL QLNFPIILQ*HLGF*KSASLSSSSPK KVSCHPGCSAVVRSACNKLKLLS*SA CLGLPKC*DYRLQSPRP/PTIFKVTM CLLKSITGVSF
12704	26605	A	12832	268	1	KCFLLALNWPFIIDYFILNW*NSLRT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						VTEKFLFMFLFTY*NMNRPGMVAHACH PS/TLGGSGGRIT*AGES*TSLGNIVIP CLYQKL
12705	26606	A	12833	654	321	LVGIRFLKVKVYFNKIFPHLLAISPSELVFNLQHFYIYFLLEIYF*ETRSCSVA/RLECSGVIIVHCSLKLGGSSNPFALASQV AGTITTAHCAQOHCFICLEKSNLCITYPFL
12706	26607	A	12834	867	201	RQMSPTLRKTSRDVAKSSSFAMAWGKL FTFWDFPMSLSVLSQPGGPFHSPQ* TQ GR*VENNQEPPLATFPFGPERSLPQGPRL EPAHSGKRRGLPLEIRFPFVNVDIHGDP SGAQWLVRGVEAGPWA VGGQAP*SEGFS PSPPLDVSPDPGSSLPSSSP*MDLRA*LSLTF*TFCKGSGN/DPASSPA\GKPG* EWRKIKGPPQGLLLGPEMWGQARVLS
12707	26608	A	12835	328	1365	YAFCLMMLDKQI*AVLFEFPMVHKA AKTQNTSNTFGPTANKHTVQWMLKCF CKESLEDEERDMHGKVDNDPI*EP\Y *TT*KITEELSVDYSTVIRVVQHSKQIG KVKKLDKQVPEHLSGNQNYRFEV*SSFM LRNNNPFNLNIRVTCNEK*ILYN/RPAQW LGPRQQLQSQFPKPNLAPKKRSLVHW/ SPVGLLAPILDPTYSFLNP/GGETITSE KLCSGKLKMGHGKQYLLPALVNRKGPI \LLHDNT/RDCVFAQVQKLELG YK VLPHPPSPDLSPGDFHFC*HLDFELQ KH/SGHGAENAFQEFVK*STDFYATGI NK/LFSHWQKCDVNCNCSGCD
12708	26609	A	12836	7	328	RRERERERERERERERERERERERERER ERERERERERERERERERERERERERER ERERERERERERERERERARV*EKST RYKSPPPRIPPLRR/RRV*RKHPHARAL SFFLYKKCTGGERAPSPVCVGGFTW
12709	26610	A	12837	219	350	PFNHTYATWSIIISNVQVCFMRKADLYL LIYLFAGSCSVA/RLECSDMIIMLHCSL DLPGSNPPISAT*I
12710	26611	A	12838	189	359	LGLDGMVRVGCPRALGFS*EEKSSRVQW LTPVIPA/LLEAEGGSPVRSRPAWP TW
12711	26612	A	12839	368	77	KNPNFLKFGSKFMGPPIYSPP\LEG*AG GFINPGF*TPPGYMGKPPFLKYSNLPG LAAPGGCSPPFGGLGRKISFTPEMEVSI NPGSPLSLPPEQON
12712	26613	A	12840	16	173	KTDVHSKTCTKLPFAALFLVIKWKHLK PP*VD/EINKMWNHIVEYILAIS
12713	26614	A	12841	425	45	NSVFVFFFLFENRVLTPVAPRL\CTGV IL/APHCTLPALPEFRRFLVPSALLSSW DYRPVPMVWNLNFCIFVETGFH\HVAQS VLKVLVSLK/LPSPTWDVPC*DFRYSVR CGGLFF
12714	26615	A	12842	237	375	LLLWVYVILKRLW/LGVVAHACNPSTLG GGGGWII*GRFESQVNI
12715	26616	A	12843	21	325	TSFFFLSVAQKQWCDPGLQPOF PG/SQ/DNPPTS*G*VAVTQ/MHHARL IFVFCRDGILLYCPGRSKIFPSCSIRE LFKKISDFLLTMIIFCNSNG
12716	26617	A	12844	369	58	FISPLQFMLPFLKNQSPYGFPPFKKKNF PPPFLGGAVLKTGPF*NFLFKKIQRGFP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PPFKKKKPRERFKPCPKPG/SPPPFFYPGPPPPKGGPPPPPPPPFF
12717	26618	A	12845	211	409	NALKFKIHFFPSGGGLKGIWVGNTLLDILGLHRTFFP*GDPFYAL*I*AENALPGG GDCAPHLOVK
12718	26619	A	12846	200	33	QKTNATCKWGSGWATGTLIHF*GEFTRVQSHWKIYNKFL*/SLNILE/PSSSSSSSSSSSSSVKNLCLHKACTWMEIALLLLLAKTWQOP*CE
12719	26620	A	12847	416	125	KIPTFPKGKGPFLYPRFFKGLNKGILGPEFGTPLNGKGSFFFPQKNKNWBERGGPIGPPSPGG*VGLTLKGEVSTKLDSPPAPPFGGQKWLP
12720	26621	A	12848	85	397	KIHFFFLVLSLLKGLSFLTFSSKN*VF/SFIDFLILCVCCIEFYCPILILPHYFCLFGFCLFLMFVS*QCSLDFFYNSF/YIF*YKIQCYKF/CILIF
12721	26622	A	12849	1	246	RPRRHVASLVLTQLNGSSPLFKKISWAWNLMPVITTFWAEAVGGLLEPSSRO*AMISPCPPAWAT
12722	26623	A	12850	161	1	NKTISSQIN*PMPIVSTT*EAEVGSLEPRS/L/KLKCAMISPVNSHCTPTWTTK
12723	26624	A	12851	65	244	STYYLHSLPFLDISYKWNHTC/SRYFMGALFLIAIK*QKPKRPSADEQI*T/IMWYIYTLEVDLAIKRNEILLHAATWMNLKIMLSKRSQTKT/HVV*PHL
12724	26625	A	12852	235	34	TTIAVSVLILKELMEP*TLQDPFLG/WSLITESVDHVOHAPVIPALWEGEVEGLLEPRSLRPAAWATW
12725	26626	A	12853	168	453	CQLRGASGTQGPGLSESQCCQPC/PEC RPSKPRPCGCRISPARTSPQSPAAASMALPFTNRTFPFALK*PK/CPKQSPQSAKSKSPKSTERTAK
12726	26627	A	12854	244	3	ELQVYMH*TYI/C*SIYTKANIYIKYMHCVYIYTHITIVCVLHLYLLRRHGGCWMLGKVRGCGGMAHLKMQQGVW
12727	26628	A	12855	376	428	KNEFGGHTSFFFEKGLVLNFGRGVLOKTRP*GGCGGKFNENFSGGREPP/PPPGGGGKGGPPPPGVVFVFLKGGSPILPRLGVNLNPGAPKGVYTORGGIKSGNQGATPLSFFLKVMF
12728	26629	A	12856	129	395	APPNIHPLSVNSAQVIRPQPPEVLSPKPC*DYRGRPPASLIHVNRSQT*KVAP/CSKPLAAAAHQSGPGATETTRCPPSRCGPIF
12729	26630	A	12857	363	97	GLATLRLVNSNSAQVIRPQPPEVLSPKPC*DYRGRPPASLIHVNRSQT*KVAP/CSKPLAAAAHQSGPGATETTRCPPSRCGPIF
12730	26631	A	12858	322	361	KSEKQS*VMLAVCTLDMMRKT*FISVVF LPKTHN/LMSNYKNTKQIPMEGHSTIYLTRIPQNCQGHQK* KSEKQSQESKKK
12731	26632	A	12859	88	417	HFTFFFFFPPKRGGGFFSPRLKRLGKNFFFLDPPPG*RDFFSPSPKGGG*KP/SPPLLVFFFF*KKRGFLGAGGF*TSFGPGETPELSPSEVWFYGGTGPPTFFFF
12732	26633	A	12860	217	2	LI LINKLANMHCFLVVETSLT*AGVQW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						HDL/GLLLRLAEPFRFPFCLILPSSWD YRCALLHPATREDEA
12733	26634	A	12861	375	145	LSFFFFF* KPGSCSVQAQGVQWHAHSSL QLQTP\GFSDSLN\AFSVARPVRVHCHT RPLSPFNI CWRARPKQKVF
12734	26635	A	12862	525	852	NLLSIYFFETESRSVAQAGVQWCHLGSL QPLPRF* IKKPSNTALFM\NLLSIYFF ETESRSVA\RLCEGSAIIAHCNLCPLPGS SDSPASTSRVAGVHHHSHLSSWDYSCAP PCLANFFVFF*VETGFHYVSQDGL/DTS *PQVICPSRPPKVLGLQA
12735	26636	A	12863	3093	204	EPDKTGPVLWVGGAARVFGMAETLSGL GDSGAAGAALSSASSETGTTRLSDLRV IDLRLAELRKRNVDSSGNKSVLMLRKLKA IEDEGGNPDEIEITSEGNKTSKRSSKG RKPEEGVEDNGLEENSGDQGEDVETSL ENLQDIDIMDISVLDEAID\NGSVADC VEDD\DA\NLQESLSDSREL\EGEMKE \LPEQLQ\EHAIEDKETINLDTSSDF TILQETEEPSLEP\ENEKILDIL\GET* RSEPVN*ESSELEQPPAQDTSVSGPDRK LAEEDLFDSEHP\EEGDL\DLASST AEHQSSKADSLAVVKEPEAQPGQGER TDCPEVGLPEVQGS\SVAASELAEASS EELAEAPTAPSPPEARSDSKEDGRKDFD A\CNEVPPAPKESSSTEGAD\QKMSSPE DSDTTRKLGKEEKORSQ\RKFLGLVG LSSTTRATDLK\NLFRQIWGVGGAPRL WTNARS PGSAFVYGFV\TMSTAEATKCI NHLHKTLEHGKMTSVEKAKNEPVKKTS \PKRGSDGKKEKSSNSDRSTNLKR\DDK CDRTDDAKRCDESVESK\DKNDQK\P GPSERSRATKSRKSRGPKRTVV\MDKSK \GVPVISVKTSGSKERA\SKSQ\DR\KS ASREKRSVVSFDVKVKEPKSRDS\ESH RVSERSERQR\MOA\QWERERERLEI ARERLAF\QRQLERE\RMERERLERER MHVEHERRREQERI\HRE\REELRRQBE LRYEQERRPAVRPPYDLDRRDDAYNPEA \KRAALDERYHSDFNQRQERHDFDHRDR GRYPDHSV\DRREGSRSMG\SIREGQH YLERH\SDPEFH\QQDSLRL*LGWGYEL* Q*RLS\BGRGLPFP\PGAGRWGDTWLE DEDDPVNGKGTAEGRPWMDR\DEK\RWQ \GGRSNSHGSGPGHMDRGCMSGRGSF APGGASRGHP\PHGGMQGGPGQSGRGS PSDARPTREY
12736	26637	A	12864	2	456	IHLGSGSEGDGSSGGLGRGNSTSRFS SSWARGDNVPRPPPAVCSWISGDVQN PGLGEAGAGSSTPGDGGLRY/WPGLLG A*GRGIGDDDDRLTLGLAGVQCCGK/ RRGPRGPGRGQPRPRDLGLRGPRRAQ GAA/SATAAPP
12737	26638	A	12865	388	1	LTKMTVKKTAITK*RGWGRTGAFIHC SWECKMIQPLWQTVVQLLKLKLIYL\WK QPKCLPM/VKNIKLYISMDSYSAVKKK ETLMYTTA*MTLEVALLSERSQTRKGER GHILWDSIYINFCQMOTNL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12738	26639	A	12866	198	3	KKQKQTKNPKIS*ALWCVPVVPATWGA KVEGSP\PRRSRLQ*AMITPLHSSLCN RVRTGRTRTG
12739	26640	A	12867	415	973	NPVNCAQFSLPLLTTEYMGHREVGATSHG TCPSVPPNTHLHTGWMLQHHRSCRAWG RGGSHTRCPQRPVDPGEHP*YIYAVHGE PP/ESPQPSPSLSCPPPQGNLYALREPP QGLPLPGTLFSPHPFFWHICKTHSSSR HPFFPGCGLELEKGVGDFI\HPPLTLF KLPNPLKPEPTPTPQTHI
12740	26641	A	12869	715	893	PCVAPHSIREERFKLTSESTNQKVLWVG ID*Y/VILITGNWQKRHLKSFFLGQKP GGMAD
12741	26642	A	12870	342	58	KKKKPKENQSIWMDNFRFSDI*TTG VLEQFRE*GRKIIFKRIVRENSNLTK /QINLLTQEV*TTT/HKNMKNSTPIHII IKLMKTTTKEKI
12742	26643	A	12871	110	401	SFYSVMILKASRIVCLFT*LYAYIHTL YIYTLCTIYYAYVNIYCTHI\NIHII HVYTYIYVASYIYSMYSAWYNKVKSD RQTYENIALITYY
12743	26644	A	12872	439	256	SYPMKFGGDKISXLYQFLTRSRKWKSTC PSMDEWINKMWH/ITIMEYSAS*RYEC SYMRHE
12744	26645	A	12873	356	43	GTPERHSHSHSQGSPIIGAFMGIRASV YSLLS CVLLMLS PQRVLYFYSAPKQQQS \WSGKVAQYNSNTYKGAGSIT*GOEFK TILGNIARPCFYKKKFLANS
12745	26646	A	12874	341	205	REIKKMVLNKRFFSLQFLGKKKNFWEFF LKKKKK/VKAPPVQF*VP\IF/CSF*KK KVFGFFFSFKIFFFFFFFFFTESTSV TQEFNGTILAHCNLGLQSSSSPSAF* VAVSQDCATELLDGRGLCEKKKKKK KKNGFGKKKSQNLFFFLKKRKMGT
12746	26647	A	12875	474	206	PIRANGVVSPPPPPPAGVTCPHPLVIM LSRLRQSHPHVTVPQWTSGLLPSPPA* LSLETHQFTAHYTFP*H*SSGLGCMG SPVGGEG/HKPLCLQPAARAFAWEE GTKARRHEGLPPAPCAWGPAPRDAGSL EFTFLPTI PVSQSPGR*HGAGGRPSCLR AFVPSRGGQASAAAAGCRQSGFDLALLP LGSPILGQQQNFASARGR
12747	26648	A	12876	257	467	YRVFTLLPRELYIMAHCNLDLGGSDP/P QVAGTTLK*LSRASRVAGTTCVHHHSWL IFK/YFL*RRWRFRSL
12748	26649	A	12877	867	1409	GFTVLVGGODWNSVLQOPRAHSFTTRGG AGGLGGGVYLHKPIFFSGELLGAFPCQK QYRVPPLEAQLLRQARSFAFY*AAVL CQAQGPSPSPCSPMVS PRPSGRAPHLGA APQSGQKALASTSPDAEPV/SVG*WCP SNPALQGGQNGABPRAVSITSGLSLYD CFLDGWWEGRSLOP
12749	26650	A	12878	1416	740	IRNPRWVOLDVFAAAPMGRSSPLFLLE SFLKTVLRGMSIPSTVPS/FHKGPAQCL YSLSLRS*SQAAPSPAPSSLPTPSPHPG LTQPGRRRRKADIS/CSHSAFYVP/SL PHLFWACPLSLPQPVLSILFCVLE*F GVLLCHPG\WSANARSWAHCNHLPGFK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
						QFCSLSLPSSEWVDYRCMPF\GLG*FLEF*VEDGGFTILVRLIWS*PQVHLPPFPKVLGLQA
12750	26651	A	12879	961	31	PSFVRDSCVANAGERGRGLGGSGVWRSHARGPGLMRGLPASEPAPCVLGSRPCFRVAFETPTWSPASCMPFERCPLWRPDLVAAGLDPFLLSSTLTAVCPDRDLIRSWKKGC DVCDSRNCWSTHSRPAACRDAILAPILAGRGECIGLWG/AAAACITGV/TPVSGLTFTSTVDFPSSARG/V*GGLPRSTGGFRVRGPGQVPVLPGLPAGVALAPLEGRPQEPAPALSHSLTGSLLFGAWLCCGCTRHGRAPVLLEVSIVACGQLCEAAPQIFIQPLGQLPFTSATSPAYLWVDVLLTLPVIRQKRVISPLTKE
12751	26652	A	12880	232	28	PALWVPVVARFDGMEETGQNHWSKEKAWPGVAHTCNPNLTGG*GGH/MT*GQFEFTSLANMAKPRIPP
12752	26653	A	12881	331	1	KNGPFFKNPPEFFPPPKGVPPNPPTPYFPWPEPIF*LTPGPLKKQKIPFQ/KGEILLGWGGKMGNLFPWKWGGPPRESKSPRFYKTPPPIFKKKKGGSSRSRSTSRV
12753	26654	A	12882	370	287	VSILAGCCGVAMIDNTVLVHKEVKILRK*IIKK*CI**FRGHSK/HNPSG*ANWLMVWQHRPR*GSLRSLRPANATWQDPHLYEK
12754	26655	A	12883	656	1168	EPSSGVWPHEDARINSGKKKSKDKKRRDEDETOLD/IVGIW*TVTNFGESGTIAIKVDEGTIYHALMNLGLTLCAPHK/ERIALKPGYGYKLSINSEDLVV/GRSDAIGPRBQWEPVQCNQEVNRGGPAEMGEKRN GTKWREDTDTHTSFPLFPSTGQPKAHSNWRKVCH
12755	26656	A	12884	205	452	ASGSAHRFRTFSFETGRVLDKFSQTDHTNRKRGGPNVK*SF/L/NLGAHAACNPNTLGGRGRRTA*AQEFRTSLGNTRPCLY
12756	26657	A	12885	112	290	KYNIQYNIIVFSCHDPLVSPNLEFFFFFKGKGFPLSPRLKARGRVWGYLNPPLPGKRNFWAPPQGFEEKLGLPPP*SPFPGGVGQAKNLGPGFQPPAPMGKTPFF*IKQNNPNWGGQPLNFKTLGGGGPKISF/PPGGGLNNPKSPSPSTWGGGNPLSKKKKKKD
12757	26658	A	12886	406	190	TRSLARGGGRPLQKPYNQSPFIMAKK\YEQPKCPWTDKWNKMSILTVG*YAA MKRRDLVLTATICTR
12758	26659	A	12887	440	160	RVCVCVCVCVCVGVFFCALWLSLIYN*VYLFLFVHNLGRVSFSYFNLIL*FFHVHV/HNYVQMIQNTSLYLKSYLETFF/CPD*FPFILLH
12759	26660	A	12888	201	411	HWVDVLLRHLLNFLTSTISCIYIKWLDVAHTCNENTLGGQGG/WIT*SQEFKILGNIQDPLSTKKK
12760	26661	A	12889	138	464	SCYNPSENRQKAPFNNRNRHS*APSTHKMNRMVMSQMKLPSTKKAEPPTNAQLK KLTELA/TKKSLNTRGTQSKNMLFALMIVTGCAGVPSSSKETATIEDKP
12761	26662	A	12890	146	366	FSVMRYFV*TH*FYHL/KLLMYL*Y

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						GFLAINTSQNISCSQKIMKLHL*GRGVV AHACNPGTLGG*GEWMA*AEFNTGLSN TAKPYLDF
12762	26663	A	12891	368	50	KGRQSGVSSFFPGVTGTYNTNLVAHNRY LFPHSPGCQTSEVKVLA\GCSLLKASRG EGFFPLPGSGGSKCPPLAYGCITPISASS CDLLLVWCVFSSYLAY*DTCHNI
12763	26664	A	12892	227	456	KLITLLKLFER\IEDRTLSKSFYEVSIT *IPSSSSSSSP/ISLINTDAKKINKIP RNRIOQCICKII\PHKFSGTIYS
12764	26665	A	12893	461	89	IYQNL\SRKDNIKCW*RCTEIQTLHC W*CKIMQLLMKI\WQFL*/ELNTEVY DSIPLDMY/PKTEC/YTSTQTLIYCN NP1EYSAIKRDKVL\HATTWMLENI/ ISKRRQSQKSTYCM\IPLI
12765	26666	A	12894	222	185	RIVMQYHLNLGACVGVVFCB/CVCL CV*MCVHIHIYISTHYIHIYVCM*ICR LS*CEFY
12766	26667	A	12895	186	166	IFFFFFEMGSHSVTQARQVHNHSSKQH PPP\GASDPPTSAY*VAKINIFFFF
12767	26668	A	12896	55	485	TCWDCRDEPPRPALESVFLTFLDEFS IEIADLVPHPTCPHSLQPP*VIYFC S\KPLVTGSSPPRKPFFSLHEPKSASL *PPSSTIQVRSSPKG*PSPFLA*VQPF KGMTIPTLCLSPVLVPVSTIFLNVSKP LPFY
12768	26669	A	12897	923	312	VDVIRKVOIEITLRCHLIHVRIATIKT RANKC*GCGEGALVHC*WEC/NYILV QPLWKTWRFSLKLIELPYDPAIPLLG ISPKGNEII/CCTPKFIAAQFTIVKIQT QPRCSSMGKWIKKL/W/HIERSIDR*LE YYLAFKKKAVLSFAKTWIDLEDIMLENI SQTQKEYCVISLIGIKKKKKYIEIE NKTVIKTVIRWRK
12769	26670	A	12898	320	3	ESWRKGRIVRPHSVPGETWLCVPVPGPF NAPQCSFLAICVFPFSCRL/CPP/DD CLASAG*CGFPLRTEASPHHSWACQ EQPWPPOCKLVGAPNSTALSGOS
12770	26671	A	12899	138	447	IFVHYKTONIYNEDTLHVIITNLWCYF GSYIKSTGRIRPEVERGLGPTTMC*FS SIKNIFF*KLKSYRKL/WLGTVAHAYN PSTLGG*GRWIT*GQFNRD
12771	26672	A	12900	279	1	INQSIHNNIKSTYISQCKLIQ*WKIIV RFIR/NLKIELLVVPATPPGV*LKEIK SAC*RDNCTT/M/FTAAALFCIGYGSNLG NSTALIGSRVLP
12772	26673	A	12901	235	183	IINYGGGPFPEKKKGGKKIPLIFYKKIK KFLNPKKKLFGGAONPIV*AHHIFTV* IDVDTRADFTSATI\IIAIPGVKVFS* LATLHGSNMK*SAVL*ALGFI
12773	26674	A	12902	180	19	LFYLYFIYLFICEIRCFVTOAGLQWL IIASCFSALLGSSDPPTSAS*VKGI
12774	26675	A	12903	406	949	APVFGHGFCVSE/CGENGSLYCPGRS* TPGLKLCSCI\CLPESWDYR/R*APVPG \LGFVPHLT*LKPPFFKDYMKSLFQFLK YLIQG*CTLV*GVRYSSEIFFFFLRR SLA/SVTQAGQWRDLGSLQSPPPGPTP FSRLSLSSWDYRRPPPCANFAFVFLV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EMGF\TVLTRMVIS*PCDPFASASQSA GITGVSHRARPKFVLVYFKDNGEPLGGVL HRSHIAVHM
12775	26676	A	12904	265	385	GNSSPSLRWIGVLGRSPFTELRH*PIF LTHASRRSLDRVSPMCTQFLSEPLSIE GLVSYRLTNLMERIPILYRN/PENNET M/PESLYCYRVLIIFLSKGYRVRKRLDTC YSPVRRSPAKKASFLPDAPRLACVKPVA SVHPEPGSNRTG
12776	26677	A	12905	363	137	APGMOA*WCM/HCTPGAQAEAGWETEP RSSRLWCTVIMPMSSHCTPANATW
12777	26678	A	12906	315	565	TFVDHGNLECSGATMAHCSLFLGSRDP PASASRVAGTGVCHHSQILFLFFVGTR SNFVAQAGIELLG*\VILLPQSPKVLGL
12778	26679	A	12907	376	412	DAWPTWRNL*FGVVVMDR*EPRCMITY LTA\PLKYFKSGVMAHSCN\PSLTGGQG RWIT*GOEFET\LANMEKPCLY
12779	26680	A	12908	215	2	NIHINGQKLEF/WLGVVAHTYNISTLGG RGKIS*TOEFETSLANTVRPHLHKQK IALPLPLPLPLPTVR
12780	26681	A	12909	307	379	KR*KQCPYLTEEWINKMRHV/LQYYSI LKKKEIL
12781	26682	A	12910	279	123	KMILSWARWMSIIPAAWAEAGGSVEL RS*\LRLE*AMTVPLRHFTPAWARE
12782	26683	A	12911	1	194	AKQHIPLLARLECT/GLFTNTVTAHCSL ELLASSHPASAS*VARMTECVHRAWLE WIFYLCVIL
12783	26684	A	12912	206	388	IELSKQGPVYKVVVRITPPYPPFFFF ETGSCSVT\RELECS/GTITAHCSLNLDP LSYSTPAAS*VAN
12784	26685	A	12913	238	426	TPLLFSQQWLKESLWLGRVHVACNFST LKG*GGRDS\RGQ*FETSLGNIARPCLI REKFLKI
12785	26686	A	12914	115	1436	AKDRFPTEV*IANQMKRCSLSLGMREB QSKIVRTHLSE*/R*LFFNGGCMQO/ CKK/QDLHCHECMQVPLMNIWA LF*NIHTCICHASGIALLSIYPREMKT TKTCIRMFIAALFVWVETWRQFIYPSLG G
12786	26687	A	12915	282	21	IKFPFPCPSTWGTGKKKLEPKKKKEVMKML CFHFNLIQVNIQ*YRLGNEISDKAG/PV AHAWNPSNLGS*GELIT*GOEFDTSLAT IVKL
12787	26688	A	12916	254	150	TLFGRSSDPSLPEV/YLKNNH/WLGVV AHSNCFSTLGGKGGWIT*GPPHMLKVSF LPDTPTRVKQLYNVPHSTVLIALFT KNPG
12788	26689	A	12917	181	24	AQWCDGIPVSKGNL/WLGMVAHACNLST LGGPGRWIT*GOEFETSLANEFHRTD
12789	26690	A	12918	75	298	LFILFPTS*VD*MRPTHIKENNL/LAQST NPNVHLIQ/KHPHRHSQNRVWPHVWAPH G/QSSCHIKMTIMARPSGSQ
12790	26691	A	12919	251	9	KFMFLARCQGSRL*SQLSGRFRRAHDLR PGVQNPQGQHSSEYLPKSTNFCRVWMC TPVVPATREAA\GESTEPGRQRLQ
12791	26692	A	12920	198	211	RFCPSVGDEREGKRA/RENNKTERKQ TEDTETQREERDRDRK/ERETDTERER PREERHTEREKK*KAAFFPQTLGCRAQD

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12792	26693	A	12921	438	127	FFKQLFPSRGWGVPMIVLL RVVMERIFVRPHIKDSMMWVRSTLLGRG DALNDLFLYCWEKEDPRYKERP\REKER ERERERERDRCEWK*APGWRERPVSQSLR ACHPPWHRFALAGPVPSAQ
12793	26694	A	12922	158	460	EARVELLSRCKPRAVITAETOPAVYR LQLEIENFGPLSPRLCSCGAIATACSLD LLG*SDPPNSASR\AGTGMCHAQIVNS CKADVLVLLSSRGLTHR
12794	26695	A	12923	33	484	GIOACIPIGLRLSPADACHRRHIPSFP PSSTAPRDDVGPQMITPDNFPQDDPL\ TPPSQSLPHRAP*PGSSVDLPGLLFX LQMPQPTPGGEVDTCVQIHKTSKARE VQNRKTPMAREGRHRAAHRWIGALGAP QSRRLRHITVG
12795	26696	A	12924	335	332	RTKVYVRGHAKE*LRPGF\VAHTCNCHT LGQQGMRTQAGQEPFETSLD\GRPHLYK KKKKKGGPF
12796	26697	A	12925	302	407	AQWLMAITPAPWEAEAGGLLEPRS*\AW VTW
12797	26698	A	12926	766	244	RVFRLPPPAL*LEFSPSGLRLARSHSFQ LRSSPPVPVPPST/PSPHRSPLSLLS LSVPS/PLHHSFSGRAPHILPPPLI FPSSPPPPPPPPSSSSSSSSSSPPPP /PFINWGTPRFFPPPPFNPPPEINFGG PKKKKIFSPRA*KFVFLKGPPEFFFFF FFFFFLGINLL
12798	26699	A	12927	127	720	WGGLLESTELQQLSPLGLYVSIVFGKIF YISGLGICCTKIFPSALPSAQPAASLPL PARSALGIVFFLHFC*IE/CNYKLPFI HHI*LIKTFSYGLT*LFFFFFFKTKSLIF SPRLNCRGPFVLN*NLCLRG*GNSPA*P FGGAGIEGAPHKAGLIFGGGGGAFLKKT G\LHHVAPGGASNSGTGNSHPLNPPK GAGE
12799	26700	A	12928	308	49	KEHW*AVGHFNICVTGGP*GERKKGTER VFKEITPNPNNLQTIKPKTQETQHTP SRRNTKI/TPRYIIIKFLKTSNKEKILT TAR
12800	26701	A	12929	375	2	GCWLSLKTINILEVLANLQAKKIKRRK LND\ROADTFTT*FCVROKTKSDKL VKLI/ERFYKVATVINFLKKSNSFHT ATINC*KQIPFIMATKTKYLINPRKK CVRFVGGKLTETEP
12801	26702	A	12930	202	379	SSENFSGKTVNLCCLRHLRMTSLWHTV AHACNPIT\GWIT*GQSFETSLADMVKP CLY
12802	26703	A	12931	209	376	TUGEKMYLKVKRI\WLGVAHASNPNLL GGQGGWIT*POEFETSLGNMAKPHLYKK
12803	26704	A	12932	280	31	ISCKVTKVTLLFELKYIWNKFYIYERVS IVGTTEDAAECVTSNVITGPGAVAHACN PST/RGRWIT*GRELKTSPIANTAKPRLY
12804	26705	A	12933	1	189	QMYTESEP*CKLWLTGDYVNM*FIS* IQCTTQAGNVNIRE/RLCMCSGGEYMRN LCAFLSILL
12805	26706	A	12934	108	409	HHSHLLKLVNWFVSFCHPIVTVFLSL* RVFVFPY*IFLSSSHFLSFCEFCPIMFIM FFPKFILSCNIVFI*NIIFFL/VH*G

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion
						*STLVSLFVFFFLQLQF
12806	26707	A	12935	225	11	ILLCEPSEFLFWFGFICFVKTGSHYIAQ VEVLWLFSGMIKVHCSL/KLLHSSNPPT SAS*VAGNTGSSYCTW
12807	26708	A	12936	74	12	GTHASAGVINILVFILSFVFLTHSLCI HISKYMPVYICVICTRTDFYTEKSFCE TFCFFGSSFFFLKPKFVLVAGLEEQKGD LG*KLP PPPRLKKFSCLTLFG/AWE*RT NG
12808	26709	A	12937	166	311	PHS*WECQMVRAPEALENMCFLTKPIRGL PL/DAALPLHM/CHRSCTQLFIALLI VAKCNHHKNL*ANEWINKM*YIHTTDTY PLAIKQNEILIHATTWMNVTL
12809	26710	A	12938	51	296	LCMYLHTLYMHATICIYAYICVTKYKTHR Y/LHT*IPEDANSVKHKYTHTHIVVHTL VPHRTYLMCSYIYSNVCCVCIYTT
12810	26711	A	12939	426	28	KGEFLVNPVPFSPRF*TPAPVYFCGP ICKIPFKAGCKVSDLSKRAEFPFLK TGSCFVPA/RVECNGLITAHNCLLPRSN DPFFSDDLQVTGKVPK*AKLEFFFLW*M GHHHLLDQGETCLSLGLQWR
12811	26712	A	12940	11	213	ATAFGLSFSEFFTGFCFSVDGAGVQ*HDHG SLQP*PP/GSSDDPALASQSARITGVHS CKGPEHTSLT
12812	26713	A	12941	416	38	WLNNSHRLGFPNCWDYICKLRLGPDVA SLLIHNS*GTWYGATKLESNWYFSPI YKDHO*FAFTWQQQYTFVLVDQVVS SAL*HNTVHRDLHDLDNPQITLVHYS DTMLLDLMSRKQAL
12813	26714	A	12942	361	74	ITHFSFVSSSRNIHKNAVPAALGGYSVY GVAILLPHYFINKLAFTTHCGLA/LNSF LR*IQEPPLG\SGSGPFSCNVFLAPTEG TIVQKPDMPATFG
	26715	A	12943	125	401	SSFFPRGIPLNFVAMQKESVNILCSPR SQEFLESRIKIVLTDLTQDEL*GQAQ* LTPPIPS\IWEAKAGGLEPFSRLRLRSC HCTFAWTE
	26716	A	12944	92	306	KRTINSFWGCSAY/GVAILLPL*YL/KL LAFTLLHGLPSNSFLRKIQEPSLG\SGS GPIFGNKLVAAGGMIVVS
12816	26717	A	12945	322	24	NFKNTNLNPLFLRGYFPLKGGGFLTFK KVGEPLKKKKKLNQOFSYFLSTYTVK* NN*/WLGAVARTYNPSTLGGRGWIT*G QEFQTSIAMVKKILAK
12817	26718	A	12946	2	448	GGAPKKHSGSLDRNRYKVTITRPSQLFLF QLYHNLYLKFAEATKEYMHRKETLCLPC PATQSFSPKSNLYRGLCMTHQNM *HYRYITVYVNHIIYCM/YRAICTYIT FE*KYILQKICILLCIFLFLQYLYKVS YLNHRHFLIAA
12818	26719	A	12947	155	415	LELTGGNAGCSSMHHVLLGKTHRYMGGS RPTSLMAG*/GPPWLRVRVAGLRGRPL GLRYGPDYSYGRQW/EYCTMGASLMQR RVRD
12819	26720	A	12948	247	250	KYVKYTHIHWKCVYIFTHVGVYTYTLT DVYKYTYLTDV*ICICIKYCYLYWYI YIHLCNIMYIYIHLCNIMYIHIH*YI HIYI/HVYIFYIFYTVYK*HIHYEVC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
12820	26721	A	12949	25	407	EYIYTLWLKLEALSLLLLLVWGLLLGIARKMYQQMNLVQYCLLVLP*P*NL*EQKRFEVEGLDHR EP*FHVLCIHSKSRFSW*EL*IRK LTLVA\GGVAHTYNPNTLGRGRIT*G QEFETSLGNVVRPLFL
12821	26722	A	12950	370	106	ILXLETLKSFISIRSFVSDSHFEKSS TVGRMLPNSITCTDPT\FNKKKSQMLMW SLLLPFSQKLQSPQPVQQPSPSRQGS IPATR*QLA*GSVQVMLFGSILPTVELF SKWSETAEKLLILINDFSKVSRYKIYV
12822	26723	A	12951	280	319	DQPSQHGRKLF*VSH*KKRKGW/EGVY AINERFLGGRGWIT*GGGFETSLANMG KPCFY
12823	26724	A	12952	337	113	TQLATSLLGICPRDLNITVCS\SDTCQ MFSLVLLMWAKR*KOPKYLQIDEWINKM QCIIHMSYLVSKGRKYLCKL
12824	26725	A	12953	9	186	DPTVCCLDQTHEFYKDTNKLKVMGWTKY /CHANGNQKRAGVVQIEYP*SKSLKSE IVQN
12825	26726	A	12954	46	381	NENTYSYKNTOMFIALFLVTPNNKOP TCPS\SGEWINKLL\YHLMVYYSVAVKN /ILVYVATSVNLRILLGQDPDKRVLTV*PHLYRKYKLISSDRKQIHGRLEVENK GK
12826	26727	A	12955	19	250	CSDMVLKACIKKLMYSYRMHQIAMDY TAL/NKEL/LMYATI*ANLEIMLSKIR QTQKDNCLMVDCIYIRYAEQSSL
12827	26728	A	12956	173	163	GAHKSASGTGWIRKDFTRPGAHAACNP STLGG*GGWLSRSEFETSLTNMVKL/CL YKSI CCTCLGCGFPAALSKAID
12828	26729	A	12957	301	79	EKDNOPLLTFRNCNVLHAISENHRIT ELKVTLRDPDAVHTCNPSLTLGRSG/WI A*GOEPEISLAKVKPCLY
12829	26730	A	12958	314	126	KHHHFKHNFRVLCCVCCVCCVCCYKHF YLPSLSFSQ*P/CI CC*CVCCSFLLCF *SATYLKII
12830	26731	A	12959	529	1697	VPFMGHISNFFPSFLRQKYLALLPRLG VQMG*SRACNCLRFPFG\SSNSHASASRV AGITGACIEHWLLFVLVEVPHHVQ\Q AGLKTP*POV\SACPSLKCDCRCEPL CPATSSILNL*TMNRL/RSEPRGQ*NL LVSFMCVAFYREGQHVYFQSLWCKREF IYRSPWAINLEKGGIRMGAV*TRIMNL TLT*GFCTEDEKTVNSRVNQLKTP*LG DE*DVKREKINDEIKLLTCNSHYTKSY RLGR*IKLGAFCFPM\VPMGQTGRNGQL KVQV*TGTVAHVCNPSLGG*DRRTV QEPETNLGDHSESSSLQKIKLARHGAAR L*SLSL*VSWDYRCSPPWF\SNCFIK\ RDGVSYPWPKA/WS*TPDLQSAHFSLP KVLG
12831	26732	A	12960	1	395	GTREPRILSEKFKKELDFFFFFKQSSP PPGPKQTL/C*QOTTPTKPKNTLGP KFGGQPKKPKISHPQIGPPKKNTLNP* GQPVWNPGEKKEGPTPKFKDPGANLK VMGLKGGVKRKGKTPPQRA
12832	26733	A	12961	90	436	LWRLTSPKSAGWAGNLETOESMLQFKS

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						EGHR/PAESPLA*SSVLFSLSSTDMRPI LI/MEGDLLYSKPIHFNKISSKXTYRN TNNVNVPHV*TL*PSQSD/CLK*TITPI VLLTCTH
12833	26734	A	12962	415	463	LRAKDVLPRILVLC*TLFFCAQIKKKK K/WPGAVAHAYNPSTLEGQGGWIT*QGE FKTSLGNNVVKPSGIPPHWI
12834	26735	A	12963	774	316	SISPTCSGKIGGKLNHRHFSKEDKTG\RY MNKCFISLVISECYLKP*EDTH*TP\LR MAKIKRADH/DKC*QRYKMTGTLIQC*R ERKMVQPLWKTV*QFLKRLNIHLPPDSI PLLG\IY*RMKACVHTNTIWMPIASL LVKAK\AKQPKCPSR
12835	26736	A	12964	44	395	MYFTLVWVSLGPKLGGHQLQGQGFLL HFLKAL**FFPQTFGNGGGTPAKTFP PFFTPLSSSSPCPSPAEGGSREPSLSTP /SCLHLIYGGAASNPSPPSPLPPQCSG LGYPVC
12836	26737	A	12965	424	50	MAFFPLSCAPDAINNNKKKCCREINNEE PPNEPLKWRHIMIFFEASHSFAR\LE CSDAISAHCKLCLPGSRHSPASAYRCPP RHIANFSAFLVQTGPFRVSDGDKLQTS *SALLMPLDPATP
12837	26738	A	12966	245	44	QSKELGNYLPLSPSPSPSPAFHGLPFP SPSPAFHGLPLLP\SWTVQCP*RLTAT SLDPBPASPRFG
12838	26739	A	12967	205	30	QEGASLSRIKRGPGVGAWLGMVAHCNPF STLGGQG/SWIT*AQEFETSLGNPHLYQ KYKN
12839	26740	A	12968	114	465	DPVSNPETTKPEPKKTTES*P/EPKSL LNLPS\P*NSS*CANREQPPSPQHPLP HPLPTSLQVHRLP*SLPPNLTPLYD /SPSPSLPVIQFPA*TSFP*PPVYSSP PSPTCPLH
12840	26741	A	12969	1618	1038	VHVQDQDINLNNQFLSGTMLLFFKETS HR*DRGPGDF*SCLYSAPIQTQPLLE*Y LPQNFIEG*PS*NSRKGTSLKTYISRV PSFFPFL*DGVS\TVPQAGVQWHDLS LQPPPPGFKRFSCLSLSSWDYRHPFLC PANFLD**RRGFTMLARLVSNS*PCDL PASASQIAGITRMSHHTLPHVFLPNV
12841	26742	A	12970	197	411	EQALRSTVCYCLNPLFPAPLPRQDC\G PCRFRWMPGGRTWLAPVITL*EAEAQ VWLEARSLRQAWATW
12842	26743	A	12971	616	777	MGHGVHRNAQLNFVFFVEDGGEWQLTC TGAGDSSVVLGEP*VFAC/PKNVLFYLH P*LFG*I*YIQLKITE*NYEGMVPE/FVF RFLFETRSLSPQLCESGITTHCSLEL VGSINSSISAS*LDGNT\GVRHNAQLNF VFFVEDGGEWQLTC TGAGDSSVVLGEP LRYKBRLLIKWYL
12843	26744	A	12972	222	389	VITEALGSELEGRQLWN*TKHSQVQW LIPVIPAL/LEAKAGGLLEAKTSRPAWE T
12844	26745	A	12973	425	145	QITFPLPQKIQNFQKASFPKKNTELGQ TSKQNSAQISVFKKNSKMITDLNVTH *TIQLTKN\NIGKNLQDQGLKEIILN TLKQASTKG

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12845	26746	A	12974	322	411	NNKKTFMSTG*KFFVCFIVQLIPETILS VVRVLSIILINYL*YCIICIFPFLPFL* T*EIRKVKTKFTSPFOIEEK*KCRR/WLGT VAHTYNPSTLGG*GGRIA*AEHFTSLG NTGRLPSPVOKIL
12846	26747	A	12975	428	1	SRKSSSQRLSFFPSHFLDLGAKGAVSQ DRAIALQPPGPRSR*S*RPSPRRCFR PRPSRSRKNKERAGEKRRPRSLQPRPP HIAGP/VPRKQGPSAGPEAPLATDEPP PQRSGIRGGSANIRSKQTSLSLRFRVRG RVG
12847	26748	A	12976	60	294	NHCTETVLFG*LTVCVCVCVCVCVCVT ERI/CFFKFLGKGTGCGIYLNWPKTIL IFIYILYSPRGRSILKKKFFFLT
12848	26749	A	12977	6	341	DSLTLPLGLECSGAISACSLCLSG/FK QFSCFSLPSSWGFTG/VPRMPQLIFPY FSVKTGPH/HVG*AGLKLIPASASPK CWDYRREPPRPGDLNWF*PTGFKLRFPQ FPL
12849	26750	A	12978	296	42	SQFASLGFKSVLDPLLAVCPLGKITLTL WDFSFIYYIKQE*WFRAGIFMPYNPST LGGGRGRIS*AEQFSTSLGNIVKPHYLV K
12850	26751	A	12979	20	373	KLYGGTWGFFFRGLNSATQENQGHN LG*LSPPPG*\RNFASASGEPIGTGS IHKAGIVFYIHKKPGKLTTLQKFTPP SFRHHQAPMGPVYSEILGEKSLINGWD PQTKKG
12851	26752	A	12980	380	96	PVFPFPWRAQGGSGREIRPPRGNOGR PGPP*KKKNYPGGGGGPPSPFFEG** PKKWNPPGGTTP*TEFPWPSTRGGEK KPPSKKKKKEK
12852	26753	A	12981	331	71	ELIYSWWNCPTVVPVATW*GRELVGRI T/KSRRLRLQ*AKIVPLHSSLDGRVRC PPPTTKKLANLCPWTEGSLFSYLLLEQ FHSC
12853	26754	A	12982	383	189	RRALKSCAHSFTAGPKNAALSOAQWLTP VIPTL*EAERAGSLELRSPLL*AMIEP \CTPAWVTE
12854	26755	A	12983	144	6	ILAQ*KTLVSVVAHTL*S/TLGGQDGR TGAQEFKTLGNTRRPLCYK
12855	26756	A	12984	341	509	ETLYTME*YTAENKEMTSFAGTWLELE A/VIL/SNLV*EQKTKMLPCSPMLGWEL K
12856	26757	A	12985	387	125	DLPPPTPPKLEPRTCSVAQVEVNCL/GSL QPQPPGP/SDPPA*AS*LAGTTGRHHA *EMFFP*VYFVQTS EHLGINPPGRHTK VANEV
12857	26758	A	12986	151	350	GRGGF*PLP*IFPPGQERPGFTPEKAPP PLGFFPPG/FFFEKRLRLSPKRWDR LGLQPPPPPTFGY
12858	26759	A	12987	251	1	RMSLLEKKRRSN*EARV/CGRVIVVATE VIKIMIGISMVAHVNPS TLGGQGRRIA SAQEFETSLGNMTNCLYKXYTHKKRA
12859	26760	A	12988	320	3	TPMGVKDFSPPPPGEGVFFGRAPPPR *KFGNFWKKRGFPNNVRGVLFKFWG/KNF FPPNPLKSLGLRFKPGPP*KAFFPPFL FFFFFEMEFLRCCPGGSAVAQS

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12860	26761	A	12989	353	183	EYGHILTAAITFSAKRWahr*GSLTDEWVRKNSIQSMYY\SAIKKNEVLLHAA P
12861	26762	A	12990	377	2	LSILINFPFRSLQRGKYPGPPPPKKNF POKTPPRAAPKKKPPFFFFFSFKKNF PFFFKQSGKGGPPSP*PLIFRF\NP PPPCKIGFKAWVFSTPPPIWGGFFFF FLRWSLALLPRLEC
12862	26763	A	12991	134	298	PPNSVCDGSIYTLIPKSDKNITRKEK\ P/YLMTIDAKVFNKVLNRIQQ*IKRI I
12863	26764	A	12992	892	171	QT*SH/SLSRLEYSDDTIAHCSLKLKMS SDPPASASQVAKPTGHCTT\MPQHTEGF
12864	26765	A	12993	269	2	GLWCFFVQLKLTETCPHPAVPQFPLGIS KIPISILFFKKLL\NPGTVAHCTNPST LGGRGGWTT*GQEFGLMFHHPWSKFHHG QHGET
12865	26766	A	12994	324	4	SLYPLLFOAEIYFLVLTIHRRSMESCIFY FBVVVPLDSLQV\IHVKI/HIKGIML*V N*QNCFKINISE*L*YIWPSTVADTLGC QGEITRAQGFKTSLSNMTKPHLY
12866	26767	A	12995	106	531	WLLNLFAPLNDKGFLVPMNRSRIFSQQK VKQRSFEGCSSFNDVSGCYVTQAGEQWL FTGVIGTL*PGTPG\SSDPPASASQAAG TTGS*HIIQLNLLIYSSG*QTI*LL*TI DSTHLIFASLYAKQLITFYFQATSLQPC T
12867	26768	A	12996	1	367	NTEPFLNIFFRDKVS/CSIAQAGGQWRL YSRCSLKLGSNSPSTASLVAGSKGRH HYTRL*LFFYVSRPQDYLWSPVFFPSF FLSFFFWKGSFFLPPSWKARAPIWNGS LPPRVKIFLA
12868	26769	A	12997	3	379	YRPSFSETKAVLVFFSFFSFFFLGTGPG KQPPGKAPNPTLTWRGKNFPI*KKKP /RLI*KKGP\PKMGFKRERFWLKP\KGP QFGKEGK/SPNYPHPRGDPKAPSLWKK PQFPGGGGGAPKKAS
12869	26770	A	12998	230	409	SCRPKKLAF\LKSSSTISQRWKQPIYI/ PSTDE*INKMWHIHTMEYY\ALKRRTKVL THATT
12870	26771	A	12999	310	343	DPVCTII*II\CDI\NL*IECSKVW*SLKF YKILILFNVCWSPVSGNCHKWLCDCV* KQW/LWPGMVAHCTNPSTVRGGGRIV* GQEFETSLGNIVRPSLYNNKSCI
12871	26772	A	13000	390	289	IKLCQPRGVKLDSEFRKAPPPFFETRS CFVS*AGVQWCN/LGSLQPTSGPNINPA TSA*LSLIFMCSNSVVCIVK
12872	26773	A	13001	1	289	GILRQISVNYLPVGRSLAQAGVQRCDLGS L*PLPPKVQGFSCVAGTTRGCHAWLII FIFSRG\GHPVKGASSDSPTFGFSKAG ITRLSPRALACT
12873	26774	A	13002	359	105	RQKNKNSPPPGGGGGGQKPG/PPKPPFN SRDPPPKNQSPFFPKKKKFFNFY*KAK NP*KPNPPLKKGKPKGFFSPPPLKKP PNV
12874	26775	A	13003	243	293	MNSQFLKRL\RIESPYGSVISLLGTYST EK*KACPKCTCTQMFTSALYI\AKKNW KCPSTVRW/IKLWHINTMEFFCQ*KKEH

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12875	26776	A	13004	465	307	CIDMPQFVHLTVGHSPLFCYYI SEACFILKLFMPG*CLFVC\SILLVF YFVFCFVLFCAIYMOFFNQCLFG
12876	26777	A	13005	207	3	DGSLTMLPKLEC/RWLFTGVIMAHCHLE /RLGSNDPPASASRVAGTTGVCHHA*LI FIFVVKMRSHYPTTP
12877	26778	A	13006	2	56	DLALLFLR*CNMGITAHCNLK/RPG*LL GSRDPPTMVS*STGITGMSHEARFSPS CDF*RCSVCVQVAVQNHDISSL
12878	26779	A	13007	402	74	FGASLLKRHLFFFLSKPLVYNKKIPRL VELAKT*PPFGRATPFYCCPFHKEGP GFOVKKEG*PKG/SPPQFGSGTFFPFL GAFKKPKVLTTFPKKCKPKLTKGPPF
12879	26780	A	13008	356	145	RPFPPFFFTFVSHPVHAGVQWHHSS LQL*TP\SSREPPASAS*VAGTTGVHYL PGSQLPILEHSFR
12880	26781	A	13009	227	353	GNSELT*/SN*QWLTPVILAL*EAEG GSSEPRSLRSAAWATN
12881	26782	A	13010	249	32	NPDHSHWAWNCASVVGQKARVGSLE SRSLRLR*AMIVP\CTPAWVAQEPPLSK KPPTIETLFPSPQDSQ
12882	26783	A	13011	247	403	TPGGGKGYFFFWGQPKNRGGFGKNGG GKTRGP*QKPASSGFAPPPFWAGPG FSPPPRF\KPPFPVFLQPKKKIFPP PGGLFFFLLGGPPSPFFFFFLGGGPL FFPGLGAMGPMAGFRSLAPGNLSKKK KSEGLGEGGNSVLT RVLLISSYQTFGPN R
12883	26784	A	13012	206	386	TREAQTFWFPLYS*KAL/WLGTVAHT*N PSTLGGQGRITSSQESSETLANMVKH LLEI
12884	26785	A	13013	354	31	YKMNWDIHI*HT\YIPVPVGRKERK KLEEYL/QDINTKFNLMKMNIIYQ EVQQTSPRINSOTSTPHRIIKLSKYKT GREGWILSVMLALWEAEVGGPEVRS
12885	26786	A	13014	1	419	EETSPGAKCLFGYGGHPRRLRSRSL LS*NPILSHPPQGPQPPAGSHSSPPPT STCSCEPFAACTGRTTGPFWASGP AELDASGSSV/KALTSGLPARGLWGP AGLGVPFRLLGWMTSCWMLPPFPSPARP
12886	26787	A	13015	109	426	TSLENTAREPH*QTHMATTREVFSPSKD ST*LRHLPPPHMCF/PD*SLKSN*Y*H YLVNP\IWPMLTLLVCLFPCRDRVSL CCPGWSAVVPSRLTAATLWQVILPP\ RLAN*IFFLRWGLAMLPRLV*NSWAGDI LPP*PKVLGLQA
12887	26788	A	13016	149	422	LKRIFFLKVVFTDITAPGDNDMCPYSC F*NQIIKSLGLFFFKKPHL/WLGEAYPC NPTLLGGQGRIT*QEFETTPANMAKP LLYKYYKN
12888	26789	A	13018	162	377	QSPGYPERVSKLETTITQGMWMMHQP CTSL*NV*TGWAQWLTPVIPAF*ED\AL AGGLELVKNLRPAWST
12889	26790	A	13019	205	427	IQTGQGFARFPLWPAWPKK*RVFPFGG PPKKKKKT*PPHPGGEREGS/PFSKKKK KKTPKKRAGVFFPGGPRPKGPGMGPPR LDSEKVPAGPEPGRNGNGPKIFFPGPP FFPLQPKGRP*PGGEGGSSFFFLGVPF

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12890	26791	A	13020	248	358	LGEPSTFCLDLPENA SRGGGEAQWLLPV/I/PAP*EAEAGGSF EPKSLPAPAWT
12891	26792	A	13021	2	434	ITEAGSDTQEIHHITLTHLCVWRRFTK KAVVKKVWHM*PGLLORLEMGGSLEP RSRLQGAMTLPVTST*QAWAT
12892	26793	A	13022	162	410	LTQKTAASQIILSPSSTSLFKIPISSES GGGGSVSTQAABQWVHSLQ*TPCD KRSSLGLPHP\SSWDYRISKDWMPV
12893	26794	A	13023	250	40	LTKLNFSCSLAINTSSCMTSLFKYFAH FSFF*IDFSSYYILDNTPFRN/GITN ILSSSVTCSFILVVV
12894	26795	A	13025	264	1	VSTTHGKRLPEVE*CFIH*EEKVFE SYFEY/PCOTFLRKETVRPGAVAXACNP STLGGQCRNII*EQEFETSLCIAAALR VTLR
12895	26796	A	13026	110	523	CIDSSSWTQDRCKEDRLCPGTGTGCAP GLLFLSAPPLGPF*PSQAHPSFVHLSG PSGPLRPQLDILPHPSTSIAPRPLPGPA S\LPRLPEHPSPSPGTACFPPLPCLGE QRHWPLPTSLWLGLDGHCLATPSVS
12896	26797	A	13027	52	53	CPTLLQLTLC/LPQASAMVDAP*ARP LPSSILACCTSGGQSVVGLAEFPVK YNLLVCRLLRPLEKCGIWAVERFSLYS LSWLPARK\NPLTACASWR
12897	26798	A	13028	262	381	HFGRLRQVDRLSPGVRDSLCKNVK*QI IYTF*FVSLSVINTYKOPSTVAHTYN PSTSGG*GKNIA*AEFE/TSLCKNVK CLY
12898	26799	A	13030	1	846	FRFIQAGRAPWALTLPQMGTTEGSPALL SHSSRCIDMGNCNTHAVDSTGEGPFHK GRNRESCLWTRPGCLITKVGQPGNMG RRRRSRSRQHPGRGHSTWASWLRQC MRKLQWASDLLSQLEMQIPSLPGESE SLGLTGPRLH/CEQTIGLSPTPGESWS EELG\GGIVGGGRGTVAGRGHREAGNK PSGTWGRQCCASGDKAMSI*LTSLYAR RGEPPGPRFVRKWLRESSQNRIGGGEGR WE*GQRSREGRECPVGWGGKKPLRWG LMWS
12899	26800	A	13032	308	1	KHYHDFWCWITLALSDAQSLDHTCV/CV CVCVCVCVCLRDQGSLSCL*CEG*LVP HFVPGPVLCLLSPVIYVFCISLTCKVE SLSNFFKLKALLRHCI
12900	26801	A	13033	763	244	FLGPRITGLRHSIVETQDHKSAVRGNN THDNYENVAGP*PKAGKTDKELYENTG QSNFEEHLYGNETSSDYNFQKPRPSEV PQDEDIYLPDSY*L/CQNLDFCYWMIN IHCNFSTAKTRNTQTC*STVDWIKKMW TYTIBYYAAVK/DTKLTWEQIKYHIF SLKSGS
12901	26802	A	13034	326	58	EHYKCNVCQKIPQKL*/HL*SKGHVYAE DKYKYKDGVPVLLVSQLIYTFYTRGK P*SSCSNFPQNGIYIGQKCKCNKFPN TFKKP
12902	26803	A	13035	199	3	RFYNNHKVCITFLPHFFY*KLVL/WLG TVAWMTSTLG*GGRIT*GQLESTGL DNTARPHLHTV

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12903	26804	A	13036	94	448	GSCATSMAFKIDTRKTAVEPGVVHGI KPLEKVCADLITGKKFKNL/KVGGPVC PTKTLKITTRKTPCGESSKA\WDGFQMR IQK*LTNLHSPSKIVKQIISISGAGPID SEVTNADG
12904	26805	A	13038	964	1717	HLKSCVLDLDDFMRQAGS\VTFA\DAHR PKLNBGVVEFASGYDLNNAIEKLSGK\ EINGKWNLLKQSKVPRSRSSSDPG TOKSPLPGRSPSPVVRKP*QVQCBAR SREPGARSGVPPVK*GPPPCPEKPEQK \RGSLSQSKILSPPSILWIRPEVSGPRS KVPVRSVDSGN
12905	26806	A	13039	2	725	SLFLSPVLPLFLPLFLAYILQNLKPLQF SPDLKSKHLFFCNAA*POYKLORSSK* PENGTLNFSILQDNNNSCRKIGKWEVP EVQAFF\SHQSPLSLCAQCNS/CPNLP SFP\VPVSUPTPSVTESE*SSFTDPSD LSLPPQALLARPS*VPILPQPPLLHP IILLSPPLLTTPRAYSFIP*L/CPFPFAQ QFTLKKVAGAGIVKVNAPPSLSQIR*H LGSFSSNIKIQPSBWLWQQP
12906	26807	A	13040	1131	2	DGVSLSPRLCESGTTISAHCNHLLCLN DSPASAS*VAGITGPATTPPLIFVYFFF LVETGFHHVGGSGLELPTD\SDRPPASD SQSVRITGVSH\AYLACSQF/CTRC*FP II*EQCVNMNINSSK*IFILISLYLRWM NKDPI/VIERLLVRMEPGQSHAA*NK TNKQT*LELVLVSTSCGVSVRFNLSIP *VFPET*EGHMRVNPSTLT*FIPQVA *TCQELGMLKIQTNGLDPSIVSDHQT Q*EPVVKOVLDSHDKLPMLELHPCR HTLASGKOISGVPRITIFLNHFHFQFY /CIFEMESCSV/SQAG/VQWRDLSSLQA RS/PGSR/RFSCLS/LPVQHPPPGPAMF \CIFSGDGVSPC*PGMSQSPDLVIR
12907	26808	A	13041	97	626	ICFTQVKVLNDSGVQCMFVVVATWEAG AGGVLEPGS*EL*/CPVNSHCPPAWAT
12908	26809	A	13042	2	431	HDPDTHSQIKVILMQSEFCGWAM*LT PVI PALWEAE/AGGSFVRS
12909	26810	A	13043	405	1319	RYRKKLQNKPLWLH/CLLLPNSATR*T LQK*SK*ISPLESSA*KEPPFLSVLSV TSVKT/SAIPMPHWNVNTQVPYQLIP LHNQTHEYNEVANLFGKTMDRNRIKRIQ RIQNLDLWEFFCRKKAQLKKRGVPOIN EQMLFPHGTSSEFVEALCIHNFWRINGI HGAVFGKGYFARDAAYSSRFCKDDIKH GNTFQIHGVSLOQRHLFRYKSMFLARV LIGDYINGDSKYMRPPSKDGSYVNLVDS CVDDTNWPKIFVVFDAQIYPEYLIDPH *FHFQISVVKALFFFGFAGRLQSSSH
12910	26811	A	13044	23	450	RSRAAAIQLGQRLRLPGPDSRLTGRQL EPGTGRGSRKRGPCSIFFRFRRETTPOR EGGRLGATISROAPPCCPPRPQWELDAS AKAAVAAPFKKVGFKAVSRDPRAEALGG KQSP\GGKGSKGVFAHR*GGLOPL*GAP EAI
12911	26812	A	13045	172	16	AHVSPEVDKTRFW/LGPVAHICNSSTLG GRGQQT/R/QGFETNLNMEKPHLY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
12912	26813	A	13046	181	9	YKMGFAMLPRLKCRATIGSNMAHCRLLD LFGSSDPSSASQVAGTGTGCHLGARGG MV
12913	26814	A	13048	2	3507	YVRVSLPPPPFAAGFGCAAVADAREEE REAAAPPPPPPPRLAARPPGSPQPRFP AAGEAQAAMNMQQQQQKAGEQQLS EPEDMEMEAGDTDDPPRIITQNPVINGNV ALSDGHNTAEEDMEDDTSWRSEATFQFT VERFSRLSESVLSPPCFVRNLFWKIMVM PRFYPDRPHQK\SVGFQFLQ\QNAESDST SWSCHAQAVLKIINRYRDEKFSRRISH LFFHKENDWGFNFMAHSEVTDPEKGF DDDKVTFEVFQADAPHGVAWDSKKHTG YVGLKNQAGATCYMNSLLQTLFTTNQLRK AVYMPTEGDDSSKSVPLALQRFVYELQ HSDKPVGTKKLTKSPGNETLDSFMQHDV QELCRVLLDNVENMKOTCVESTIPKLF RGKMVS YIQCKEVDYRSDDREDDYDIQL SIRGKKNI FESFVDYVAVEQLDGDNRKD AGEHGLQEAEGKGVKFLTLPVLHLQLMR FMYDPQTDDNIKINDRFEFPEQLFLDEF LQKTDPKDPANIILHAVLVHSGDNHGGH YVYVNLNPKGDKWCKFDDVVSRCETKEE AIEHNYGCHDDLSVSRICITVAMLVIR ESKLEVLQAVTDHDI PQQLVERLQSEK RIEAKRKRQEAAHLYNQVQIVAEQDFC GHGNDMYDEEKYKVTVPKVLKNSLAE FVQSLSQTMGFPQDQIRLNPQAARSNGT KRPAMLDNEADGNKMTIELSDNENPWTI FLETVDPELAAGATLKFDDKHDVMLF LKMYPDKTRSLNYCGHIYTPISCKIRDL LPVMCDRAGFIQDTSLLIYEEVKPNLTE RIQDYDVSLDKALDELMDGDIIVFQCD PENDNSELPTAKEYFRDLYHRVDVIFDD KTIIPNDPGFVVTLSNRMYFQVAKTVAQ RLNTDPMLLQFFKSGQYRDGPGNPLRHV YEGTLRDLQFFKPRQPKKLYYQQLKMK ITDFENRRSFKCIWLSQFRESEITLYP DKHGCVRLLECKKAVELGEKASGKLR LLEIVSYKIIGVHQSEDELLECLSPATSR TFRIEIEPLDQVDIKENEMLVTVAHFH KEVFGTGFIPFLLRHQGHFREWVKRI QSLLDIQSEKFEKFAIVMMGRHQYIN EDEYEVNLDKDFPQPGNMHSFRPWLGLD HFNKAPRSRYTLEKAIKILN
12914	26815	A	13049	30	477	VRAEHCAVWERNFEETURWTSVKFLMTS PETASLSWQMKVKGENTYIDCKWFG GSRTWDRRTGTETSGVQVPAACDYKE VVERGVQTLVIGRGMSEALKVPBSTVEY LKKHGIOMRVLQTEQAVKEYNALVAQGV RVGGVFHSTC
12915	26816	A	13050	179	389	NIETIQSMFPI/DNEMKLEINLKKATWG IHKYASQVLWFMP1FPTLWEAKVGFEFL PRSSRSVNETWRDPI
12916	26817	A	13052	466	1489	PGKGEKTRTSPSFLAIVRPQRASRPLL CAVSPMASASGATAKHEQIIVLDPPIDL KFKGPFIDVVTINLKLNRNPSDRKVCVKV KTTVPHYRCVRPNSGIDIPGSGTVTVSVM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
						LQPFYDNPNEKSKHKFMV/QIFAPLNTS DMEAVVNEAKPHELMDSKWR/CPNENDK LNDMEPSKAVPLNASKQDGPPTQPHSAS LHDTETRKLTTECKRLQGEHMLSEENQ HLRDBGLRLRVAYSQKPGSSTASFD VTSLLPSLLVVIARITGPTFFWRRSL TLVAQAGVORRDLGSLQPPSGGKQFSH LGLPSSKWDYRPPPHANPFCFSRGGVS PCWPGWS
12917	26818	A	13053	892	189	SYDPGALGCRPAPRSGRGKSGATRDMH PMSRERAKPVKSLG/YCKTRELMLHAR CCLNQKGTILGLDLQNCLEDPGFNFHQ AHTTVIIDLOANPLKGDLANTRFGTQL QTLILPQHVNCPPGGINAWNTITSYIDNQ ICQGQKNCNNTGDPMECPENGSCVDPG PGLLCVCVADGFH/GIQVYAPGLVLTAY VLRDSGSHSIRLHSLGDPAPKSQDFM NYIGLTIDLRSI
12918	26819	A	13054	423	12	SFNQKNPLQKCSLRTPRPAQSGLATWF GQSTRFEQALPWLNDPQSKRAE/MQL EPHAHTWTHAHTOGHTGA/FCSAHEV YVHLHSPVHAHTHARTHSPPVHTCGRL HAHTH/PQTPSPGGLLSLAVARPOS
12919	26820	A	13055	16	349	RRSGKNDPWTQSPRAAASHTRCPHPAV AAAAMPKRKTEGDAKGDKARVDESKRT S/ARMSKSAASKAYAKPIKAPAMNGEN VFNGIQRLKLEAFYDLOACRHLTRLIDFA
12920	26821	C	13056	716	594	MMQTETGVMPFQARQCLEPPGAGTGRKD SBLVPSSEQSWL*
12921	26822	A	13057	353	2	IGNQKKTETKFPFPPKFIKSFMMFLF FLVKTRSCYVAQAGLQTG/SSDPGASA NQSAGITGVSHHTOSIILKYTVFCLTPQ TPEYTIPTWSIPCCSHFSCYLCFLFAC FLRQSF
12922	26823	A	13058	864	529	EVSTSKTAGRCGALVISMLCIIFPQGL FTRALLRTRCSALLHADWPESIFVVVVVF FKTESCSVAQDGVQCDLRSLKPPPP/G SSDSPASASPVAKI/TGMHHHARHLKS
12923	26824	A	13059	2714	1376	GRYDGLVEQLGGRATPAVGFMGLERLV LLVQAVNPEFKADPVVDIYLVASGADTQ SAAMALAEIRLDELPGVKLMTNHGGGNF KKQPARADKWGARVAVVLGSEVANGTA VVKDLRSALAVGVILGVGALIGWRWNS HQVDSARSASLAYQNAVTAVERGKPDISI PAAEKFAENKNTYGALASLELAQQFVD KNELEKAAALQQLGGLADTSDENLKAVIN LRLARVQVQLKQADAAKLTLD/TPIKGE GWAIAI VADLRGEALLSKGDKQLLSVTL LSGCCLPNSEEDVVMKSLPTVENQFTF TIANSTSDSGIGNFYSLNHLHPALADNVV YAADRAGLVKALNADDGKEIWSVLSLEK DGWFSKEPALLSCRVTSWPNNQTEKEN KQRTSPAVAEPEQACVRRVLYPFTGG YERRRACQAEERPAARCATTEHOSIN
12924	26825	A	13060	99	254	RNHLVAFKELSAKVKRVVDNAPWIMPV IPAF/LEAKVGRSLERPSSRPAPAT
12925	26826	A	13062	127	386	FSYIIYFFFLFFLCVVIPTGEPFLMKKL GPKPTIMLKEKKGGESYSELFETDQME

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						WL/TPVITLWEABVGGSPFHRSSR
12926	26827	A	13063	1	209	GKYLILLKVFCCFLRQGLCHLAHCSRL PGSSDRSASQVAG/ISITGVHHHARL NPFVCFEFLVCF
12927	26828	A	13064	132	1	SHAMCCNVLRKRGWARMMPV/IPALWE AAGRSPEVRSRSAL
12928	26829	A	13065	269	134	TLNVSFASV/WAMWLTTPVILAPWEAKAG GSEPVRSRLICKQKVL
12929	26830	A	13066	853	461	RLNRSVSQFLCACVMCMVPSVCVGLAH AGTYAVSTCVH/MCVCMCARITLAKI CSETSGNLLFRKIISLDLFTLNFISIKY KVQLVLSRSLAWGRIKLLLSRPFSD VNTFERINYWLINDISIIR
12930	26831	A	13067	57	2066	AQPTGRQTSVAPTATARSRGGRVPFIF PCPHAPITLLSTSRVTPASPAAMKAL RLSASALFCLLLINGLAAPPGRPEAQP PPLSSEHKEPVAGDAVPGKDGSAPEVR GARNSEPDGELFCQVDPALAAVLLQ ALDRPASPPAPSGSQGPEEEAEALLT ETVRSQTHSLPAAEP/EPAAAPPQPTP ENGPEASDPSEELALASLLQELRDFSP SSAKRQQTAAAEETETRTHTLTRVNLES PGPERVWRASWGEFQARVPERAPLP PSQFQARMPSGPLEFETHKFGGVSSPK THLGSAALPSKAYGVGAAPFKARRPE SALLGSEACERLLQGLAQVCAERQRA EATROAAQEERLADLASDLLQYLLQG GARQRLGQRLQEAABERESAREEEEA EQERRGGEERVGEDEBAAAEAAEADE AERARQNALLFAEEDEGEAGADEKRSQE ETPGHRRKKAEGTEGGEEDDEMDPQ TIDSLIELSTKLHLPADDVVSITIEVEE KRNRRKKAPPEPVPPRAAPATHVRSP QPPPPADAPARDELDPWNEVLPPWDREE DEVYPPGYPHFYFNIRPTLQPPSALR RRHYHMLPPSRHYPGREAAQARHAQEE AEAERRLQEQEELENYIEHVLLRRP
12931	26832	A	13068	282	53	PGFPQGGKFRKKILPDQYFPQGAAPNSK ARPGGVGPGIPL/LWRVKKGGPLRSGG PGFPAGKGTFFLIPNTKKS
12932	26833	A	13069	177	2	VSLCRPGWMECSGVISAHCNRLRFGSSN S/PALASRVAGITGARHALLNSLFKVL SRA
12933	26834	A	13070	789	302	PHPEFYYSFYQIFYFYFISFHTRHFIVH YFISSHFISCHLASSSSSSSSSSSSSS SSPAPFHYSFHFISPHLAHY/HFIIS FHLFHLFSFHSISFRDRDLQCPGWSV PFPAPFHYSFHH/VHVMRHFILRQTRS IAQAGIQWRDLCSLQPEVSSSRA
12934	26835	A	13071	193	2	PPLYKSHSQVDLSFGVQDQPGQHRET PS/LTKN/TKVSWWCTPVPARNEVEVR ESLEPCSTRA
12935	26836	A	13072	122	1495	LLSDEFFETE/SRSIAQACMWCYLSS LQSLPPGFKFSCLSLSPSGWDDRCPPPC LANYCIFSRDRVLPCWPGNSRTDPLR
12936	26837	A	13073	178	347	ICCLCNDNSVLLCMYYLVCMAHCHALY IKTWK/MQLGAVSHACNPSTLGGQGEWI T

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12937	26838	A	13074	165	34	FILSFPPFTVS YFAVQAQVQW/LI IAHCSLDLPRSSDSPTSAP
12938	26839	A	13075	205	105	GGWVQWFM IIP/AIWEAKAGGLLEPRN SRPVWAT
12939	26840	A	13076	3	357	HERREYTAQEKRFIAFFFFKMGSCSVIQ ARVQRHDLSSLQPP/RVAGTTGTHYHTW LIFVFSRTDSRLPSSPSRPLTSVILII PSLIIPITTYLTTPSRPSTSPSPSPSR AFLTSDP
12940	26841	A	13077	3	477	STPALTARGLSGGSRASVAAMVLLSEBQ FLTELTRLFQKCRPTSGSVITLLKKYDGR TKPIPKKGTVEGFEPADNKKLLRATDQX KKIITVVSSKEVKNFKQAYSNLLRANMD GLKKRDKKNTKKTKAGSNSS/ATTAAP AAAATAATTAATTAATAAQ
12941	26842	A	13078	1077	1566	RQVTSLDLPKTFPRTSLEFTSPFGOLDS GATAFTVVPVPSGAPTGRGRESAAHQGN/ YPVGQRS/RMAGLSPRSPCWWEVSFR/ SHSC/ICWVLGKSAVL PQQSRGPGAHE GSRRRGGSSPPCPPLQTLQVFS PQELSM SAPIHRLSVTLQGD CISTGAPSRCLRA
12942	26843	A	13079	3	396	HERGKKVSVT/RLIQRLRNWSGHDQL GKQLRYQEISKRTPTTKLPEGPSHKL FNNYY/CTDRGRRSVPPIIMSSHKAL VSRMPAYSFAEAATDKKAVTPAPSIYRG EQSSDHPYLRHCTLT/VTRL
12943	26844	A	13080	467	109	SLVPVPSPHLKEPSCRYLIENVMVLPEKE QEFWSKEAGSLFSPVPFYCWTPSIVFS SSSFFFLFRCVCFPPFFFCFFFFFLFLLF FGTKKALYLLRARGCKQYKQKLIWYLT FLSLLVK
12944	26845	A	13081	458	51	VSLFCTVAPLLLLPEGIFFSCSLLEVKKA PMRDSGVFLLTFLYSVLFFPLGVFFFL FFFLLPBPKLIFFFPVFCVALLFFSPAP GAVFLF/SLWSSVLPQGVGTFACSSFFF FFFFTFLROSFAVQAQRMQR
12945	26846	A	13082	23	327	RSDEGGRRGHKHYFFPIVTHHTHTYIPI YTIQIYICLHYVACL/ LICHIFISIIYI HTYIYISIIYIHYLHYTHIYLIHYIHT YIYIYLIHIIHYSSWCKGS
12946	26847	A	13083	352	153	KKLVEYYSATKKNVLIH/VSTWMLRKN I T L S L K T O S O R H L Y I I P S V R N V O N R Q V H K Y R S L R V D S E D
12947	26848	A	13084	121	417	DYDYCYCYPPKLYITKLIFYFY/VGNIIY THIVRHVYICETYPVTHIHTYIYICIY IYIWKETTWLFSOGISKTYRTHDLAYTY LVFCLTHVTHVSST
12948	26849	A	13085	242	12	LSSRLPMLETKETITSKILPSRKL/LEP GWCFKSKITWVSQIRNRL/AQWLTTVI POLNEA/SGLLKPSRRPARTW
12949	26850	A	13086	274	340	GGKKTPGGFLBKSSFGGGIFGPPP/P TKRGVFPSPKPKFFFPPTKNFGRGGG KIPPPKIDFFSKNPPGVFFSPP/YKKKK IIFPPPVKLGPPKDFLKSPPPPFFFPF FFFFFSSQEVNLKALSSTSEIIFVYLV
12950	26851	A	13087	241	405	PPPSKIHIGNFRMSDVKNATGAWMLT PVIIPARWAEAG/VSLRPNRSPANAA
12951	26852	A	13088	537	375	KSLITLSRLLECKGTILAHCS/L/CTSL

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						LGSSDLSLQFQQIAGTTGACNHTHLEKI F
12952	26853	A	13089	448	186	GALVFFSSQAPPCPPKMQSFFFFFLL ETGSRSVSKAGVQLHGHSLQPPPPGFER SSHFSVTII/TYLYHRLALRVFELHIN GIMHR
12953	26854	A	13090	365	191	GOEREKEREREKRQKKREVE/REEKE RVRDLESESNNRALERERSALVDRAPLSR PG
12954	26855	A	13091	148	316	DKMESCSLAQTGVQWHD/LG/YLQFSPL GFKRFCLSLSSSWDYRWETSTEPQQA VF
12955	26856	A	13092	712	229	FVAWVKMAEYLASIFGTEKDVNCSPYF KIGVCRHGDRCRLHNKPTFSQEVFTL QEKYGEIEMNVCDNLGDHLVGNVYVKF RREEDGERAVALESNRWFGQAVH/GEC TRGGFCNFMHLRPI SQNLQRLYGRGPR RRSPFRFTHGHPRENRHVRFP
12956	26857	A	13093	835	405	ELTERLGPNQKFFLLMWKMPSPSNMKA SAALLCLLLTAAAFSPQGLAQPVGINTS TTCYRFINKKIPKQRLSEYRRTTSSHC PREAVIFKTKLDK/EICADPTOKWQVDF MKHLDDKTO/TPKLLNHDWNLNQAMT LRKPN
12957	26858	A	13094	1137	424	LCPSPHFAPITTLTPQGAHNMCCKISRFK RDLGCRITCLVNMKFTSSILGKSHRHSL VSLNGGNALWKAAG/VLSWKAGYCVQG FSFCDLKYQ\SWDEKDLTPQPDTHQCA SVLRNISKRGKPLAVETEGRATGLPLCA PWGTE/CLGYKTPIV/HLPNSEMG/ENR PYGGRARHVCSNAALLFTPLRLCLQGEK HKSGLRAHPVTVLSLELNYDIDSFAHMF FADLLLIITLLSCYIPFC
12958	26859	A	13095	1	324	ARGERERERERERERERERERERERE RERERERERERERERERERERERERE RERERP/RPRVLFFVRGREGSHPEKCN KKERAPFSRALRKISITETRGVSIITTEA CVFVIGAHVRVCRSVYIYI
12959	26860	A	13096	508	840	DGVSLCRPGRTADCSGAISAHCKLRFPG SRQSPGLSLPSSWDYRRLKMPRANFF CIFF/VKTGFHLVSQ/AMGLDLLNS/SI PPRLGLPCW\DYRREATAFGQELLNR TGM
12960	26861	A	13097	53	254	WPQTASCLVAQGVQWSDHSSLQQRQTFG \SSHPPASASQVARI TGMHHCANLHLII LLRAHGSSPLC
12961	26862	A	13098	329	67	GGAPLLKGKELLKEPPPRISPVSFAF FANGPPPGYCFLLKGQPPF/VFPSPFPG KKINSPPPHINGAKTFPNPPLLFSSF FFP
12962	26863	A	13099	253	444	EGAFSLGTFFYIFFLVLSNTFLLSIKNQ QVWNKRTVW/PSPFLPTLIALTLTLLPI SFFLLIIL
12963	26864	A	13100	341	590	PWASSQICIGRIPFFLYLKYVFWPGKV HTCNPRTLGGRGALITQQQKFPENSLAN/ MAKPHLY
12964	26865	A	13101	55	184	RLREPTFLYSE/HAPTKCYRMAHDNYPH SDPIPQRHRYRVLL

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12965	26866	A	13102	433	762	RNLLNCKRGLERKGCGRASWAPVPLFLQR RVWPRPTAELNEACMLAQHNCQNVKME YPQLSFTKRQEI/NLGVVAHACNPSTLGR G\QGGG\IACSQFEKTIIPSSKVRPCFYLK
12966	26867	A	13103	349	250	DLFFSTKPPPPPPPPKNGLPV/GPFGFP FQEG
12967	26868	A	13104	3	236	YPOHYPSCTFTQYTLTKNNHFLIFFEV GSCSVVQARVQWCHHGSLQPP/NSSDPP ASAPQVAGTPGVSHRAPPKNGNF
12968	26869	A	13106	154	4	KKVNTVHYNGKYLKSNQSTFLKEIL /MLGVAHTCNPSLTGGRSGRIT
12969	26870	A	13107	391	150	RPFKPNKIKSGITSGIKMIVYTRKYL TKKAMSOALY/V/HAVPAIQBAEVGG SCEPGSSRPCTMTWIMETHCAPAWT
12970	26871	A	13108	90	252	KVGDGGRCLVFCFFKRCSTFVQAGVQ W\ATIAHCSLLKLLSSDDPONYEDSGT
12971	26872	A	13109	197	414	LYEFIKITVLLGLCPGRVGCSSNORFF SLEMFPHTVAVARVQNHDLSQLPLPPR PNRFSCLR/VPOSSWDYR
12972	26873	A	13110	2	317	GRVGANVHGKHQRRTYGVSVPHILPLAV LKKTFSLRDFHFSVSLKK/NLVTCLHL FL/GVTRPRNDPFVSMMLLFTAFDLRPS TILGTGLLYTEGLTVALRLAYLR
12973	26874	A	13111	413	162	LILLPQPAECCLQASATLDCGLGFLPC RDCRRSLVHSLVNGAGAGVQWRDLGSLQ PPPPS\TCLGLPKYRDCSLCPAATPSGK
12974	26875	A	13112	40	296	ESRLSALYIYHICVGVYNNRHLLVGIHM /SIHTYTHTHTHIYIHMRAPELDEKF ICSLCSRDNAFLVSLVKLRQNYFLT RR
12975	26876	A	13113	2	288	FEPRCKNSARGKVPRGFSFNLPHVTIVET PEGSKTGFELSR/RRHRQIHSSAQCLP TAVPGAGDAIPEDASGWTWLP\LAHQNC FLLYIQAEQPPPA
12976	26877	A	13114	685	340	LSPPRAGSARPTGPPTDAPQORSTWTCG ALKPRRRRLRDAENLFQELQEHFQALT ATLNLRMEMGNRIEDLQK\NVNDL\MV QAGTENS\KEQM\KKTVTANMSVFGDGAS YRSH
12977	26878	A	13115	65	3021	GVLT\ONGDEKDSWKVTLDEILQEKRR KEQEEKAEIKRLKNSDDRDSEKDSLEEG ELRDHCWETTIRNSPRRDESDMEDEGEE DDSLAIKPPQOMSWKEKHVHRKDEKKEK KCRHHSASAECCGHARVKEHEHERRKH REEQDKARREWERQKREMAREHSRRER DRLEQLERKRERRERKMEQKQREQKE RERRAEERRKEREARRVSNHRTMRD YSDKVKASHWSRSPRRPRERFLGDGR KPVKEEKMEERDLLSDLQDISDSERKTS SAESSAESGSGSEEEEEEEEEEEEGS TSESEEEEEEEEEEEETGNSSEASE QSAEEVSEEESEDEERENENHLLVGKN LPQDRVPVPSRFRDRDSESEAESEEVG EGTPQ\SSALTEGDYVPDSLPLSPIELK QELPKYLPALQGCRSVDEPQICNRIEEG TYGVVYRAIDKTDITVALKRLKMEKEK EGFPITSLEINTILKAQHPNIVTVREI VVGSNMDKIYIVNNTVEHDLKSLMETMK

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						QPLFGLEVKTLMIQLLRGVKHLHNDWIL HRLDKTSNLLSHACILKVGDFGLARFY GSLPKAYTPVVVTQWYRAPELLGAKEY STAVDWSVGICPGELLTKQLPFGNSE IDQINKVFKELGTPEKINPGVSELPVV KMTTFSEHPYNNLRKRPAGALLSDQGFDL MNKFLTYFPORRI SAEDGLKHEYFRETP LPIDPSMFPTWPAKSEQORV\KRGTSRPR PP\EGGLGYSQGLDDDLKETG\ FHLTTT NPGGLLPRGPGFSRLRVAEVSLEDPVIGR NSAGDHRGRLPAWNC DGRNSSSYEVL PCFVFVFLVKCLSRISKPSLLWRKELCF LRDLPRAEVRGIFRGAHVQHKPHHPL PLSTRTGLGWAVIKGTGGSRVDCILFG AGDFLCWDERCLAPTHSSRPALSTTS PRPTTQPLLPALEQVFFYKVVGVLK CIKIFEE
12978	26879	A	13116	469	202	MIIVGLCEYTKSAVLVQHS DPLPPAPG VFLAVLDVVDIKIVVHPVCLFVCLYE MESCPVAQAGVQWRDLGSLQPPP\PGSS TSCF
12979	26880	A	13117	193	383	AARMASTFFVFWFSTF\SLYSICVCV CVCVCVCVRMHTVQLYFPQVGCSSL LNFLPFMN
12980	26881	A	13118	146	350	HYLVKFLLLAHPGSKAPPLNTLOPPPLA TREQPPITVIFHYPPTSYKMAP\PYLPS LTLFGLSPAPR
12981	26882	A	13119	124	254	HALLQTLRDLSDQANWHALVIPATW\BAE AGCSLEPRSSRPAMAT
12982	26883	A	13120	150	45	SLFLECSPTVLAH/C/NLHLGSSDS ASASQVGGI
12983	26884	A	13121	336	446	IPLKISSWACHLTVPV\IMPVWAEAGG SLEVVSSGPA
12984	26885	A	13122	181	39	QNLTAQDGVCWCDLGSQFP\LPSSWDY RRESLCPSFFPIFWKRGFT
12985	26886	A	13123	463	2	GPAVPSGLYLKGGKPMRLCASHSPESH HDKGQGTLPRIPO/PLLEGGSRS/PLAW GAVAGLPSNRPRIVPLPAPTRSGTRVRP HTGHQPGMSPGCGESKNWPSAAWPEA YPHFLLPFPFTGCEVLGPLYTADPWVI CVSLLPSCPNSATVDVD
12986	26887	A	13124	429	263	DHFSFLCVTGSQSVQAQGVQW\LYLAHC SLKLLASSDDPPASVFQSTRI\TGPFLESFT
12987	26888	A	13125	310	486	NKKTTRGESSKQQRQPRVSHHPGNGTVAP SGFTAASAS\RAVILLFRPPE
12988	26889	A	13126	124	461	GSPLQLLPLSPLAALTDCSCAPMGCSV AQDGVQWRDLGSLRLPPGFPPSCLSL TPAP\FPSGWDYR
12989	26890	A	13127	2	337	RGAAFAAMAVTALAARTWLVGVMGVRTMQ ARGPGSDQSENVDRGAGSIREAGGAFK RQAEERFYFRAQSRQALAKK\HDE EIVHHKKEIERLQKEIERHKQKIKMLKP
12990	26891	A	13128	681	422	CRSDRWAKEHRRGKRGDSSKDVMARLME APKQTAQYFFIFIFFFETKSYSVTQAGVQ WLDLGLSLQRPPPG\SSDSPASASCAPQ TAH
12991	26892	A	13129	299	579	LVMFCKVTKIERLNLWRPGTVARVLWSQ HFGRRFAVHVWGVRDE/RLTGHGETP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						SLLE\NRRTISQAWCMFVVPATREAEAR ESLEPGGQRLO
12992	26893	A	13130	268	438	KVKDKSMKMRKNRPKNAENSKNKKASSFP NDCNSSPARVQ/SWTNEFDKLTEVGFR KW
12993	26894	A	13132	1108	1529	KIHSSFVLLNAKLVAARPTKPYRKKKT DLPTQTYSAQTAVEPIVSAHSFTFRSF IHSFTI FETESYSVAQAGIQWHDLP\ PP GS\SDSP\ASVS RVAGTIGVCQQAHLFF V\FLVET\GSFPHLSPLMTIRNKQLFK KGH
12994	26895	A	13133	497	370	RPSTVSPRLECSGLILAHCS\LDPPASA SQTAEITYGHHAS
12995	26896	A	13134	217	373	CNHTETTYNNKKHRPGTVAH\SLYNFS TLGGGGLITQAEFTSLGNMTLS
12996	26897	A	13135	257	507	PVSFGFPLCPVPHFPLCHPCRYFES PGCPAAQHCAFPQCPNPRACSSGLP RCPFACHHAPSCLLCVCPPLPQCCRVOG
12997	26898	A	13136	137	309	FSFPTHPOCFCLFCFLVFETE\SSIVA QAEVQWCDLGSFDQSSASSPPSASSLPL SIW
12998	26899	A	13137	297	419	GGSAVYIWEIVQVLMMPVIPT\WEAY AGGLEFEPSSRPA
12999	26900	A	13138	213	492	QVGINYQPTTVVPGDLAKVQRAVCMLS NTTAITEAWGLPGAISAKCALVH\YV GEGMAVGFESEAREDLALEDYETCGPW NPVTEAEARR
13000	26901	A	13139	246	534	DRVLPLLPRLCSSLAILGHCF/APASQV TGTGTGTHHTQLIFLLYCWLCPPLASE ASASPPLLPRGFLCFSSTTSITAI PA TTRDYVDVSRSGS
13001	26902	A	13140	1	206	SLEWFFFFSFSETGSHSFTQAIQVQCNH SSL\SPTSASQIAGTGVHHAQL/VFV FCFAFMSPQLSNSC
13002	26903	A	13141	164	582	GLVLVNLVLRSLYLMVFIYINSRLQVTD ASRRERRENESSWFCRSVCRM/PPVGPGF SCVHPCS PRGISISPTCPHCLKTQAPA \PPRPLRVGPGPHLDQCCVAAARPLYD PILVAHSSWPAPSPVPVQEDTEHGA G
13003	26904	A	13142	235	367	LALNTFCWLGVVAHACNPSTLGGQGEWV TRGQE\QANMAKTCLY
13004	26905	A	13143	91	403	GALQFATAPWEFLPSGLAEAGAISPCLOG G/SGRGASBNRGCTPRVPGRRILNR PRMWSWPAFPQSGRSPALNCPRAEE CGRRVWDQCALPAADANVPU
13005	26906	A	13144	558	147	GHSFONWLLGCFQLQGHILLPPDASEE CGSPWPTPLRPHIHPASGPHGTHK\HA GGCLFPLRPSPTPCGPPVPLPWSQ\QA PLCFPHPIHSPHDWECDGKSAIIPPA AQSPSRILIKHAANEPCSPRNRRPGIP
13006	26907	A	13145	321	421	GCAQWLTVP/IPALWEAKAGESLLFRSL RPAAWI
13007	26908	A	13146	3	398	IELLQSHDKTLTDKLLLLDQKRNKFL MESTPGEDVNNVELTKOLEYHINLDD\ KAGFERIDSNFERVSAVG/KMLSNSIAC YREIFHRSVKVANFTVAILPQPHKLSV TINLI IQQSTLRQDLLLAIR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13008	26909	A	13147	228	261	SKIQRSSEYFSLVVCVVCVRVCIIYIY FFFETEFSL\APQGVQRCDLSSRLRP PF\GSSDFSTSQSAWYRRPQRPTS LHYFVQLKHNLHRVKRDLNTR
13009	26910	A	13148	3	275	KHLSDLGTLRLGLSSKTRKTRVSHPAQG RSIFPLLRPSVDWIKPACMDGNLLFSK TNLAWN\TKKHPHRNVQNVWPNVWAP WPKEVD
13010	26911	A	13149	218	382	ANDHKLSEFYTAKEETT/RMKQPTWE KIFANYPSEGLVTRMYKELQIYRKKI
13011	26912	A	13150	391	29	FCFLFLFMFLFFFMQDGVQWCLSSPQ PPPPG\SSHS PASASQVBAENCLNPGG GGCSLGDRLRPQKRERERETERKRKR ERASCAFCAITFVNWMCQKHHTCNHLP WLTVFETNKL
13012	26913	A	13151	351	157	FGYSRFLCVYNFRTNLSIYNYICIYIN LYL\NIHTYTLIYTYVHTYTHIFYIY IGILTGIT
13013	26914	A	13152	402	111	TFFGGEKFFFTLRLPGPPRRGGGGPPGF REGGFVRVPLGAPGSRPK/RPEKSGPV WAPQIFLWGGKSRAIKESGKGFPSRIT LLVFATEKKKKTLF
13014	26915	A	13153	310	141	REHEKQKPLSQVRWCTPLVQAQAEAG GELEPRSSRLQCSMT\TPVNSHRPPARV T
13015	26916	A	13154	153	21	LNKCVISWLGAVAHACN/PSTLEGRWIT QQGEFKTSLGSLAKPHLY
13016	26917	A	13155	429	275	SVDIPELKTINKDVFEAAFKCKVS/R QARVKFKKRYKPVKTKWFFQKLWF
13017	26918	A	13156	303	42	YERAFVYFIIINIAFGPHKQ\YTRAHT THTHIRMAHTHTPAIIPAPAKNGLGT FHKGRTYNDKVKPRLSCAAIPSNLKS REPR
13018	26919	A	13157	198	13	SHGVAILLFFHFLNKRAFTVSPAMNS LCEIQBPSLG\SGSGPLSGNRMSGKGR KYFAKI
13019	26920	A	13158	192	2	ISNSHRKDKDPEVLLIEQYILSGQWQ WLTVPVIAL/V/EAEAGSLFPRSLRPA WATORDSVSK
13020	26921	A	13159	40	190	RVDPRVRESRSVAQACMQWRDLGSLQAP P\PGSRHSPASASQVALPLANK
13021	26922	A	13160	1	178	PTMWLSPADKINVA\ANGKVGAAHAGY GAELERMFLSFTTKTYFFHFDLSHGV SSYL
13022	26923	A	13161	411	41	ESLQICVGLHAKPSSWDACRPWLQAWER YFLLTLFGLVFLVFWFSKIYFLYHLK NPSLSSCYNLD\FTQYLYKCKKKRLG AVAYACNPSILGSGQGRITRGQEPETRL GNMAKPDWVDP
13023	26924	A	13162	372	218	FWKRSWISKKGLFKRGVSLSLSL/CDT HTHTHTHTHTHAHSGYLCLVRKVK
13024	26925	A	13163	247	89	QGLVLSPLKCRGGITAHCGILGSSHET TSA\QVAGTTGTQHQHAKKFFILLIIL
13025	26926	A	13164	122	409	FFSTAANSH/CSSPGCSAGVATIRLF LRSSNKAL\LYGLAL/NSFFCNQEPES \LGLSLGPLSDNKNLCCFKSPSWLF ATAVLGNYSLSNTVRSGRDPGTNACS
13026	26927	A	13165	69	313	PSVSLFFPPNNHNVHMLGLKINSIFGE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GLALSSRMCECVTTITVHCGLDLLSGGGP PSAAS/RVAVTAGTCHHSWLMFLSFV
13027	26928	A	13166	310	26	IKSMTPLPALNVSLSYLLPPLPCRCRRG MVQDRFFCFLFCCCCCFIFSETGSHSAAQ AVSQNKKTIGWAWMLTPVIPATHEAEAG VESLERGQRLOQ
13028	26929	A	13167	296	68	KNGPLNLATKSLLLITMKCLGVVLOGKP NCSKLKRMKIKTKRWGWAPWLTPIPLPA/ LLBAEAGRSLEARNLRVWT
13029	26930	A	13168	2	235	GATPCPREPSLFFLAGNARLSCWAPPFH CTGQTTTPGLMGTOAPLAIIGGNARSP PMFPLPLSGTRALSAQBCPTE
13030	26931	A	13169	248	406	TERCGFDLLSQGVQWILTSVTPALE/EA EAGELLESRWRPAWATWQNLISLKK
13031	26932	A	13170	33	308	NSLQGAEMAAQSLSLPSASEGYRGRGR GRGRGRPGRG/RSEGDGRGRGRPGRGGR RKVLILLRI CWRRLRLMNRGRIGVGRG VTYLMESI
13032	26933	A	13171	294	56	ICKRNYLFFIYFLREGTLTPRLCSGA ITAQCSL/GSSDPPTASSTVSGITGACQ CALSSRDALISLCYPGWSSQAPGLK
13033	26934	A	13172	71	476	DSLNDNHIYQMPFLIYNNGLAVTISLL G/ILVYRSHLISLLCLREGIILSLPIIA TLITLWTHLSLNIIVPITAILVPAACEAA VGNEECGFRSRPTALILEGLPLRSCQPT CVRRPACTRRGPAPVGNRHSIGG
13034	26935	A	13173	86	318	NNCNCVCVCVCVCVCVCCHICIVV/YV YICITTYKYICITYTYKYICICIVIHVYM YMCVVYVICIMCVYICIDSKGR
13035	26936	A	13174	466	726	NCKMFGAVTRIG/DLEWEINPLSSCSLL REKDPPTTSGPQTDQPKHLTNFKSGKR PLETLFSNLPHYPTSTSFSPQSWRHTSIS PFS
13036	26937	A	13175	128	325	FLRVILICRKMVGVCVCM/YACICNGM CITYMCVCVKSWLKPELCLCISDEVGW VLTDWAGREEN
13037	26938	A	13176	134	311	INSNSEKMGSHYVAQDGVV/WQGLFTGH GIAHCNKLKLGSSNFPASISQAGATTGI VANG
13038	26939	A	13177	577	1052	SPSTFTTSGVAMWLSQPMGRITCRSKV ASKSLRHGPLIWAHPPIVRCMILRHNY/ KQAGRGRLSLE/LRVAGIYKVAQTIG IS/EDARRRNCST/QALQAKVQRLK/ED RSSLLILFPRK/PLAPKKGDSSASELELD TOLTGPMPPIGNVYKKEKARVIAD
13039	26940	A	13178	496	578	TLNFVWAQGLKTRTPWKNAPVPFVITV/R LRKNKLLTLKGEICSDPKWYCYCLPWKKT KKNLV
13040	26941	A	13179	192	421	GIYTFFLSFFFLRLQSLTSLPRAGVQVC NLCLPGSSDSPASASRVPG/ATGT/CHH GSANFLYFLVGRVFGYGVGR
13041	26942	A	13180	144	5	LQLATLKLKMLGVVAHICNPS/TLGGW G/GRSQQEFETSLANIVKP
13042	26943	A	13181	351	51	KKKKKIFFGTKRRRFFFLKGVGVPFPPK VSPPPPPKISPNPPKKNPLKA/IKSPQ NWLFFPGPPCKFFPPFPLNPKNSPWN PPSGGEFSPKKKKKSAI
13043	26944	A	13182	2	218	IHFSGCFVLLFFETEFCSCHNGCRAGVQW

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						RD\LAHNSLTFPFLQ\SSDPPTASQSA ETGMSHIACPFFKKGHS
13044	26945	A	13183	33	304	EKGHIFRAVKILCMILQRTVATHLSRP TGYTAPRVNPKLWLTQNDVSM/SGSLI VTNTALGWLLIRRSACMGQDMGNLC TFLSILL
13045	26946	A	13184	277	13	FSFFLIVEMSGCYIAQAGLELLGSSNPP SSASQAGITGMSHHPAWLATLKRFPVS D\NSLSFPSSENAHLSILAGHFCMGFF FFQ
13046	26947	A	13185	140	361	ITCCCVCIYTHIHTYVYVYVYIYTHYI RVCV/YIYHTHYIHIYIHVFIYIYIYT FMHTYIYYPVCMVLLQLTL
13047	26948	A	13186	64	759	CLSAESAPTSTMPMTLGYWDIRGLAHAI RLLLEYTDSSYVEKKYTLGDADPYDRSQ WLNKFKLGLDFPNLPYLIDGAHKITQS NAILRYIARKHNLGCTEBEIKRVDILE NQVMDNHMELVRLCYDDPFEKLKPKYLE ELPEKLKALTS\EFSGGKRPF/SQGDK ITFVDFLAYDVLDMKRIFEPKCLDAFLN LKDFISRFEGLKIKISAYMKSQPLRGLL FGKSATWNSK
13048	26949	A	13187	41	426	LFFFFFESGCPWVQAAGRR/WNDHGS LQPGFPGLGKSPCLTLRRSNYRPGMCRH TQLVFAPFFFPREKKFLGAPTGFKTRG LRGPSRPGFCQGGNKGQEPFPRAGLIF LEPERGQAFGVPFGPTQ
13049	26950	A	13188	39	197	FFLEFKTRSCSYCAGVQWCEHSSLQPV TPQ\SSAPRASACAGTTEAALKL
13050	26951	A	13189	221	396	GYLQGAEGLMVDVNSFFCWRLRYDQKT YHECRMWANSCHP\PPKGLLRDITPRCW AP
13051	26952	A	13190	2	826	PGSTISSRRRGACGSRGGHFPSPRGSSG VASLERAESWSTEPAKAIKPIDRKSVHQ ICSGQVVL.SLSTAVKIKIVENSLDAGATN IDLKLDYGMDLIEVSGNGCGVEENFK GL\TSLALKHHTSKIQEFADLTRVETFG FRGEALSSLCALSDVTISTCHVSAKVGT RLVFDHDGKIIOKTPYPHPRGTTVSVKQ LFSITLVRHKEFORNIKKIRACFPFAFC RDCQFLEGGPAMLPVQP\AKLTPRSTPP HPCSLEDNVITVFSVKNPGGSR
13052	26953	A	13191	235	1	SPCARQCCPFNAQGEPRRRLERGPGKW WPRSIFKPLPAV/RARFPLLPSPAPLRQL VSGRVGGRVGRPGKAVQVSGGLN
13053	26954	A	13192	2	386	VIYLLLFETESCCVQAARDGVSPCWFG WFQTPG\SSDLPASAPK/VAGITSVSHR TRPDVRGPKK/QLQLEMSHLALL/TT SHRFWYFVLLSFVSGKFFIFFFLFFP FFLGKGFPPFFPRGGGGGQI
13054	26955	A	13193	749	506	GQTKAFVLSYCGASPSIKQ/FCPOAKDH PLEPSMHPEGTOLGSCSTMGLGPRLSSE KQFLLPPRSHLKS PMLRACKGLTS
13055	26956	A	13194	73	297	RMFGFALGSPFSCQRIECFCVAGAGSC TYASFCKCKEYKCTCKKSECGAPGNG GAQCSQRREPRQAQGAQO
13056	26957	A	13195	670	390	PRETYIKFPARSIGCFPKPTIHTFSRRP STRPAPRAPHARPVHTP/APSVMHSDRP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						STCPFSIH\RPPSPDVSRRPOYSLSFSTS LALPGQSCIGR
13057	26958	A	13196	2	438	LSFTSYEFCHLLFLNQLICNYVIFTKSS TISCEALGRLLVVYPWTQRFESFSGDLS TPDAVMGNPKVKAHGKKVLGAFSDGLAH L\ PPLKPTTFATVSELHCAKLHVDPENFT LLGNLVLCV/MKHNFGK
13058	26959	A	13197	57	499	SFSWPRSSARPCSHGCLLPLGWDHGKAP CLRAARHSQGHGFRKGRKEGCGLWAAGW TKNPVPTWRAG/SRRPGVTSPPPVPSV QNFP\ PQRRHGGSQATRFVLTFTPPPKH MEGPNAPILGSDQRITAPFPBILYPPFRA ATCDALRRG
13059	26960	A	13198	34	465	GILPYSFCVLRAFNPKVRKCGCTTPRH L\ CKATKCCCTTPRAPLAEFKCCGCT PRHLSRQLNAGALPRGHINETKCCCT TPRAPLNATKCGCSTPRHLSRQLNAG ALPRGHLKTRKCGGATPADAFYETKK IGGGL
13060	26961	A	13200	177	1075	PTSSMAFFPKKKLQGLVAATTTPMTENG EINFSVIGQYVDVLVKEQGVNIFVNGT TGEGLSLSVSERRQVAEWVTKKDKLD QVIIHVGLSLKESQELAQHAAEIGADG IAVIAFFFLKPWTKDILINFLKEVAAAA PALPFYYIHIPALTGVKIRAEELDGLIL DKIPTFQGLKFSDDTLDFGQCVDQNRQ QQFAFLFGVDEQLLSALVMGATGAVGST YNYLGKKTNIQV\ EAFEQKDFSLALNVQ FCIQRFINFFVKLFGVGSQTKAMTLVS GDSNGPTPASTCRKPPGPEFT
13061	26962	A	13201	35	464	VQEFKTSLGNVAKPCLYKKKKKSLPGG GVPPPPKKTVGGT\ SPQKIRPAGPLIF PPPLPRGQGEPLSPIKGGGGGGSS\ Y PPPPCLTGRA/PPSPISAKSSPSPPP CQYVHPPLLELFFFFHLALRRATAPLFL FLVRA
13062	26963	A	13202	1153	259	AGSVLRGLGVVTSRHMSDSGNQGT\ CTL EFAVMTQCSCVDADRKSQCQVAGQDV EVHLEDQWLVHHT\ LPSQEQVALL\ EST GRQPV\ KGMG\ TQGFSESGQGV\ APGG GLGTVQGVVRFQLT\ PERCLIEGT\ PG LEPGLHGLHVHVGVDLTNNCNSCGNHFN PDGAS\ HGGPQDSDRH\ RGDLG\ NVGAN AAGGAFFRMEDEQLKVWDVIGRSL\ IID EG\ EDDPGAREGQSLYPKITRELPGSLR SCGI\ IAKSAGLFPEPQSKICSCDGLT\ IWEERGRPIAGKG\ RKESAQPPAHL
13063	26964	A	13203	281	420	VDGSKKYNEMPV\ PALWEAKAGGLL\ EP RKSRTAWATREDSVSTKN
13064	26965	A	13204	3	1125	SDSPQTPMRVMA\ PRTLILLLSGALALT ETWACSHSRIFY\ TAVSRPGRGEPRFIA VGYVDDTQFVRFDSDAASPRGEPRAP\ W VEQBGPYEDWRETQKYKRAQQTDRVSLR NLRGYYNQSEAGSHTLOWMYGCDLPGDG RLLRGYDQSAYDGKDYIALNEHLSCTA ADTAAQ\ TQRKWEAARAABEQRAYLEGT CVELRRLRYLNGKETLQRAEHPKTHVTH HPVSDHEATRLRCWALGFPAETLTWQR

SEQ ID No: of nucleotide sequence	SEQ ID No: of peptide sequence	Method	SEQ ID No: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond- ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond- ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						DSEQTDQDELVETRPAGDGTFOKMAAV VYPSGEQRYTCHVQHEGLPEPLTLRWE PSSQPTTPIVGIIVAGLAVLAVLAVLQAV MAVVMCRKRS SGGKGGSCSQAASSNSAQ GSDESLIACKA
13065	26956	A	13205	417	13	GHFRVMLQCHMGSSASLSIMTPFPIRSYQ PALTRSSATKPA/TSAPSITPMTFVTAN IS/VWMTANTTTTTKLGNPTSS/STLSTP IWHPSILPAPPSTPAPLTITVTNSATTST ICFHVOLFOAHHHCHCIAAALEYTS
13066	26957	A	13206	1139	559	GLSELSTHSPVARVOEGHGATFERSTIPW PGGKPRRGGRTGLRWEGGSGHRSLGQT KKKGAKAKRDHCAHGP IAAFGPPFRAT QLLSFCHGCSWKENQPP*GPPGHACTAW EKTVTGHSRCRPVTKPSDPGFGVQAPGT KGNPAPGMDGCAGFRISCHPVPITKPLS NTGICVLLCYEFGFLIAIVGCWGFK
13067	26958	A	13207	306	332	ENGEIRIYIYICLVLYKKHWEAGCGSV HL*SQHLKRLKWDYLRGPVDPQGHRR ETPSQKLNK*INDDF
13068	26969	A	13208	48	233	GKQNHKLKLCRLFLLSAVISRNYYTL T*LSLSLSQCVVCVVCVVCVVCVCAIL ENYPR
13069	26970	A	13209	250	2	YCEBGLGSSRPGVSKREFFSRPRDKRM PWPQAVIYAYNPSTLGGRDGWIA*A*EF ETSLGNIVKPHLYTHTHTHTHTHTH
13070	26971	A	13210	615	120	SVFWPLLGGSVWSGYYTEVRGPLEKAVCP LSELEYCAGRSAAALFAIRLFPKDALSLL KLCPQPPFLGALSP*EALVCVPLHV STCLS*WCTPCPBERSWCLFPMVPR VCPDGLLPPVPLRGPGVCVPLHVSACL LSLPSNLLRLRTCGVNFSPVPLVC
13071	26972	A	13211	239	429	PILLRNKLQGTAVACGNESTLSSQGGK IA*AQGFETS LDNWKPCFYLPQLKKKK KIKNLGV
13072	26973	A	13212	954	503	VQLLEPLCGRDLYLFAFNLPYRCWQHL SKPRAPILAGGSDRWCPCCPFWLP*WC HVSAAHAPQPPFCAKPEALPVGCPSP PSLEAALLILRAGLVVLRAPFCFSAHLL SCHSQCCQPCSEKRSCLGGRDRHAASN PLSAVWPGE
13073	26974	A	13213	1844	1147	LHSQIYSTAKKASLSMKGSRDKTRAASS RPVPSVLGVPWSTLLQHPQNMWGPAPQ QGGQPSGRQAWCTPGEAPGAEAPQ*QP HPEEDHSGGQASAAALAPPSPPSQORDV QGETMGOGRSAPRSASSACCACRSRL PCPQLLRHPGLRLVSPAHSRPPGPAPS SSSGSLVPGYLPQKGLAGLSAGAVLCP PGLLRVHAGAGYGPSAQLHARLSSSSL RGRKRLRF
13074	26975	A	13214	413	60	LCSSKCHGFSAMDCETLLTFPLFYPIIL HMPTVPQALFVHTPFL*KLPLLPGLPI SCHSPFLD*QGESPPGGLFGHPFGSG VLCIWFHSLKHPVLGSSSVTPGASAPS RSRL
13075	26976	A	13215	67	196	GLSLSSFKVTHNATLNGCIPQK*KAIFY HSMQKKIILLFNMA*P*YPLDFGQWNP LHGSHAYSTIL*LDLFCCKKEE*DEIYP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13076	26977	A	13216	161	2	V*CFMLLNKSTTM*KRIILLFNMA SVFFFLFDRLRLYLKSWAAYNSSLTGG RGRRIIT*AQEFKTLGKNKARPRVVO
13077	26978	A	13217	57	184	CLTVCKDKVSLCYPGWSFPV*SYLTAAS NSWSKAILPPPPPE
13078	26979	A	13218	292	400	LKVKQGRGHLDLNQGLDL*SNLPLSH TPSHRRTV
13079	26980	A	13219	186	394	YLVLSFLPYFLFIFLSRVSLPIFFILEI *LGIVAYTCNPSTLGSQGGRIA*AQEFD TSLGNIVRPPSLI
13080	26981	A	13220	315	448	RTKDLGVVDHVYNPSTFGG*GGRIT*GQ KFETSLDNRRARSLYK
13081	26982	A	13221	3	13	LRLPLRSFVSVERLWASCCGLSELVVDKTD KRKRRLSELSEHKQEIADAFELPDTDKD EVIDYHELKVMIALGSPDKADVLNLI KQYD*VTGKISFGHSIEVDFQI*R
13082	26983	A	13222	1	715	VDHHSKGSPELTHASTHAGKHAPWAS LRLVAPWNGRIRGTHRLGAAPADGNO KKKRTTLQFLTNYFYDVEALRDVLLQRE MYKVHEKNRSYTWLEKQHPYGGAGAFFI LKQGGAVKFRDKWIRPDKYGHFSQEFW NFCEVPVEAVDAGDCDINYEGLDNLRL KELQSLSLQRCCHVDDWCLSLRYPLADF VAGAFRWAGCPRIFRGAKHGFHHLQ*D LSSGWATCPGTSPT
13083	26984	A	13223	1019	1238	LTGAETKSDGLTESVTANLEPEAPKVF SRLDDEAPVTVLPARLFLPAP*HTARP PPQRRRSMQLAPARPF
13084	26985	A	13224	1534	1181	RWNSEPDYSAGGPRAGRGARLLPVKSP GGGGAVAPGPQTPLRAERTAVRLSISS* NSSTAPADPGAAPLHPQPAEAGTWVSA FLRVIFCFPSLGFQCEKKAIAFVPPFPPT DEKCL
13085	26986	A	13225	328	22	CLESFDRPRFQGPAPFKHPHPPPIAFLSQ PGKVQYFFESNCKSLSSQIKNSRSVPT SPAPSPPPPPFLYFSLTAEGGEV*KET LDSDRAPPSREAPICQV
13086	26987	A	13226	180	5	NSIDYKINVKNSNRPGAVAHTCNPSTLG SQGRRIIT*AKEFETSLGNIVLLITIIY YI
13087	26988	A	13227	237	528	VGLQDPLLTLTDSFCSVLGGSHLAF HKILYVHIDLWYFRRISFFFLTSAAI CLSLVLSHILSPFL*LFYCAITTLYL LITTLFFLIPKV
13088	26989	A	13228	140	366	NATCLWHPMSFYAPTY*C*LSGOLLRW LAITPILVLMILISSYMHVSISSGFTFRS NFFLDQIILTLFIYELHIV
13089	26990	A	13229	257	25	LPAHSLGRDLQAQYSPMRPGGELRAEG QSSLCSVARSSL*LVUCVVCVCVCART CVNVFACVLLSTKVCILHELPE
13090	26991	A	13230	561	52	WPSCSSSGSPMLPPVPPPSLG*SFSP LPAAAAAPAPCAAPRAPLPCGPAPT AAAPAPAPAAASLSAARAAGSPGPSR PSARGARRRPSGPCAPPEPLRGPRAPGS APRTRTPS*GRARSGGSGNAPARRTP QGPRAACSLARSWINPAGRGSCGRAL GA
13091	26992	A	13231	335	103	CQKYSTSYCNKWLATLVICSRKI*FDGL

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						KGQAWLVPVIMLWKAAEAVGLPEARSL SCPCNMRAPALPKFLIGGV
13092	26993	A	13232	452	712	VGLEGED*PFPSAQSGSLSCWPDCCSP PSWPPDQRPGRPPDPDPESHGAEEG LPERPSDA*ARPQFSLHPGVFPQNAS TQ
13093	26994	A	13233	480	2	SCFSEDWNLKFKLQLSTLSYRKSHTL HCAHHFRGQCHSD*AFLVFSLTCLQLQVG SLRFTAGDVSPSPYPEKRLVL*EGRVADP HVMARKGQQAALAILLQNAQTGYVWVLT PVI PALWKAKASGSGVKPSRLRQTWQNGE TRLLDREGESASQAGMTGM
13094	26995	A	13234	692	824	QINALFPFSPFPPLVLM*CKGGKIPFPF SKNPRTCVGNVTI IKA
13095	26996	A	13235	657	872	PRGPRLDVLYACEPOLITCLEGLTPLKV RFWLEVVVDHTYNPSTLDGQGGRTA*GQE FKTSVGNSKTLSLKKK
13096	26997	A	13236	168	365	QESLCITQCTCAHONLK*RFKGSKSLR AVAHACNPSTLGGQGGRII*GOEFETSM VNMVKPYLY
13097	26998	A	13237	31	338	WYIYIVYCVVCVCIYIYIYIYI*YI* YIYIKHTVQ*H*HLAFSTFTLLCNCHHC PSLELPHYPTLTLYHTH*ITPHCSSC*Y CPLFYFHLVFDYSRYLV
13098	26999	A	13238	714	1001	SSGVSCNLRAGWITGVNHHISLVLLKR EK*TONIITEVCLMFLLLPHLAIEATVT WPGMVAHACNPSTLGSQGGRRV*AREFE FSLDNIARPC
13099	27000	A	13239	250	406	NLA*HGGVHMWSSASQVAGITGRCHAQ LIFIFLVKMGFHHVGGDGLNLLTL
13100	27001	A	13240	256	193	WINFISLPSSLT*TLSLCVCACVYVCV CVCLEPQCVHIVGMLKRYIVFARSVTLG CKFTLLHSLIINNDT
13101	27002	A	13241	1	257	GMDLQWCKHLSLPLIFFFFFFSEKTRS NFVQAGQLRALRDPD*ASREAGITG LTHVHRPGQIPKKIGITLPTLLPLLR K
13102	27003	A	13242	319	406	KRGWT*WLMPIPTLNEAEAGGSPDVR S L
13103	27004	A	13243	228	56	KGAPPVLKPGYKPAKXNPTFPKPGSKV GENPPLP*NPCPGGNNPPTFPFPPFF F
13104	27005	A	13244	1687	612	ILGNQCCFKDAYNALANESWTMISIKLNE *VREREREKEKERVRERKEEREKKLL TSSKGTGSTATFHV
13105	27006	A	13245	220	1	TKDPSSTMPQPNPLSFKSQIFLIFL FIKKYVGWQNLPLVIPAL*BAEAGGSL QPRSSRFAWATWRNP
13106	27007	A	13246	204	375	ASWFPGLQYELRIKCLLHCWTRAMIF ERERERERERERERERE*VHLKRG A
13107	27008	A	13247	158	2	IWVFKETFFQNFPPFFFGKNNFNGFFF FFFFFFFFFF*DRVSLTLHPSLGVR
13108	27009	A	13248	221	3	NPSGGPFLKIFFFFFLRNSLSPRL* NSI*KN*KI*KISWAWNRTPVPVPGAWAE EPGESLEPGRQLQNE
13109	27010	A	13249	81	341	GELNDTHVKYLG*YIKVL*RNRTNRVC VCVCVCVCVCYACTQKDL*GTGSCNC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GALVRFKSAQASRLTKTQTVVIRSLKAVC
13110	27011	A	13250	299	1	ATARLRLFLHGAWWYASVVPPTQEAERAG FLDPRSSRME*AMILPRCTPASVTDKIP SLASQIHRPSRVACVILLSSSHAPTEAPS RWFPSPPLCPAGSRA
13111	27012	A	13251	106	146	LCVLKQVKQATWTKYSSSQIFAILDCMT TLSSHPALKYCNLYLISNGSPNHLRL*C SGMISAHCNCLCPG*SNSPASASRVAVC FKASQSYLD
13112	27013	A	13252	217	158	LEIEICLPFFFFFFFNFPPFETRSHSVSQA GVQWCKQGSLOP*IPINFFWKEGVIDK LILISYGNACQGPKVAVTPVCTTALQPGR QSETLSOKRN
13113	27014	A	13253	150	56	TILILLLLYETESQSVAQDGQWNCOLGS IQSPPRSSCHSPA*AGVNRRLQNGMGSF EAEIVLSPDRITLHPLGLQIETLSHII IILILSTISFHOLH
13114	27015	A	13254	174	145	PCLKNTTYDFKSALEIAFFCCTAILRLVK LLIKVTHFKWLRVAHDNCPNTLGGSGG RITWGHEFKTSLANMA*PTTRSYSQVRG IMGITIPDEWMSRTQPSHRSRGP SKVYP
13115	27016	A	13255	179	273	GQWLTFPVISAL*EVEVGGLETRSLKQAWAT
13116	27017	A	13256	264	382	GLKIGKGCSSWFTFVPIPTL*EVKARGLL EPRSLKSAWAK
13117	27018	A	13257	1199	1563	YLVVGFAPVPLDLEFGQACATCGFVSHY KIFAKLWAVGSILDMPGPE*GSFLSVF TSLCFIYGVTYPFHSQEPHPASPSASGL LLLKGRAANLVSTLCTGSPAPMLTGIFP HKVYNQLFI
13118	27019	A	13258	194	242	ILYVETGSHYVAQAGLELLGSGNFPAST SEIAGIEA*ADEFIYGVWSODECKISM KQVAHASIPAISEVEAGGLPEPRSSRA
13119	27020	A	13259	322	120	GTPVLDLAFQKLCLSPTSGQQADGITPA FPIRKQGGTQMPKPVIPITLWEAKAGREL *PRSRPANAT
13120	27021	A	13260	237	1	TSKKISLGHWKGKGIPTGWEG*AKRPF PGKPRVOWTQVPLDPSLQKARLCLKK KKKKQKQKTLKLTCHSRITYSRA
13121	27022	A	13261	52	318	SAVGIRHRCDDGSH*P*PTEHKQLSPFLSL PSSNDYRGITRELFORFPWIFLQLITAV ISSESTVLNLELAARVGRSHVRVIMMAV PINPF
13122	27023	A	13262	274	1	KKKKNSPWWNTFVPIPGSP*AGELLEP WROKVOLAQVVPKLVVPTKVVQGCPL ALQPGEBHQIFVSQKKKNPKTKRYWAL FCSLFSC
13123	27024	A	13263	717	877	NSTKEMARHWPGVVAHTCNFPTGG*GGW IT*AHEFETSLPMVKPHLYKKYK
13124	27025	A	13264	288	131	SLYIWSKRLITITNNKISGVWCLPVV SSTWEVEAGGSLEPRR*RAPANATK
13125	27026	A	13265	80	287	FMNGEAS*KTSILSQAWNCAPVTPAQ* NEAGELLEPRSEWLWATRALRISGRGL RFRRLRRFTSTR
13126	27027	A	13266	3	241	VGLPLFFPFETESCVTQAGVQWCGLS*L *PPPPGIRDSPASASQVAGTGTTHHTW LIFLYE*SSGFHYVGLGRSSNS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, = possible nucleotide insertion)
13127	27028	A	13267	103	359	ICVYVVVCIYVYEMKATSKDPLNQWFS FLRTVAVLFEEXLIVL*MWLSFHHIYI HITHIIFIYVYTHVLIVYIHTYSYMC IHIYI
13128	27029	A	13268	172	12	SARSSQATIQKQSVTSQGVKPN*QS*P TPFLPTLLAL*TL*LLPISPFILIL
13129	27030	A	13269	2	203	RTEIRISYKNLAALFMTAKRMGTQMPH NFEWINXMYIHTLEH*SKDKKKKKV RAEIPKLIQK
13130	27031	A	13270	236	365	KIYEQGAVARTCNPTLGGQDGMIT*GQ KFETRANMVKPHLY
13131	27032	A	13271	371	15	QNGINFALILILINTLALLLIITF*LP QLNGYIEKSTPYECGFDPISPARVPSI KFFLVAITFLFLDLEIALLLPL*ALQT TNLPLIVMSSLLIIILALSAYE*LQK GLD*AE
13132	27033	A	13272	2	16	PRVTSRSSRAALELIFFFFLGPNPLFV YNGPLGRTKPFGTGLDITGGSPILCVGQ RHPYKGGAKPLAPFGKGGGP*GTRPLA GPVPPKAGLQSEMPGMAPFCGSFG*PT RPD
13133	27034	A	13273	329	290	SSALVPRLECKGIFSAHNCNLCMGSSNS PTSASRVAGITGVAGQATDKTPQTL*RS SQPSHMDPVRVSP
13134	27035	A	13274	175	13	APCDHRPCPPENNPL*L*FSITFNPPIK RPHLYPL*LL*FSDSAHLHPGEIEQR
13135	27036	A	13275	355	861	PLTTTPAAPRAFCPPSRKLSGGQPLTGPT GSRSLSPNISRQGEPLALTVOHPLST QGPVPSLELPICQPG*GQCTPSPQS A*GGVLSCTPESHTEFKPPPTGSGRWA RLGLNGAT*GREEPLOTRLPAPYPOGP IDPLQPPFISTASHATAFSDPLLGRDP A
13136	27037	A	13276	865	667	KFLCILLDFLFFIF*EMRSQHRLESCA IYAHCSKLKLASTDPPTSAS* IAGTGM CHCAQLFLTF
13137	27038	A	13277	103	375	WSRRLPWRRLGYIELFQGLIRHHLFL GPHYLRRTCQGPVPSLELDGQWDYMS PGV*DQPGQHDETPSLQKI*KTSSAWH APVVEAT
13138	27039	A	13278	177	3	QQTGSRASHNSHRRPGAVHASNPNPL GGRGG*NI*SQFKFTSLVMVVKPLYGR V
13139	27040	A	13279	379	372	SR*WVCNVAHACDPSILGGQGGRT*AQ EFETSLRNMVRPCLCLGNINIIYIHTH TYIFIGN
13140	27041	A	13280	83	1184	PPAHAAARASPPSYTLWCYEVKIKRGRSN LLWDTGVFRGPVLPKRQSNHRQEVSSWE CRKHLISKMSGGGLSTVYFFHRRFQITWF VSNVNPCLPCVVKVTKFLAHPNVLTITIS AARLYYYRDRDWRVLLRLHKAGARV MDYEGERCRCGQSMGTGRNSLRDGIW CNAIYASLHRTLEKILR*GSPSGLIVLLS PFAHPEDSPGNEEWLCPTMEVTKHHA VFRKGVFRWQVAFVYLPK*ELSSSR RKIKNT*HTNVEVNTWTSWSPCEGAGE VAEFLAHSNVNLTITPRLCYFWDTDY QEGLCSLSQEGASVKIMGYKDFVSCWKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FVYSDDSPFKPWKGLQTNFRLKKRRLRE ILQ
13141	27042	A	13282	1558	1824	SFPYLASFPPCLGLPLETLFHLPLGL*RD *SDTHTHTHTHTHTHSHTHAHFSPFPDP LPQSSPFFSSGFI DEYKYPHLNPVMSVTC CRFCV
13142	27043	A	13283	1	519	PHFFLPQGFWGFSPFPPL*KSSSPLKAL IFLGGSPFFPPPKRFFSKIPRGVFFP PPKGGKFFPPPPG*IWPPQGFLLKGPFS SSSSSSSSSSSSSSSSSSSSSS
13143	27044	A	13284	349	159	CPLEPKKNYFFCF*ETGSCYVA*AGL VLVASSNPASASQIAGIQGTSRHAQPC RIFLSKT
13144	27045	A	13285	748	869	WGVVVAHACNPSSLGGRGGQIV*POEPE TSRGNMARPQSL
13145	27046	A	13286	315	410	VQWFTPVNSALWESEAGGLLEIRS*RTT WNT
13146	27047	A	13287	355	499	ARCGGMHLYSQFGRLRWEHCLR*KVLS QVMWHAPVFADIWEVEVGALLERSRL *CAMLMLPVNSHGPPTWAMQ
13147	27048	A	13288	880	701	KSYFSSHLHFEGKKCVSYLL*SLVLML CSWLMNYTHHTYIYIYTRTHICVHVYV HNF
13148	27049	A	13289	379	434	KRGPPPKKRGCFSEKFF*GPKPTFF FFFPKPKKKKKKKKKKKKKKKKKKK RLADAWADAW
13149	27050	A	13290	253	344	GLFYNLQKIKIFPVVKNLFFFSNSITEA GVQWPNLGLQPPPSGNSDPASE*RIV V
13150	27051	A	13291	561	745	AWEPSLVGETNVNSFNQKYINWPGVAH TYNAGTLGGQGGWIT*GQFETTLANMV KPSFY
13151	27052	A	13292	289	2	TLPGGEDFNKVFVGSIKRQLQINL*NTD FIGNVFQSWAQOYT*PVVPPSWVAEVEGS LAARSSRPLCTIITPLNHCSLAWATQQ DPAGRVGRPRV
13152	27053	A	13293	281	229	LKNRNVNKEKLRQGVVAHACNPSSILGGR GGWIT*GEM
13153	27054	A	13294	276	441	GLFPFKLIQKINQNPDAVVHAYNPSTL GVQGRWIT*GQ*FKTSLANRGRKSENK
13154	27055	A	13295	258	389	NMVEKRLGQAHAYNLSTLRGGERIT*A WETFSLGNVVRPCI
13155	27056	A	13296	358	353	SFLAPFNGAFPLRGRFFWKITFFPGGVCM RNPFL*KKKKKKKKKKKKKKKKKKKK MKRNIGGEERGGG
13156	27057	A	13297	196	1	LMGKAFLLGGFTPPAFFFFFLKKKKGGPG AVATCNLSLTLGGRGWIT*GQFETSL ANIAPCSC
13157	27058	A	13298	182	436	GVITLNVRRHRKVTLYRLDKKVRKCP KLHGNLRKVFQAGIASSKTLGHVWML MPVIPAL*EAKMEGLLEARSLSAWATQ
13158	27059	A	13299	334	440	RHYWLN*AFYHSSLADAPGGGGHWP GITPLNSLHVPLNLNTSA*LASGV*LT*A HHRLVFNLRALIQALRITRILGLYSTL LPA*KNFEAPFTISDGVVGSFAFF*ATGC HGLNVIIGSTFLTICFIRQLIFHCTSQR *LWLEPPAWDW
13159	27060	A	13300	359	372	KKKICGGKNPNPNKKVKRGEKTPLK

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						GV*PFFCLGCFSPHKEFFFPFSPNYC SPKKSFFLKFPFPALFFFNLPFLKNIPSP PFLKKASP*EIFFCGPPFFFPFNTLIF FFPFPFFFPFFFPFFFPFLDKFAVY
13160	27061	A	13301	233	406	VTVEGMEEVLGSGSEGMSGRPTS*V*FL KYLGLAVAHAKPSTLGGRGGRIT*AQE LKTSLCNKVRPLRYKINK
13161	27062	A	13302	92	429	GSHFNSELIMKFIYIIRNPIILNCFY LIIKHQHFHYTKFLVSVINKF*LATVAH AYNLNTLGGQGGSA*THEFKTSLGNTV RSLCYKNLKMWSVWVWCTAIWEAEVRGLP
13162	27063	A	13303	302	140	GGAVNSVQSQAWNHMPVVPWPAEATGL LKPRSLSL*CPMIYHVNSHCTPAWAT
13163	27064	A	13304	115	312	LRSFSFVLSRLKCGGTIMVHCSFDLLG *RNPPALPSKVVTETIGLHALLRLILF FF*KWVULFP
13164	27065	A	13305	90	246	PGVVAHACNPFSTLGGRGGRIT*GQEFKS SLCKIAPPPEKGRKEGKKKRG
13165	27066	A	13306	19	310	DSSFSPTMCPGMSVUNKTGLWLGGKKKKK KKKKGPP*KKPLGGPNLPGGKKKFPF *RGAKKNPPGDFWKKTLFLGGKLGPP PQK*NPPFGGKIGPTPPPKIKPFGKKK KF
13166	27067	A	13307	179	56	WVLVYKQKSLG*AQWVMSVISALWEAE AGGSLVSTSLRIA
13167	27068	A	13308	425	290	KKNYLLAPPGYFWPPQRFLLSPFPFPNV VIFPFFLFFPFFLFFPFFFLIQAEGIG VMRGCEKMGK*W*KFFGRVNLNIRSI LLANFKHVPVY
13168	27069	A	13309	214	371	IVF*RNISQAWMLMPVIPKLWEAEAGG *LEPMSLPQNYETSL
13169	27070	A	13310	975	572	ANGMVGVGKHSVLSLCTEECASTALS LDKSGWNEAAREEDVLCDERCLLCHV PAGVSGSLKPELGSRRKGNQOQSGSKPS VPSLGPQPGPCPNALSKGTRPN*AICF LCOTPADHSAKKOAPHILPIR
13170	27071	A	13311	270	10	TPNKS*LI*RLQFSNIGLANLGLGTMAHS CNLNTLGGQGARITSGEEFKTGLGNIDP IPIESKVIKTLAGMVSPDPAWDAIKRTG TSG
13171	27072	A	13312	103	290	LTEVVSQVIL*NCIYLLPOYTSVRUHV IHTYIHTHTSTGLSSTSVGSTHNSKI FGGKK
13172	27073	A	13313	136	1	SNTSSSLVTOAGGQWCELGSL*PLPPKF KRFSCLSLPSSWDYRL
13173	27074	A	13314	88	183	RVSTLLKSCFFPFFPFFPFFPFFPFFP PFFPSSQKKQNLKNKRE*KKSCFFPFF PFFPFFPFFPFFPFFPFFP
13174	27075	A	13315	481	517	LLSP*RPQKPKGKKRKNLKEKKIGE RGKERQKTPORTGQKKRRKYRIRGR RNYR
13175	27076	A	13316	307	196	GMHLYLPRTW*WVRVLPGRREIEVHAPL EPGQRLVLAEMTPMHSSLDNMNKSPPF QPPKTEKQTKNPPKPHIA
13176	27077	A	13317	2	209	PARALDLKSGPYMESCSDAQGVQDSIY GDHL*LRAPAV**GQTVFVSPSKVGGI TGASHHPLGFLF
13177	27078	A	13318	3	178	SFCFSLREIYGQSLIMKTLTP*ITHTHT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13194	27095	A	13336	298	349	KTPFPYGLRSGKIGTL*CSGVITAH*SL KLIGSSDPLSLVAQAARTTGACHHDQLT NAFFFFFLERVPTPLKKNFFLWKGKVN WDL
13195	27096	A	13337	865	518	KSATRMVVEDTHKMPAMGGYSGSLQGER GELGSLPCP*PESPPPLIFLKLPSNPL DCSPLPCTQGPGQAPFVSIHTSLKFPN AKLSVCLSRATIEFS
13196	27097	A	13338	154	354	FNLVQKPDGVYFVLFTCHILEPDSKSGKA PGAPCHSRNFHRIKTLGQWQWLTLPVILA LWET*FSHQENGLGVAHTCNPSTILGN QGGWIA
13197	27098	A	13339	262	11	OHFFSRKLT*KM*LSAHSNSTHEAIVA FPKAHKPGLNSKTAF*LGTEAHACNPN LGGQGGQITRGAQFKTSLANMAKPRLY
13198	27099	A	13340	358	164	TKKGKPRFFLKNKSKIRGWWAPVISGP WEGEGGAFV*TCRPFKWLTEVGLPFLNL GKKKENPF
13199	27100	A	13341	147	2	FRPQKVSVRVGLAHACNPITLGAQGGH II*GQEF*ASMANMVKPSSC
13200	27101	A	13342	367	17	TSRSWNLFHVLVRFFPTADKIDIRETGSFT KKRSLIDLITPYANASFTLMMEGKKEQV TSSINGSRQKVRSGSGLLSLTPSDFSW AHWLMVPFPAW*SETGSLFEVRPSRPA WPTW
13201	27102	A	13343	166	492	EGTQETLCGCIICLVRGDALNLPHLKCS WVGWGAICMELRETAQKLSVWKLPL FEIVFSFSNNPRPGAVAHICNPNTLGG *GGRIARAQEFETNLCLNIVRPHLFR
13202	27103	A	13344	804	1124	TFFFCFFL*DRVMDVAPGWESSDMIMG LQALTSWGSTDPPTLGLQSLGLDQDQW PYPYTSFYFFFLQSRGLTMLRLVLNSC TGAILPQPGQRSTPISLNT
13203	27104	A	13345	280	448	GCGGKKKKTKPPLEKXNFSDFP*FFPP KKQIKIPPPP*GCGGKKKKTKPPPLEKN NFSPPPPKPKKQIFFLPPPLSWKKKGD PPGGTRPLAPL
13204	27105	A	13346	232	400	AELLRYCSGCHF*SMARYTKKPGVRWL TPVIPVFWAEAR*IMEPRSSRPASATQ
13205	27106	A	13347	138	332	RAVVKFSPEIFYFF*RAHT*SCVCL CVCVCVCVCV*THHTHTHTHKTHDY
13206	27107	A	13348	314	395	WLGIVAHAYNSTLGT*GGMIT*GPEV
13207	27108	A	13349	388	371	IMNGWQDKELSVRIQTGIKK*KPNNRP EFRAPP*WHERNGKERERMEBGRKER XKGKGERKKKACAIYKVKIETSNLA NLIINVER*DRRRPDILSWLSLRVSS VFIALVTCLTSPQFFLSHLNLFLPLG KNL
13208	27109	A	13350	412	40	LVFRFWMCLFSRELFGCFSHLLTKMSQ M*VVAFGDIMYTFDLFLKKTNNCKLW QGCKREGSLHCWRECKLVQPL*RP1*R SLKQLQMLPYDPAISLLETYPKERKSV Y*RNICTSGRVG
13209	27110	A	13351	372	148	FFFFFFFFFFFFFFFFFATGSCRVA*P GVKWLISGTVPLLISTGVLTCSISDLGQ PVHTSLGNLVFYSQELPY
13210	27111	A	13352	209	206	KKKKKNFFSPHGKNPGNGGPFPGPPPPP F*TFKKGGGLPKGPPPKGFNNPQNG

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						GGGP*PGGEKKT*PKPSLGVL*FFFFFFKFF KKRPTAFFLLKKKIFF
13211	27112	A	13353	43	334	KKKKKKKKKKKKKKKKRGGGPFIKIS GAQFFRGEKKFFFFFLGGGKKT*PROFPE KKPPFWGONFWPPPQKNPPFGEKKKFL GGGGGKNRVFFWGEKIFSLGFFLK* KKPEGKNFFPPKKNPVFSPPPP*KKFFF PKGBI*FLGGGPKIPPPKKRFFPKKPPG GFFSPP*KKKKKFLPPEKLGPPRNFYK RPDP*FFFFFFF*FFFFFFF
13212	27113	A	13354	264	496	KPTILRVTHFLGCEKYEFL*LVAFSNF SEPLKRYYYWLGABAHVCNPSTLEGRGG QIT*GQEFSETSLVMVKTICLY
13213	27114	A	13355	183	9	IRSPKIF*EIRVFFFSRWSYALVAQVGQ WGNLS*MHPPRARFQPLSSLSVPST*KY R
13214	27115	A	13356	208	378	EICLEPKIIDEMDKCGKWLGTGAIT* NPTITGGGGQTT*GRAFETSLDIMEKRY L
13215	27116	A	13357	256	341	KGCTQWLTPVPI*TLWKA*AGGLESRSS TVGLFSESSKGGQHVVSQWYLRLLTYR FLFPLFSCLCCK*FFFFFSPT*ECFVPO AGVQ*HNLG*LKPPPPQLKQPSCLT*PS SWNYR
13216	27117	A	13358	78	344	AO*LMFVVVDALYEAEGSSLEPSLLS VWAT
13217	27118	A	13359	259	291	RLFDLGNKKTSS*PVONSNAKYEDSLOF YCRIVYIVYIVYVICIHCYVM*TYMCM YICIMYTYTHVYTHVMCIHTYMCIA* YICVYIYIF*KACLP*LAISTLSSGH
13219	27120	A	13361	125	262	FSFOASVEFTSKTVWSVOWLT*FIIST *EAQAGGSLEARNRPD
13220	27121	A	13362	362	46	ARAKGPKKIGFSGKGGPP*GAPFFPMGK KI*ITPPKFLFFFLGKTKIKNPPWGEW PFGFPKKRGGGAR*KTSPFREKPP QKLKRP*TPFFFLFFPMNRP
13221	27122	A	13363	378	48	FKAAREKVS*TRKRGFVCLFDFWFRQ SHSVTQAGVQ*CDLNLHPGSSDSPA SQVAWTTGTHHTQLIFIFPCRNKISP SLKKKYKNLPGVAVAGACNP*SHLG
13222	27123	A	13364	174	396	SLIFILEKRECY*PSRLFTVANFT*AKR *QTLNCPSTDKWINKMCHITVEYYS DIKRNEIPMRATCROT*LA
13223	27124	A	13365	76	280	PLLPFAQWQVGGCHYV*KL*INCYFR ALLAFSEYMYIYIRTHHT*YIYIYI YIKLTYSHLKVG
13224	27125	A	13366	133	324	YLL*ILVYCSHL*FLPSLLCE*LLWVFI IATLITNTHSLIN*VPIALDLAAGQ AAVGLALLVSKKKKPP*PLKPPGAGQ IPANORKFP*PKRKP*IKIRRGTF
13225	27126	A	13367	488	190	FSYAA*FLPQCVFVCT*FYILHAG*WLL IIFPNSVFLCHSCMW*VCFLLQ*FLM NL*FSL*FLMLMHPVS*MECSIY*FSSLI IFH*SLMLL*FPCFMI
13226	27127	A	13368	229	372	YVATKDFSR*PRAVAHTCN*FSTLGGGRQ IT*GRQFETSLANV*PKPOLY
13227	27128	A	13369	122	2	KREC*VSGT*WVNPV*IPAL*EAEGRSL EPRSLRPAWTEK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13247	27148	A	13389	454	367	NKKKPPPPPP*PPPPPLGKTFFKKKNP NFFRGGGNSPGSPSGGGKGKDPPPGGF PPPPYPFRGEGGNPFKKKKKKRASLD P*WSSQPCPAYEKELNFPAPVLATVTLPP GHSS
13248	27149	A	13390	34	354	HTLLALLLIITTF*LPQLNGYIEKSTFY ECGFDPISPARVPSIKFFLVAITFLFF ELEIALLLFP*ALQTNLPLIVMSSLL LIITLALSLEY*LOKGL*TEY
13249	27150	A	13391	1089	792	THGFGFVGSGFLDLKQPKANFRGSPSLG NPPPGCCQSHGAGGE*VPPGPRQPVMA SRNLCLPLALPRTHPSPGQTRDKPRTQ DRSCWRDPRNGPGV
13250	27151	A	13392	299	428	WIRCRGRGRSCLFVPPHSAFALLSPVLVD GTRRREAGGTCQGGSGCMGAHNLGGG EGSGCRSQUALPREAAAREFPKHGGIPR H*LTESLVSUVEFRHA
13251	27152	A	13393	382	413	HGKTHLYKKFKNKKFKATMPA*WLPVPI PTLQEAEEASLKFKNSSRPAPWVTWQDPS LQKI
13252	27153	A	13394	64	401	GGIPKEDSQAGAF*TGIGERQOGLVPIPL KNGQLSTDACVPPWGRVGERAGPPNQF AGEGGGQGECSLGLPEANRCHPCNPS TLGGRSGQIA*GQFEISLGNTRSCPY
13253	27154	A	13395	146	18	FSPGVVAHACNPS*TLGGGGQGIT*GQAF KTSANTVVKRRPQ
13254	27155	A	13396	1056	679	DIQVPERPL*NVPEPEARGEPPDRAVGE HIDRDCRSDPAQKKRI*FTNKCEARAGR QREMKLTCERCSRNFCIKHRHPLDHC SGEGHPTSRAGLAAISRAQAVASTSTVP SPSQTMPSCTSPSR
13255	27156	A	13397	440	423	IHSPTQRRV*QREERERERERERERH ALAEARNRTREGISGTTGERGNMLVGH LPGPLSRRLGFCPDGFGGQCLAQGDQ VRL
13256	27157	A	13398	2	256	ITELGSAVEFIPYENTYGTLYLKKNRNS HMQQPNRKHILKLYTAANA*WLPVVI PALMAEAGRSLESSRNPNVSTYKKIKQK
13257	27158	A	13399	102	922	LSFFLFSFETGSCSVAQPEVQWCHSSLQ P*TPGGFSMQQLPQEQQRTAVNHGGR A
13258	27159	A	13400	198	55	KDYSAVVHTCNPS*TLGGGGGWIT*GQEL KTSQANMVKPHLYKNPKIEF
13259	27160	A	13401	19	447	ESALNLSFAGITGVSHRTOP*IFCLNAL ALGVILERSPLQSPQVPPSHSHTKPGS LPSVTPGRGGRPRAAEPTAQGRYNSN PVILSPGSVHPASFALPAEPF*TGAPST PRPCVLRPLLLGNAMDLLCTKLSRSLFP YRT
13260	27161	A	13402	93	410	DSNLNYSLFFHGEADLGTNQVLTHPSTT AMYFEHYQPP*IVHGTINT*PPVVHKN PIHITPSPCLRASTAINLLSHINCYS *ATHPLGYQQTLYPLTVHST
13261	27162	A	13403	55	387	SNSTYSLLKKSAGITKFNQNHIVNCICI CQVVVPLEMNVNRTVILCOYVVKPRILY QHHTAILVTILTFTLRPGVVSHACNPST LGGGGGRII*AOEFKISLGNIVRCPCLY
13262	27163	A	13404	39	365	SGDRVRILLKIITF*LSQNGYIEKST

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, _ =possible nucleotide insertion)
						RYECGFDFISPARVPFSIKFFLAAITFL LPDLIALLLPLP*ALQTTNPLIGMSS LLLIITLALSAYE*LOGLD*AE
13263	27164	A	13405	32	350	HEFATSTSEMTKGT*IVKRRITHT*LC RRCGSKAYHLQKSTCGKCGYPAKRKRY NWSATAKRRNTTGTGRMHLKIVYRRFR HGFREGTTPKPKRAVAASSSS
13264	27165	A	13406	326	668	LQFKIFCMPIFTTSEVSSMSN*RTAYG SQS FKHIVLI*LATFGGALSC*IL*IHL CYLKNKTKHRAVAHACNPNTLGS PRGR IA*GQFETSLSGSIVRLLSTKNLKKKK NM
13265	27166	A	13407	170	472	KLISVNSEESSYCVHEGEPVVPQKEYS WLEIGKAEMERSTLESILGATLEALSSN PTRKMQLKLLQKASAFKEPWLGVVA HACNPSTLGG*GGRIA
13266	27167	A	13408	178	422	FYNRYF*YTKYTQENIYCKIMSFRLLV *KI*SLPGAMAHACNPSTLGGRGRII* GREFETRNS
13267	27168	A	13409	274	444	LFSQYIVFHYSSFVLLFV*LFQYI VFVHYSSFVLLFVILHNYTYIYHTHT HTYTLIFLLIFSQISLGMKILIL
13268	27169	A	13410	205	23	KEFLKPHRKCICQOVVKIWPRAVAHACN PSTLGGGQKRIT*GQELETSLANVEKPH FSNS
13269	27170	A	13411	25	426	SVWNNSLETRSSRLRLKKI*NLQNKRR KEFHRHAQRKYDLETQBDAILYKLRRR RKBBE*EKEKKRRARKEKKKKKPTL LCLKKQRNQHLDLRLPASTYVKLISVV *ATHSVVPCYGSPEKLLIQSIH
13270	27171	A	13412	227	52	EIGSHSCHPGMSTVAQS*TLTSSNS*TO LILPPQPPRELHYNCVPCPAFCRQALA MF
13271	27172	A	13413	345	67	SKCCYWAHDCILDLCLYFLDLVGCV DCFPSSSLGHY*PLFV*IFFLSPSLFVY SHYEHCVPFHSKAPFIFLHFFSPSEFP FLCIEMVYV
13272	27173	A	13414	345	33	KVFFFLIICKMRMONKQKNHGKICLLNS AMNTCISFPLRQOIMTTWLEVTQIWG LFYLFHFPIEMGSCPGWSAVA*SQPSATP VSWSQVILLPQPPEDLGNS
13273	27174	A	13415	187	415	FNQGWAFLEFPFCVIFSYPWKDRNRTIFS IKITSFQSSVLKLCFIFEVS*ILKIGLG QVRMLTPVIPALRRPQADH
13274	27175	A	13416	143	50	CMKLQSSIVMLGVVAHACNPSTLGGGG WIT*GQGGWIT
13275	27176	A	13417	170	17	KQMRKEGNGLLTISRVMQKPSQS* *IKKM*YICTMECYSALRPEPPE
13276	27177	A	13418	7	163	IK*IWYI*TMEEYSAMKRRKIMSSAAIL MKLEAILLGEVMQEWKTNLMFSFISGS
13277	27178	A	13419	901	709	SGRRTSLGNLARSCLYTRSFKIHCLPVV PATQAEAGGSLKPSRLRQ*ARSHCS PVWVTRTP
13278	27179	A	13420	236	4	VIRAKTGSNLSLFPPTTFFFGKNLCFF QKKKKKIYIQSKPGAMAHACNPSTLGG QT*DGQFETSLATWKNLY
13279	27180	A	13421	46	141	NSVISACHNCLLPGSSSDSPSSASRVAGI T*HCNCLLPGSSSDSPSSASRVAGIT

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13280	27181	A	13422	604	1121	GWC LGSGDLP*EINPLSSCSLLREKDPPTTS GPQTDQPKKHLTNFKSAPYKTTIDAELE VLTIVAEHLHPGEINSHVAHTKPVWWSL HTDAHEIWCSDSLKLVPTLPIPLEAA LRNITHSLSI PFPKNFRPNTSTLFCVI FLINIRRRQEYQASEPKPSHRIPCDLHVY AQMA
13281	27182	A	13423	214	22	IRESSSTPSSPTLPESCNSIPFPF*KFT WSGVVAHAYNLNLGG*GRKIARAQEF NSTRAGLN
13282	27183	A	13424	397	330	SEYNSECS*VQWHTLVUVAQTQAEAEBS LEARSSRLICALIIPVNCCTPAWAFPM
13283	27184	A	13425	729	885	AKCYPVRNLSLWFGVAHACNPFSTLGGQ GGRT*GOEFRTSLANMKPHLY
13284	27185	A	13426	231	2	ASVFFKATLVDLW*YIYTYIYTYIYI YTHYTHYIYIYIYIYIYIYIYIYIYIYIYI HINANQQQYIYTGRTPICF
13285	27186	A	13427	184	171	LS*YIYIYIYIYIYIYIYIYIYIYIYIYIYI QPSSQSS
13286	27187	A	13428	372	166	CKFRPRKINTTFSHICGS*KVDITEAA* HWLGTVAHACNPFSTLGGGGRWTI*VWEF KASLANLLTPLQ
13287	27188	A	13429	391	437	MYSLGVGFPHSTI*LLKDIFWGVVAHT CNPSTL*GQDGRIT*GRLETRPGNRAK LYLYKNSN
13288	27189	A	13430	39	254	EFIPRAODLETSGQNRVPRPRLYKFKNN *VWVCASVVPAMWEAAGGLSEFGRRL HSNMDNGERSCLKK
13289	27190	A	13431	336	488	DIWPGMVAHACNPFSTLGGGGRIA*AE FETSLSNMARFWLKKKLARHSGA
13290	27191	A	13432	154	481	FFFFFFFOROKNGFF*KGIFFFFKLEGR GAIFV*PNLTLP*GKSPASPL*KGKK GGAPP*LIFFFLKKKPLLLGGGGLK RALGKPPFPFSGGGGNGVKTFFGL
13291	27192	A	13433	388	280	KSKLNGCCVALCLLGLI*SVLLA*FKT *LFCVSLDWYIDTCCLSIYLSIYLS IYLSIYLSIV*SVS
13292	27193	A	13434	187	48	SISSTKFGVAHAYNPNTWGGGGGRIT *QGFETSLANMKPNS
13293	27194	A	13435	71	309	DSVSEEEEEVEELAHPLAAERYHCERA ET*VKALLWLELDERVSSRSHTEEDCT EELDFLHARDHCVDHKLPLNLK
13294	27195	A	13436	18	375	RPAVFGRPTRPINTLLGLLLITIT*LP QLSGYIEKSTPVRCGFPDIPSPRVFIS KFCLLAMTFLLFDLEIALLPLP*ALQT TNLPLIWMASLLIILALSLAYE*LOK GLD*AE
13295	27196	A	13437	373	27	THPYSHOEYQSP*PLTGALSALLMTSG LAM*FHFHSITLLIGLLINTLTIIYQ*W RDVTRSTYQGHHTPPVQKGLRYGILF ITSEVFFAGFF*AFDHSLAPTQLGG HWPPTGITPLNPLEVPLNTSVLASGV SIT*AHDP
13296	27197	A	13438	575	699	LGTVAHTCNSSSLGGRGWIT*GOEFET SLANMKTCPOKK
13297	27198	A	13439	247	168	LENLIYTRVLERHREAKVHPPFSNISYS DKRTDYFLTKTH*HTHTHTHTHTHT

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						HTRGSHFFFY*HTHTHTHTHTHTHTTRGSHFFY
13298	27199	A	13440	391	168	TKKKKHPSPRGAREVFF*QPFPFFFCVL*FFIVFPLSQGGGGGEPFPFFFPPTSPSPSPPRGVWKKTPPFS
13299	27200	A	13441	403	246	LFPTAITGGPGPGFPFPF*NPAPFPFFWGPKKKKKLSPPPA\KMVFKGPPP
13300	27201	A	13442	305	414	KNNFHSILGG*GWGIT*GQALETSLGNMVKPHIY
13301	27202	A	13443	269	409	PQTVAHYNLSLTLEG*GIMITQGQEP*ISLVNTVIPHLYQKKKKKG
13302	27203	A	13444	295	37	DPSLVANHWTFHQVSTQHTLPRPRPCLPEMNFVLSLKIWQCWPGTVAHACNPSTLRGRGGWIT*GQEFETSLANMTKTRTRGSAR
13303	27204	A	13445	256	388	FCGFWPQAEAHACCPCTLGGRRGNIT*GQEFETSLANHWKPRVC
13304	27205	A	13446	277	374	SLRTATSSRGGWIT*GQEFVTTLANMVKPLLA
13305	27206	A	13447	14	387	PQVTHSPWPKVLGLQA*TSQANWLTPVIPALWEAKANSLEVRSS
13306	27207	A	13448	185	379	HGFRNRPADHLRFGATNHPGQGETPSLL*NTKKKKRGRRPKKKKLQSLVWQNKIRFLAELKLLW
13307	27208	A	13449	168	346	ISILRTNMISIKINLRLEFIDELKKRDFIFPYPIFFFFFFFPGGNHSL*SLIVIFLIC
13308	27209	A	13450	57	176	VAESRPGPGGTATELVPPSTRLLTRAPRLDLTGKKRPPLGMRGRARVQWNHNP*TESCSVAQARVQQRNLGSL*TLPPKTKQFSCLSLLSSWEDCLSQVRDCEK
13309	27210	A	13451	411	241	PPLFFFFFFFKQKFFSVF*GGGGGWDFGSLQPPPPPRVKQIFCPKIPWPWPKKGGVPG
13310	27211	A	13452	307	298	PTHSVNNKSL*IN*TSMSCSGLKVMR R*SQKQEDP*SGVVAHACNLSLGGRRGWIT*GQEFSTFLCPSA
13311	27212	A	13454	191	108	GWSTPGLGRSSLLSLPOWMDYRMQCRGVILAPHGCLDLGSGDPPASASQVAGTAPENCATSFWLP*FLNTQCFKIYKYN
13312	27213	A	13455	242	400	ITALLDYLOTPNTGFGAAHACNPSTLGGGRWII*GQSFENS\ANTVKSC
13313	27214	A	13456	1	346	YVITARCSCWAGTSHMGAKDFYRQEKHPHADSGSIGWA*DLRLQRQYRFGRRM*FHWARGAGECHSLA*AGLWMPVVTT*FEWKEGRSLEPSRLRPANATWRNVSTKIKKKKKG
13314	27215	A	13457	166	289	VRSSKLTWVRNLVPIILTLWEA*AGGFLEPRLSLVWATO
13315	27216	A	13458	220	76	TASLKLKSLKSLDWUVAHACNPSTLGGPGRWIT*GQEKITS\ANMVKWSP
13316	27217	A	13459	219	46	SPPLKKNNFFPGVGVGAPRFFFLKGPPQNFFFFFFFPPPPPPFLKQ*EQTFLLIY
13317	27218	A	13460	126	1	VVSLGAVARSCSPSTLGGQGG*IT*SQEFETSLANMVRTLS
13318	27219	A	13461	330	420	NYCSWAQWLTVPTPAL*EAAGGSPVETSS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13319	27220	A	13462	577	766	AQWHTSIVLAA*EAAAAGGLEPR* SRL KCTMIIP INSHCTPAWQHMRPCLLKXNF SNSFISK
13320	27221	A	13463	206	387	VTVGTEAEAGRGHLLTCCVLTKQKW L GTVAHAYNPSTLGG*GGRI* DQEFETS FLGS
13321	27222	A	13464	167	41	DFWLGAVTHACNFNSVGG*GGQIT*GOE FETSLANMVKPMS
13322	27223	A	13465	480	79	SRVTSPLLLNSVISAKSLLPVSGQKS KQGVMS*QERLEPGVGEFTPGPCCL VSQGPSLCPSPPPYFRMSRLSQPGS I RVLI*RFAAATSAPPALGLPDTAFPP PLLSRDQWAAAGROGDRDKGLP
13323	27224	A	13466	3	373	DAWVAHASAHASVCLITITLLALLIT I TF*LPQLNGYTEESTPYECGLEPISPAR VPLVIKFFLVATITLLDLERALLPLP *ALLTTNLP LIWSSLLII IIALSLGY E*LRKGLD*AE
13324	27225	A	13467	214	55	TRQKITNLFSS*KKFLIPPARAKDFLFF IFFFFFFFFFFFSCSRILLHR
13325	27226	A	13468	111	358	VMKVYFI*IGELVTQAYIFVKSHQIAH I LPHSMVLP*IKMFVGTVAITYNPSTL GGHSRRIS*AQEFETSLGNIVSPHLY
13326	27227	A	13469	199	607	RIRGTSQKLLLLKKLISLTPKSPQTRGT P*TTFPPTNTNFPFPVAAATAPDPSPA HFVSSPYNPDLGSP*PECPSPGRLOREI EQCKDIQNFPPPTSTRICSNDSLKSGS ASRRRGHLFCERPVNQFSPKPKK
13327	27228	A	13470	128	256	EDWMMWLTPVITPTQGEVVRGSLFPRSS ELQ*AVIVPCTPSE
13328	27229	A	13471	94	388	KGEGKTEELNSWRSHRGTHLCLLADISA LPLHYYYYYYFQWRQSLPDQPGQHGET PCLPKIQLINRAYWHVPVPTDQEDAR *LPEPNRQSQRPE
13329	27230	A	13472	359	73	ATEPGQLFF*EESHNVITAGVQWLOH GSLOPTPCGLKPSFLIHTGITAASHYT WLNQLLPMNVSLTYFESPOLKIQRSHI LCNSIHIKLE
13330	27231	A	13473	332	10	ILSKRGFPKFGRYCEVNPFFLCVQAK*V RP*EDTSLHCEIYHTHTHTHTHTHTHN LKP*TSKELIPQKTESLFSLCIKKSLL RFQTFPDAGSTGNSVGCACFISK
13331	27232	A	13474	355	385	IMVCIQSCVH*KNN*FWPGTVAWVCPNE RTLGQGDQTA*AQELKTSLDNMKAPCL YKFF
13332	27233	A	13475	297	425	RKSAWMLMPVVSPL*EAEAGGLEPGSL RSAWATWGDPHLYKK
13333	27234	A	13476	160	1	KSTGRIGMVAHICIPSTLGSQGGWIA*A QEFETSLGKILSLPEIQKSASLITW
13334	27235	A	13477	334	79	GMKEQINFLYQKRGIKPNKIQENNVLI HYN*KLLNSFK*LQDTASI*YFFGNLY NRPQGMVAHACNPSTLGGRGWIT*GOEF L
13335	27236	A	13478	234	385	YAKFHVSINEKKPDVAHACNPSTLGGQG KNIT*GOEFKTS LANMTPRIY
13336	27237	A	13479	408	129	KRSINRKKGGELSSSHFLLLLLPLPDEE PSPPPPCPLPFPFPFPCPLPQSG*GAC GRLHPC*MDLGPCKCPARKVFSHLSCL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						VLQVCRSP
13337	27238	A	13480	251	384	TITFWRGVAHVACNPSTLGGQSRQMT*G QEPKTSLSNMVKPRLV
13338	27239	A	13481	164	300	AGDSDSDNSMGLGRTHETFFKCLGFCM TTKFIVPALWEAEVGGWLEPSTSLRLR*A LIALLCQTPA*GTVDYKYVRPSTLGSRRNA
13339	27240	A	13482	2	30	TGCHQFRFLNNFSPHPVLQVLPQDCL LIFRYFKF*LHQLM*INPNANFCGARSF LCKFRVWIS*LRYSLVSLVLFVFK*S VQI*VKKKKKKKKKKKKKKKKKKK*K
13340	27241	A	13483	39	199	LDVGTCSPVVPASQEAERGRHEFTSLR LW*AMIVQLYVSLGDRARPCLYLKK
13341	27242	A	13484	18	72	TRTRSYPGSTGCQHTFGLVSLYNCVSQ FLITNLVYISIVRDY*YIYIYLYREIYL YIYIEITYIERYVYIHI*ILGLQVANC IPLD
13342	27243	A	13485	266	496	LDSASDITQAGVQWCHNSFL*PQTFFLK *ASTSAS*VAEITGLSQHWVKIIMSVS LSSYTFIQLPSTILLYGNATP
13343	27244	A	13486	286	72	HILSHCTVLFWLTLPHPHOTTHTYKNTIGQP SIVARHTNLSLGG*GRWTT*GQEFKTS LANTVKCSDAWWRD
13344	27245	A	13487	309	6	RFFFFFPFGKGVFFORFFFGFRGFFP PRFFKTGPEIFFFGPLKKKNFPFGGK IVFF*RGAPPPPPFFFLFFFFFLK KNYLLLEKVSQPEKG
13345	27246	A	13488	183	459	RRVKTYCKCIWQNNYL*KNICNSMPO KKKKKKKKKKKKGAPFKKKKKKIS*G GGGPFF*KTAKIPGGORGGFFFGKIM LFPVFI
13346	27247	A	13489	348	1	CEGRDGLPIQFASWFKYAGFHSLESTFO SFCQTKKLEAPKELSPCSQLYRNVQLT CRRMKLDPHLLPYTKINSRPGAAHA*N PSTLGG*GGWII*QGEFETSLTMGETP PTRP
13347	27248	A	13490	313	320	KGGFFPLAQARVQVNNLSSGETSLPLFG SSNPFPSATGVAQTGSPPLA*LIFFLF *DRENGDORKL
13348	27249	A	13491	187	350	GNPVKK*IKNTSSSGWVWMLPITPAL WDAEVGGLLEPRSLRPAMATERDSVS
13349	27250	A	13492	211	83	EYAKKGKLLSWRKY*SVCVVCVCTTC VCVVCVCTTCIKNI
13350	27251	A	13493	286	407	LGVEAYACNLNTLGG*GGRT*QGEFET GLGNTARPCLYF
13351	27252	A	13494	897	1033	KFIFKQMQDDHSSLPQ*TPCLKQSSCL RLPSTWDYRREPLHLM
13352	27253	A	13495	265	3	HLILLREDLTWQRGKWLKGRVSLCSLGS *TQSLTVLKKGRGLGVVAVPSTLGGRR WVALAQELETSLGNMVKLSLSIQKLA GMV
13353	27254	A	13496	319	1	CFKLWDTCAQCAGLLHRYTCVMVVCYTH HPEFCYINIMGLPKYMMSYLWPKCHAVY HFRYIKNLLPGCVAAHACNPSTLGGRGW IT*GKEFKRRMKTIV*IGIYFI
13354	27255	A	13497	265	11	VLSEVSNQHLGAPSNRTFSEVPLAQAA QGRPSLVPPSAIVFSPYTYCYAFSLIS MFIIP*VWAEVGELEPRSLRQA*ATW

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13355	27256	A	13498	164	22	GKKRLKISGVVAHARNSSSLAGRGWNL T*GQEFETSLAKMMEIPSV
13356	27257	A	13499	277	363	TYLCYIFNI CLFVGEIEQR*LI*FHRS TLNGHILYRVPSPNPQAVASPVCTCY MPTWPEVVEESQKK
13357	27258	A	13500	1	270	YTCVLLLVTVNLLCLTIYKLNFIIGML RKKTIVYIERIQYLYLKFOASTGCLGVY PTV*PMTYTYTYMYMYIYIYIYIL CLCLDG
13358	27259	A	13501	170	383	TLVSKLTYFSPQIVTIFPCGKST*GWVW WNPVIPA*EAEVGGSESTSLGQAWA TGRKAFVFPVKEYKN
13359	27260	A	13502	31	402	GDYLYLREGWCEPARRECHQNLPHRT FTPHLCLTYNRLPSLAWSECEERHNET TDKNQTVKDLALDMKRVLPFS*GHQKVI KGVGVAVACNPFSTLGGQGWITRGEFEX TSLINMAKPYLY
13360	27261	A	13503	232	446	RNRPGAVAHACNPFSTFRGRGGRIMRLGD *RS
13361	27262	A	13504	196	390	VNKAEEKHLYFVAKRELKPGVVVHTCN PSTLGGRGWII*QGEFETSLPLKTKQK LAECGRGCL
13362	27263	A	13505	146	7	LKVVLYWLGAMAYTCNTSTLGGQGWIS *GQEFETSLANMVKPCLF
13363	27264	A	13506	177	18	SONFGRPRQDHFRLDGRHSETPSLOEK VKKLTRHGACVQSOLLRLRRDHLP GGGGCSVP*SVNI I
13364	27265	A	13507	117	338	NKTLKKKGGGRFKESKFTSPGLQGNFS FMGPPLKNSRAGV*QRREGKLGVPOLK PFEANPLFARGPNTKNP
13365	27266	A	13508	306	443	LARYEPAVRTRAC*AGWLTAIVPVL*EA EAGGPLEARNLRPWAT
13366	27267	A	13509	146	390	KMPKHGEQAHRKKKKRGRFKGSKFTS ACLQRNIFFLGPPKLNRSAGV*QRGDWK NEGVQTFNRFEENPLFARGPNTQKF
13367	27268	A	13510	119	356	NEDRLRGCCPGR*LLRTGEGVSNPAGN SGIRWCEESGGLFWVRVGTESVLSGL FVCCVFQAEKAKATGRAEVLSCP
13368	27269	A	13511	221	21	EDLQRDKPLGSCYSTCGWAEQWLYQHPG GAGSKCRIMLGAVAHAYNPSTLGGQGRW IT*GOEFLSL
13369	27270	A	13512	163	418	TFDDQCLMLQDHACVKSISQSA*YLTF AVLAWAEAGGLEPSTRPWWAT
13370	27271	A	13513	239	21	FGNLGGGGRKTACIQESLGNIVRPFYFK TKPKPKPNQNTKXIS*AWWCMPVPRNR KAEGVESLEPRRSRLQ
13371	27272	A	13514	135	11	KFFFWFGVLAHAYNPSSLAGQGGRT*G QEYETSLANMVK
13372	27273	A	13515	162	57	EGTSLRSRPFPLGGWVT*GQEFETSPANN VKRCLY
13373	27274	A	13516	424	54	PKRGFFPTFFIWPVPPLPFFPKPPPR IFFLGPKKKFFSPPGKLKIFF*KGPP PFFFFFLLFFFKKKKRLGGFFFF FWARPFSFLSLFFKETIPLYNIWMHX DSCKAVIHYYH
13374	27275	A	13517	310	349	GGGLPKKLPFSRGGGERFFFF*GAPFFF FFFFL*SSKIFIFLKSPPFFFFFFFC FFFFFSQILFFISSPCFVFFFLNYTSRT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
						CSVCAITLFGKNTYSRKARHTLW
13375	27276	A	13518	273	393	IKCLSYRKATTLGGQGRNIT*SQEPETSLSNM*KPOLY
13376	27277	A	13519	450	139	TPETALVSPFAKHTWQQQMLVRRSSKGNNMSKGNELIHPSRI PCSNHTLLRLALWLGAVVHTCNFSTLVGRGWIT*GWEPKPKSKTSMERFCILSRHKRTGSG
13377	27278	A	13520	47	427	KMKQLFEMLVFNQNTITFLSHSIFETIR*LTLEPLMFYYFKO*RTLPPKF*DRVWLCHAGGCL*CSGTVSACNLRLLGSSDDSTAS*VAGTVGAGHHIWLILNNRELPKQKFFINSSRNLFET
13378	27279	A	13521	199	98	SLPSVKLSICCEFFEDIVSKDPIPVVLPVVKRESCSLCALPNLLPK*EKTNIQVP*VFQSTIKAKAQLGMVAHCNPSLGGRGWIT*GLR
13379	27280	A	13522	314	18	QTLNIFYLKIYNTISLVHC*IFEARFQILV*V*NYPF*SLICFTFSWHETQNT**KNLIIWAGAVHTCNCTLTGQDQGRRIALAQEIEPSLGNIAIO
13380	27281	A	13523	18	231	CPPAVFGTSTIEQIQLYDKID*KIGQAWWCAPIVPTQAEVGGSLERSSRL*CAMSTSMNRHCVPAWAT
13381	27282	A	13524	239	465	RVOVSECLLHREKCLYFQLGLS*LYPQTGWLQKQKLPQTVTAHTCNPTLRGRGKRI T*GQEFETSLANIVKPRLY
13382	27283	A	13525	388	468	SLRLGTVAHTCNFSTLGG*GGWITRSG
13383	27284	A	13526	342	369	CTLNLTLLYSIDFGVSAFLATGGDITR NKVRKT*LRLGTVAHYTNPTLGGQGRRLT*AQEFKNSLNLGPHLYKTKTKTKT
13384	27285	A	13527	241	231	EYVCIVSHSSSLYFSSSLYIHM*VCVCVYIXVHTNSHIYTHMYIHTHTHTHCYIKLEEKYKEL
13385	27286	A	13528	241	231	EYVCIVSHSSSLYFSSSLYIHM*VCVCVYIXVHTNSHIYTHMYIHTHTHTHCYIKLEEKYKEL
13386	27287	A	13529	34	299	SAPASASPWGIVGLYRFLACDEFDFSPGPEANGRIETTELRTVLSPRECSTGITAPCSLDLQGSRRPPPSAS*VSETTGASHHAOL
13387	27288	A	13530	158	45	SGHRSRARWL*FVTSALWESAGGSPETKSLRNRRPG
13388	27289	A	13531	342	1	CFFLKGAFFFFFFFFFFFNFVFLVGTDLKILKVTWKWGPDKDAVPPKKNQARGLP*PDIKI FYKWLGA VANAYNPSNLGG*GGWIA*E*EFETSLANMTKPKQYKYLKLA
13389	27290	A	13532	589	742	RIMKMLRIKICGTGPGMVAHAVNPSSSLGDWIT*DOEFKASLANMIKPHLY
13390	27291	A	13533	74	446	HVGIFPSRLTSVSHPRCHKPRTSESHVYCAIEARHYQCKVSRPSDAGSEGRPRDMTQDTEVADTPPNISSITATRMATIGVGVVAHAYNPNTLGGQGRRIA*AQEFKTS LGNLAKPCLYKH
13391	27292	A	13534	1941	1040	AFHLLPYLSSGFYCSLGPCFGLGSSHMAAWHKEPLHNACDSRRSAPIRQGLGSPSATHDTHRTLAHICKEIKERLHEIKEREIDS*RG*NTQR*VEREAENKYKPTIEI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13392	27293	A	13535	1192	1476	NTEIENHKQEQMLRHAGEERENSPREAE RRCRNEKCEIKSRNSRKEARLRKKVKFK TNEKGKG*QIITVHKKEVGRERRGRQ NKRTKSTQHVTKGDMR*SVKEEPLHR RAKRNSNMKNERYVLRQDTHSCQEQE KMRQRHTRKKLARETNKQVHRHTLNREQ AKFRKKETKEIHHISAILK
13393	27294	A	13536	55	132	RAESCSLAEDGVQ*GNLSLQPPFPK
13394	27295	A	13537	7	325	SPVEFRLGEPPTKG*SSFGKRNRKTHLC RRCGSKAYHLQKSTCGK*GYPAKRKRKY NWSAKAKRRNTTGTGRMRHLKIYYRTFK HGFREGTTTPKPKRAA*VAASSSS
13395	27296	A	13538	259	274	KFEEAAVCYHCTTSL*CHTVCFLSFFL LEIGVHYITQAQSGAMIAHCSLKLGGSS NPPVPAF*VAETRSACYNALVVFVKFLM GL*ELWKDMS
13396	27297	A	13539	3	68	QASVLQKQKQMSWQKLSSTFVKFWNLV KTGRLGEEISCCLVVREYISDCLATI KLPASHLSMRKPRKDFKSTFLISTKQ GNHGHGTGKNEVNNFQQRISV*KTYFKK YNMRPGVAHTCNPSLTGG*DWHT*GK NCQNQLS
13397	27298	A	13540	268	468	YRRLISKKFFKRRHWSVSPFKFSFWLWG EVAHACNPSTLGGQGGKIA*AQEFLTSL GNIVGPCLYKK
13398	27299	A	13541	308	437	FSWAFEIGSQAEVQWHDHLSL*PLPPRF KRFSHLSLSPSWDYR
13399	27300	A	13542	7	244	AKTAPLFF*FETVSFCVAQARGQWHDGP SLQPRPPGQETSMIKTSSDPPPPASQVA GATGMGHHAQKI*FLVETGSPHVSQGG ALLK
13400	27301	A	13543	50	175	ALPAHTAVGQCSVEGFCVLSDEGDGA ARMKLVFLMKLSHETVIELKNGTQVH GTITGVDSMNTHLKAVKMTLKNREPVO LETLSILGNIRYFILPDSLPLDILLAD AEPNVKSMNREAVAG*R*G*AREIFDEI ES
13401	27302	A	13544	47	362	VAFQGLQVPATNPANFFFWKGGFFFP QGGQGEKIGLRDPWPPGVKIPGPTLS GTREKGA*PPPIYF*FWKGGQKGGP GGF*TWDPKGPSPPTPKGGD
13402	27303	A	13545	97	351	NKKKKGGPPFF*KKRVGKKKKGARAGG PPKPPFPFGGPRGGPRQNSKTPRPGK GNPPFKKKKKRNIPFAGPMGLKGGGHL
13403	27304	A	13546	214	32	NYIKSSVDGGA*IK*WT*NLKCLVLSV KNITRMVDCSSGVQDQPGHGETPSLL KTRKTSWA*WRLGLQVRKMPSPSR
13404	27305	A	13547	350	159	OTGTLQKTKQKKAQNLMTVILGL*EA KAGGLLEPKSLRPAWATWQDPYIKKFF LERKTWR
13405	27306	A	13548	367	149	PFFFFF*TGSHYVAQNWIQIPGLNLP ASASQVTATTGMHHHTRTTFFPSLTSTH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13406	27307	A	13549	321	2	QVSTASWT/LQNSGRH GLVKVTHHGIDRNGLGYDPSQASVLSFPY TA*WQ*LCPLPKQVQIYPAHPLFINDMP P*WLLKIDPSGPGTVAHPYNNPNTLGGRG RRTTRDREFETSLANUVKPHLH
13407	27308	A	13550	216	13	GYSGKETVFSMRKQQSGFCLQGFSIPM GKAGINQIIPKTTLGGRGWIA*GQEFK TSLANTVKPCLY
13408	27309	A	13551	199	391	KDFSIFTACFRPPTTSGSGQEQWLIFF HAYNPSILGGGRQIT*GQEFPTPARLG NMVKPCLY
13409	27310	A	13552	70	239	ATCVKN*RTSWAMWCVPVPATHEAAAG GLLEPRSRRLQCSVIASVERHRTSVWTT
13410	27311	A	13553	105	257	GOAQWMPVTPALWEAAGGSFAPRSLR LA*ATVPGPNFLKRAFHSLNLFLP
13411	27312	A	13554	499	165	Y*MESHFVTGGGLQWCSLGSQAFFPEV GGWLELGRQLPMKPKRIAPINTPSPG
13412	27313	A	13555	415	719	YTDKIRSTISLLPVKSGTHSMCPVKFTQ LQEAGGIHMAKLSGQVDREWRLGTVAH TCNRSHLEGKGGQIT*AQVFKTSLGNMA KSCLCCKYQKLSWIWQH
13413	27314	A	13556	224	523	DRVSLCHPGWEGCWGVSQLTATASISGQ* TILFPQSPPE
13414	27315	A	13558	355	1	QVSLQLPYCVLFQFHINQKQAALLQRCY VSAITNLLINAIWQVNSLKMCEENQVNS LQNNPF*HRNYPFAGHGGSCL*SQLLG RLRH*NCLNLGGGCSLELRLRHCPTAWA TKASPS
13415	27316	A	13559	73	259	KYVPFHKGKISERRLCSVAQAGVQWCDHG SRSEVLGSDNLLASAS*VAGITGWCWS SDPHTT
13416	27317	A	13560	205	21	VVKISEDFLGDGAKKWAYQEDIKRRLG RGAVSHTCNPSWTRGRGWIT*QDSFET SLPKC
13417	27318	A	13561	254	481	LWALLPGSSEVDSLEYGWEHFNVPVILIS KEIFILLFF*DGSHLLPRLCSGMISA YCHLCLOGSSDRRDFLKKO
13418	27319	A	13562	174	369	TFFSFSMEVPEPGFYITQAQGVRLWLTGA IIVHCSKLLALSDSPSAS*VTATTGM PPHLAFTVK
13419	27320	A	13563	371	109	LFSKAGRCILQNLCCMVSGKCNPMNGI DVTREYPTIAHRVLYTAATSGSDFLGQ AQWLMVPVPAI*EANAGESLEPKSLRLA *ATVFGPRSLQTLHRSLEGL
13420	27321	A	13564	206	486	RQLAAHVILVTPLPDHTVANYTSLSL LSSSENGVNDNTHFIGLLLRDYK*GWV *WLTVPVIALWEAKVGRIARGQBLENSL GSKARPRFV
13421	27322	A	13565	212	398	SRVRCGPPFNFLPKSSCI*ECGQGAHA CNPSTLGGRGQIA*AQEFKTSQGNVAK PHLYKI
13422	27323	A	13566	26	395	YSPVHTDKCSGVRLGLFFFFFEKEPH FFSPAWKARAKIIGNGTPLSQGGNFRP KPPKRGKRGAPGPKILNFKKRGFS MGAKVNFNPGKGNPPP*PPKGAGKGG TPRPGPFFFFF
13423	27324	A	13567	400	195	ATRVSLAPTNNKINWGWPTTVPVPPPE GEAGEFL*PQKWRVRLNKIVFLSPRPD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
13424	27325	A	13568	316	154	KTRLCFKKKKKK SQPFPGRLRWEDRLSRGVQNPQK* LMPV TPAFSGAIVGGSLPRSSKPA* ATNNLK SKVLIQGOIQCDKASKVSI VESSWGWGCG
13425	27326	A	13569	297	475	FDYFFIYETKSHSAQAGVQ* CKHSSL QP* P PGLKQSLLPWPPKSAGLTGVSYGT WPI
13426	27327	A	13570	116	332	NRVLLLPKGEYRGTSIAHCSLKLGS KR PPTSA* GDETTGWCHTTPV* FLKTF IEIRPGVYPRVGHNR
13427	27328	A	13571	233	405	TVPELASCRLKKKKKKKGEKNLKKIK GFPGPGPRV* GPEAKNPGGGGPGIKGP G
13428	27329	A	13572	408	3	TFCDYFKTPPGKGFFFINGPSPFFLNRG PSFFFFPGFPFFLNKFFFLPVVFKGG GYKRGVFPKKKQPPQPLFFFFFFFLI* KTRPGTVAHPCNPSTLGGQGRWIT*GQ EFLSSLAKMAGRVVRPNCESV
13429	27330	A	13573	273	406	IEKPFKAERGGS*NTSTFGGGGRNIA* S QEFETSLANMVKPHLY
13430	27331	A	13574	385	38	KKNSPPPPGKGNFFFF*GPFPSPFFFF FFFFFLLGKKTFPPPPSRFFFLKLP FPKNGGPKNFFPPPKKIGD* ARPPDLT GGAKGAPL FKKKKKKKLVKRGAVAH T CNS
13431	27332	A	13575	230	53	HWKVLKENQIFTKISFKMNAIKDSVQ AQWLMPVIPAL* EPDMGGVPEPKSLRPA WAT
13432	27333	A	13576	406	33	VNSIVWSSPPFRVSTFISFFELKSCSVT QAGV* WHDLSLLQLQTPGLKRS PAPS LSFYLSSIFYPHSSQTELPVCTLNAASF TNSRLLYL SLLCOKYHPLVPSLPLSTI WYPSLRVSHFP
13433	27334	A	13577	426	294	GGFPSEFVEKPEPFFFGFLKKKISPP PPGEKKIF* KAPP
13434	27335	A	13578	268	3	LQKKGFWAGAEACRCSSEVWGWKRGFD L* VSR* PSFDSHVRIGVQRLMPVVPVL WETEDISFEPCCSRPANASWRKTYIQK PQRI
13435	27336	A	13579	395	49	EKKKFFVCFPGFPGNPNPSPQFF* KGL ISPSSGLSTRRRGFPF* RVFFFLKKQFP LSPRVCENGIIPDP* PPGFVSTSTQVA GAIGPPPPPRVNFYFFVKKGLNVGPMF FFF
13436	27337	A	13580	68	466	GASPAQGSTLHLVILRYFFKPIPTVTE SFGSLVTSPPPLHLPLNKERGGGPI LPCPQLQLVGLGTSLLPVPSLPDTSQDK WPLHGVPFGHVCS* PLAGDGAWPPSPHW IPLNPGTSKSLQDAPFWNSA
13437	27338	A	13581	67	249	ATAPGLLCSYKIFSCQLQWCVPTQLAW ETEAGGSLEARSSL* *TMITPVNRHCI LAWAT
13438	27339	A	13582	359	3	RQDSQWVAAA PASVAVSTCWRLGLEP GGQNRKGSGLPQVHGA* GTENKQGG TPRPGGGPGPSAPRGSGLGAHRLPVVH TTLSSRSALPPTPRHPAPSSPKPTTEF HRTPT
13439	27340	A	13583	174	1	FFFFFVETESHSAQARVLEYSGAIPAQ

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						CNLDNLSSSELPASAS*AS*VAAXTGT*KR
13440	27341	A	13584	192	206	LFFLEVGSCYVAQAGFFFPFGSGHLPASA S*VVGSTGVPHHTQLV*SFSSLYNLERN C
13441	27342	A	13585	244	28	KKPENQEIYIFYHLFPNVHEQIRISLGP GAVAYNCNPSTLRD*GGRIT*AQEFKTN LGNMARPRTRGSTRTF
13442	27343	A	13586	312	701	RGFEET*PRTRKSSPPRPTSCSEVSUKLA RPRRCSAAPQAVRRLSLRSPKPDPPRV SSAEKCAPLPLLPCESETGALPRNSFLC QNASSPLLGLPPSPPTVQALQPRALHQ HLGSTNKEDAHVAPAKKK
13443	27344	A	13587	410	292	GYMIKQQTYYHECRM*ANSHLHLPPEGL LRAVTLWRRAP
13444	27345	A	13588	428	36	TPPPFFFFWAQKKKKIFPPFPGKIFFFL KGPPPLFFFFFFFFFFFLKKFFGLK GPFFFFVQD*QGLENPKEGSSLGWEKGLR ALLPQQRSFVPGGLGPTRLFWGLVWFPG FFFLPFGLCFFFALI FNC
13445	27346	A	13589	3	364	TAPDDQGRPYQAGEPAAHVRADSTHGLG A*RRVAGHLPPRVGAPHPHGASSREGAP PLHPPPNL*HRRPNGSCRFPLGPAAPFQ GABGGGRDRRGTHSVAQTGGPGGFGSG VTPSWRSS
13446	27347	A	13590	778	910	DRIRSGAVAHTCNPSTLGGQGERTA*G QEKTSLGDMVFCLY
13447	27348	A	13591	230	3	KLNLTIVKSLVAMKSTVSEGNMVRISP ASLGMVAHTHSTPSTLGGQGRQIA*AQEF ETILGNMAEPCLYKHSYV
13448	27349	A	13592	223	340	LTPITPEPNESEVVGSL*LTGPVAVIHA YNPRTLGRISGRIT*GHEPQTLSHTMK TRLHYELL
13449	27350	A	13593	35	220	DRASLSRPLECSGNIWAHCSNLNGSSD PLTPAS*GDGTTDTCIHARLIFTGADFC IDASS
13450	27351	A	13594	87	369	NVQKTECEISGKMQINQKSGVKTKCSNG LFNFIFSKKIASCKVKKLTR* KYKSO ARWCTPVI PATEAEVRGQLEPRSLRPAN ATYQPHFKS
13451	27352	A	13595	261	489	SWNVNRMVVG**KHETSAQWLMPITPA LCEAEVGGSLSEARSWETSLCNIVRLHS KKKRGKGRKGGNQIAPSRE
13452	27353	A	13596	238	2	NDCLWLWFRIPANVSTFGLLHMSLKVNT PGNNRFKSELGTRCLITHCNPSILGGQG GWIT*GQEFVTSMQGGSVKNQ
13453	27354	A	13597	36	687	RDVHRSTYQAGSKQDQGPGEAERLSSSR RGAYS CPVPITFAEGKTRMGDRMRLIL GLSWGPSLTLLPITNAPRRPGM*EPAL PGNSTS*SGAVRFPGGGRK*EDSAESWS CFCSHPSPSSGPNPSPSPSAVCMPLGLS GLQR*PKQLSPPALSLPVSSLLVRLSP WPPPTSHELLPQALPQSLHPQGSRAVND FSW*GNVLGSRNRNGCMEA
13454	27355	A	13598	367	468	KKQKRGREBPWLTPAIPALWKAAGGSP* VQSSRP
13455	27356	A	13599	183	380	LTSMLAVDNSSVEKTCPOAMRISRPAV AHTCNPSILGGQGGGLA*VQYEYTNLGS

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13456	27357	A	13600	161	657	MAKTHLYKN LIQGCWCSLFFSTRVFLAAIGMKSQWCR PVAMDVGYYQLRHFISFLSSLLGTENA SVRLDNSSSGASVVAIDNKIEQAMDVLK SHLMYAV*EEVEVLKKEQIKELIEKNSQL EQENNLLKTLASPEQLAQFQAQLOTGSP PATTPQGGTQPPAQPASQSGPTA
13457	27358	A	13602	121	423	MIKVNISFGLYLSQVIYIYIMKYITAIY LKDFFFDGVLTRHPWMTVTTCSLBI LGSTDPASAS*AAAGTTNTSHHGQLYSY FKKRPTVAEMEQYKIKK
13458	27359	A	13603	1889	1717	VPRIKPLSNTPFESSI*RPKPPSSTFSHP GKPSMGPPGLNRCVPQORALLPGWYOHCG R
13459	27360	A	13604	81	267	ETCCIKNNTLK*ISQMLKCKPTIVPATW QAEVGGSLDPRSSSL*CAMITSVNNHCT PAWAR
13460	27361	A	13605	267	418	THASGMVTHTCNPGTLRVSAGRIT*GQE FKTSLGNIARPHLYKIIINKYI
13461	27362	A	13606	428	24	CPESNPRKREPTLKSEPIITLPIITGLL DDGNSPTAAAGSVFAETTLQPCSSLCC* VKSSPWPATSLPQPPGSAQOTLPVRVAL IPGPSLVSTSLGPRLAPGLPGSPSPSPSP QVTLDSERYPSPTPCIAPALED
13462	27363	A	13607	267	442	RPPPTLVKVPWLGVEVHACNPRTLGGGG SIS*AQKLENSLSNILRPHLYQKQKQKQ KK
13463	27364	A	13608	3	280	YRLSVICEDPMREREQTCFPPPPSPFPN RYCSTRDGGMEGSGQDFRKGFPFA*APCR SGGGWRGCCPAGAPGSPGCGSSQGQGV SPWQKRS
13464	27365	A	13609	291	248	EKRAHGSQPMKGRENSMCKSSSEFRVVA WSLAGVKGGDGR*GSGAGGSKLG*AV* LDPEGHAGQAVFCGEAGARTQIGGK* RDQAPLPLSPNLCSGSCLPTKHSLARMP LRVKSYSQAQLGRTCTRPSPTITFDS S
13465	27366	A	13610	267	3	HTDLLNTPTHTPISPRCDPKHTALPDQK SLLEFFEMESCVSARAGVRWHDLSRLR PLPPRF*KFTCCSIPSLYCGRSRGSQT YTS

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13470	27371	A	13615	197	428	KTWVGLKTSASPHQDFTQPLNMLNSVP *TWLGSQPRFLFPPTVSHICNPSTLGG RGGWIT*GOEFETSLATWVKP
13471	27372	A	13616	445	550	ISTITGRGRNLTPTVILVLEAEAGSSP* GRSSRLP
13472	27373	A	13617	3	435	TWVLSPADKTNVKAARKVGAHAGEYGA EALERMFLSPFTTCTYPPHFDLSHGAQ VKGHGKKEADALTNAVAVHDDMPNALS VLSDLHANLKVDPVNFKLLSHCLLVTL DRLHPAEFTPAVHASLDFKFLASVSTVLT SKYR
13473	27374	A	13618	719	918	CEGRREKWKIGRERKGRGRKGEQMGRE GKGRDGGKRCPTSRPRSSSRDRSNI I ISEHASAVEA
13474	27375	A	13619	847	938	WLMFAVPALEAEVGTISLEAQSCRPPWA TQ
13475	27376	A	13620	349	409	NLWSWFGAVAHVCFNSTLGG
13476	27377	B	13621	25	189	MVLSFADETINVKAAWGVGAHAGEYGA EALERMFLCFFTTMTYFFDFDLHGSQA*
13477	27378	A	13622	142	356	RIVENEKINAESKSKQVLDQSLPTFRY LDOTVVPILQLGLAVLAKERPNNPIEFL ASYLLKNKAQFEDRN
13478	27379	A	13623	18	1353	AGAAQCEVVSAGEAGARTMS EADGLRQR RPLRPQVTTDDGGAPEAKDSSFSGRV FRVTFMLAVSLTVPLLGAMMLLESPI DPOPLRQISGIALFCSPKEPPLLGLVLP NTKLRAERLFENGLVGPESIAHIGDVM FTGTADGRVVKLENGEIETIARFGSGPC KTRDDEPVCGRPLGIRAGPNTLFPVADA YKGLFEVNPWKREVKILLSSETPIEGKN MSFVNDLTVTQDGRKIYFTDSSSKWQR DYLLLVMEGTDDGRLLLEYDTVTRVKVL LDQLRFPNGVQLSPAEDFVLVAETTMAR IRRVYVSGLMKGGADLFVENMPGFPDNI RPSSSGGYVWGMSTIRPNPGFSLDFLS ERPWI KRMIFKLFQSETVMKFPVRYSLV LELSDSGAFRSLHDDPGLVATYISEVH EHDGHLVLSGRSPFLCRLSLQAV
13479	27380	A	13624	18	1353	AGAAQCEVVSAGEAGARTMS EADGLRQR RPLRPQVTTDDGGAPEAKDSSFSGRV FRVTFMLAVSLTVPLLGAMMLLESPI DPOPLRQISGIALFCSPKEPPLLGLVLP NTKLRAERLFENGLVGPESIAHIGDVM FTGTADGRVVKLENGEIETIARFGSGPC KTRDDEPVCGRPLGIRAGPNTLFPVADA YKGLFEVNPWKREVKILLSSETPIEGKN MSFVNDLTVTQDGRKIYFTDSSSKWQR DYLLLVMEGTDDGRLLLEYDTVTRVKVL LDQLRFPNGVQLSPAEDFVLVAETTMAR IRRVYVSGLMKGGADLFVENMPGFPDNI RPSSSGGYVWGMSTIRPNPGFSLDFLS ERPWI KRMIFKLFQSETVMKFPVRYSLV LELSDSGAFRSLHDDPGLVATYISEVH EHDGHLVLSGRSPFLCRLSLQAV
13480	27381	A	13625	1	384	QSFRTGTRKRERERKMSLSNDHLAALK ADQPLTPKSILRLPETELGEYSIGGYSI SPLKQLTAGKLQESVDPDELIDLYCGR KLLDDQTLDFYGTQPSGTVHVRKSWPE

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13481	27382	A	13626	980	1089	PDQKPEVPDKEAAMRD KRIRIQLTGGLYPVPVPPHPFPQSPPIFP RPTSPTRT
13482	27383	A	13627	116	587	VCGELRADSWFPVPSQEQASGPQKQAFI WPEAPSR SARLPITYTDYDSRLQTQES QMLGSMARKKPRNTSRLPLALNPLKSKD VLAVLAERNEAIVPVGAWEPAWPGSSSE IPAYTSAYLIEEELKQLKQKQALKH QKQVYRVNQQTILRKQ
13483	27384	A	13628	150	484	VAFPGASRGVRKTEVEGQQGGQTACGGC GHOCPPPTWHIQRACHVPSPTCGAGWHL QGRASCRPPSPSQPVYQTVQVRQDPHT GVGRDSRGELAWSSFTHPYLLVCNPL
13484	27385	A	13629	330	397	ARCEWLPVPIPALWEAEAGGSH
13485	27386	A	13630	10	137	SFTGAVILITARGLTSSLLFLCLANSYE RTHNLFPLNDPFFS
13486	27387	A	13631	380	98	FQWLVSFTATLWFEERHKNKTEREERR AKGERGDKKEEREEREGGERGRGERS DKREPKKSKKEENHPKVVFSPICSCFC FLTFFFPVFF
13487	27388	A	13632	56	827	PLFEAFTACGFVHDCGLLHPEETCGLQ PISSDYIEAILQSELRCPGSDMKGOWI VPCLSGSDNRCTDREITWQPHNCQYGV LTKPQLQCCGGRKILFJGDSNTRGIMY YLIERLNETLQEWQKVHGTKFYHNVNNGG KTLISYSYYPQFVISPSPRPTFENALEH LLQSRPLNTGQTVLVVGGVQWLNSNH LQIHKVLKSPFTTLNQPVTKSCLOQIY FPRLSPTLHNSCLDLVYSPTKSNFIYFV VQFLN
13488	27389	A	13634	3	2718	SGPCRTTIVAPLLRAAPVEHCVAALRPTD STMLKKFDKKDEESGGGSPFQHLEKSA VLQEARVFNTEP INPKKCAHILTKILYL INQGEHLGTTATEAFAMTKLPQSNDP TLRMCYLTIKEMSCIAEDVIVTSSTLQ KDMTGKEDNYRGPAVRALCQITDSTMLO ALERYMKQAVDVKVPSVSSALVSSLHL LKCSFDVVRWVNEAQEAASDNIMVOY HALGLLYHVHRKNDRLAVNMISKVIRHG LKSPFAYCWMIRVASKOLEEEDGSRDSP LFDFIIESCLRNKHEMVVYEAASAVINLP GCSAKELAPAVSVLQFCSSPKAALRYA AVRTLANKVAMKPSAVTACNLLENLVT DSNRSIATLAIITLLKTGSESSIDRLMK QISSFMSEISDEFKVVVVQAI SALKQKY PRKHAVLMNLFMTLREEGGFEYKRAIV DCIISIIEENSESKETGLSHLCFIEDC RPTVLATRIHLHLLGQEGPKTINPSKYIR FIYNRVVEHEEVRAGAVSALAKFGAGN EEMLPISILVLLKRCVMDNEVRDRATF YLVNVEQKQKALNAGYILNGLTVSIPGL ERALQYQYTLPESEKPFDLKSVPLATAPM AEQRTSTPTIATVQPEKVAARQREIFQ EQLAAPVPEFRLGPAFKSSEBVALTES ETEVVIRCTKHFTNNHGFQFCWTILN DOTLENVTVQMEPTAEYEVLCVVPARSL PYNQPGTCYTLVALPKEDTVACTFTSC MMKFTVKDCDPTTGTDDEGEYDEVYLE

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						DLEVTVADHIQKVMKLNFEAAWDEVGDE FEKEETFTLSTIKTLEEAVGNIVKFLGM HPCERSDKVPDNKNTHTLLAGVFRGHH DILVRSRLLLDVTVMQVTARSLEELPV DIILASVG
13489	27390	A	13635	118	629	LWALQLHPPELFPERRGTGAAGVNTGVA MIRFILIQNRAGKTRLAKWYMQFDDDEK QKLEEVHAVVTVRDAKHTNVFVEFRNFK IYRRYAGLYFCICVDVNDNNLAYLEAI HNFVEVLNEYFHNVCELDVLVFNPKVYT VVDENFLAGEIRETSQTKVLKQLMLQS LE
13490	27391	A	13636	57	221	LHHCTPPWAEVEETLKRLOSQKVGQGIT VVNTEGGWEPLGHCGDRSPPAQGCP
13491	27392	A	13639	344	544	LSGGHAGALSSLLWHLYCLSSQQLGN VLVTVLAIHFGKEFTPEVQASWQKMWGT VCSALCFRYH
13492	27393	A	13640	319	623	DMEEASEGGNDVRNRLQSEVEGVKNIN TQNVERILARGENLEHLRNKTEDLEATS EHFRTTSQKVARKKFWKNNVIMVILICVI VEIILFTVLPAKGAFS
13493	27394	A	13641	2099	769	TRLGRVSVASRFGCRGAVGGLLVERSK ARRPILLESRVAAJAVVILQLQOQEDRSK LRSVSVDLANDVPSLQIDIPDALSERDKV KFTVHTKTTLTLPQSPEFSVTRQHEFDV WLHDTLIETTDVAGLIIPAPTKPDFDG PREKMQLGEGEGSMTKEEFAMKQELE AEYLAVFKKTVSSHEVFLQRLSSHVPLS KDRNFHVFLFYDQDLVRRNRKNTKEMFGG FFKSVVKSADDEVLTGVKEVDDFFSQEK NFLINLYNRIKDSCKVADKMTSRSHKNA DDYIHTAACLHSLALEEPTVIKKYLLKV AELFEKLKRVGSRVSDDEDLKLTLLRY YMLNIEAAKDLLYRRTKALIDYENSNKA LDKARLKSQDVKLAEAHQEQCCQKFEQL SESKEELINFKRRVAAFRKNLIEMSE LEIKHARNVSLQSCIDLPKNN
13494	27395	A	13642	210	772	SVKMVRYSLDPENPTKSCRSRGNLRVH FKNTRETAQAIKGMHTRKATKYLKDVLT QKQCVPPFRYNGGVGRCAQAKQGWNTQG RWPKKSAEFLHMLKNAESNAELKGLDV DSLVIETHQVNKAPKMRRTYRAHGRIN FYMSSPCHTEMLITEKEQIVFKPEEEVA QKKKISQKKLKKQKLWARE
13495	27396	A	13643	168	2172	SLPCEVSVDSQCFRFGCKKKHKKSDKH LYVEVEKPLKLVKCGNEVTLSTGS SGHDSFLFEDKNDHDKDKRKRKKKGS EKQIPGEEKGRKRRRVKEDKKKRDADV ENEAERKDLQCHAPVRLDLPPEKPLTSSL AKQEEVEQTPQLQALNQLMRQLQKDP AFFSPVPTDFIAPGYSMIIKHPMDFSTM KEKIKNDYQSIIEELKDNFKLMCTNAMI YNKPETIYYKAAKLLHSGMKILSQERI QSLKQSIDFMADLQKTRKQKDGTDTSQS GEDGGCWQREREDSODABAHAFKSPKE NKKKDKMDLEDKFKSNNLIEREQBLDRI VKESGGKLTRLRVNSQCFERRKPDGTT TLGLLHPVDPIVGEPCVCPVRLGMTGR

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						LQSGVNTLQGFKEKRNKVTVPVLYLNYG PYSSYAPHYDSTFANISKDDSDLIYSTY GEDSDLPDSFDSIHEFLATCQDYPYVMAD SLLDVLTGKGHSRTLQEMEMSLPEDEGH TRFLDTAKEMEQITVEPFGRLDSDSTQD RLTLAKAVTNFQGVVEVTFSEAEIFQK KLDETTLLRLLEQEAQNERLSTRPPPM ICLLGPSYREMLHAEQVTNNKLKLAQQV TPGDIVSTYGVKRMAGISIPSPVMENN VDLTDEETPEPKKTDVAECGPGGS
13496	27397	A	13644	1032	207	PADVTPKPAATEAVQSESDASPMSTINEV ILSASGACKLIDSLHSYCFSSRNQNSQV CCLREQVEKKGELKSLRQVRSDSQV RKQLQEKDLRLRVSVFPSSLLSPSREP PKMNPVVEPLSWMLGTWLSDPGAGTYP TLQPFQYLEEVHISHVGQPMLNFSNFSF HPDTRKPMHRECGRILKPDNTKVAFVS AQNTGVVEVEEGEVNGQELCIASHS IAR ISFAKEPHVQITRKFRNLNSEGKLEQTV SMATTTPQMTQHLHVITYKKVTP
13497	27398	A	13646	148	380	RGSWREVPESASLPSRGAKGKRWGLCC CCCCCCCCCCCCCHQEQDGLKHQADL WRSGRTQNQAGIWOEHQTLLEG
13498	27399	A	13647	2099	769	TRLAGRVSVASRPGCRGPAVGGLLVERSK ARRPILLESRVAMAAVPELLQQQEDRSK LRSVSDLVANVPSLQIDIPDALSERDKV KETVHTKTLPTFGSPFVSVTRQHEDFV WLHDTLLETTDYAGLIIIPAPTKPQDQ PREKNQKLGGBGSGMTKEEPAKMQGLE AEYLAVFKKTVSHEVFLQRLSSHPVLS KDRNFHVFLFYDODLSVRRKNKTMKFGG FFKSVMKSADEVLPFGVKEVDDFFEQEK NFLINYNRIKDCSVKADKMTSRHKNVA DDYINTAACLSLALAEPTVIKKYLLKV AELFEKLKRVGVRSSDEDLKLTLLRY YMLNIEAAKDLRYRTKALIDYENSNA LDKARLKSQDVKLAEAHQCECCQKFEQL SESACEELINFKRKRVAAFRKNLIEMSE LEIKHARNNVSLQSCIDLFPKN
13499	27400	A	13648	1	1206	MSTSQSPCESICDYVTSHDKSNFTDMTK LNI LRCEVILDY P APGGGSLGAKHCCSC YTVSSGVTEGERNAGEKGVKLNADGARI RGT PGRGRRAEAEAS PAPA VAAACV V AAAAASRQLASGNRTRVSSGV PAPAFLG TMNPNCARCGKIVY PTEKVNCLDKFWHK ACPHCETCMTWLTMMKNKYGYEKKPYCNA HFPKQSTFTVADTPENLRLKQSQSELQSQ VRYKEFEKNKKGKGFVAADPELQRIK KTQDQISNTKYHSEEFKSRMGSGGGM EPERDSDQSGSYRFLQEQQPHIPTS APVYQPOQOPVAQSYGCKEPAAPVS I QRSAPGGGKRYRAVYDYSAADEVSF QDQDTIVNVQIQIDGWMYGTVERTGDTG MLFANYVEAI
13500	27401	A	13649	3	394	GDGGHGLGSGRNGGSMNAPPAFESFLL FEGEKITINKDTKVPNACLTMNKEDHT LGNIIKSQLLKDPQVLFAGYKVPHPLEH KTIIRVQTTDPDYSPOEAFNTAITDLISE

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						LSLLEERFVRAGPGAD
13501	27402	A	13650	1	471	SRTPTGLREAGSGPRAPRPSGCKSPGL GTVMGLRPKALTQVLSQMTGGVOSTLL LNNEGSLLAYSGYGDTDARVTAATASNI WAAYDRNGNQAFNEDNLKFLIMDCMEGR VAITRVANLLCMYAKETVGFGLMKAKA QALVQYLEEPLTQVAAS
13502	27403	A	13651	1334	82	CYTGGTQSLWFGSSCASSVARPSSLFPS AWSCEWSVRCARACTMSVPAFIDISED QAAELRAYLKSKGAEISEENSEGGLHVD LAQIIIEACDVCLEDDKDVESVMNSVVS LLDILEPDKQEALESCEKLVKFREGE RPSLRQLQLSNLPHGMDKNTPVRYTVYC SLIKVAASCGAIQYIPIELDQVRKWI WNLTTEKKHTLLRLLYEALVCKKSDAA SKVMVELLGSYTEDNASQARVDAHRCIV RALKDPNAFLPDHLLTLKPVKLEGELE HDLTLTIVSAKLASYVKFYQNNKDFIDS LGLLHEQNMAMRMLLTFMGMAVENKEIS FDTMQQELQIGADDEAFVIVDAVRTKM YCKIDQTRKVVVSHSTHRTFGKQWQQ LYDTLNNAWKONLNVKNSLLSLSDT
13503	27404	A	13652	1	377	TTASGSGVKGSTMSAEVPEAAAEQK EMEDKVTSPKAEAEALKARYPHLGKPK GSGDPLAKRLQKQKQVPSGDMMAKAK MKNKQLPTAAPDKTEVTGDIHTPPQLP QRKPSLVASKLAG
13504	27405	A	13653	424	596	SLKNYGLSCRKKKKGAVKKIIIVQAW LMPVITVLWEAEVGGLEARGLRPTRAT W
13505	27406	A	13654	190	448	LRSPYAPHLGSPFLRIRKRGHSHCLAG AAGPORTALCGLSAPLCPPSPTPPGAGA PRYCSGSDAPPCLLRGAGPPIPGMGDPE TS
13506	27407	A	13657	1612	563	SMPGWRLLTQVGAQVLGRIGDGLAALG PGNRTHIWLFRVGLHKGSGTWDEHLSE ENVFPIKQLVSDDEKQAQLSKLCPKDE PWPPIHPEPGSFRVGLIALKLGMMPLWT KDGQKHVVILLQVQDCHVLKYTSKENCN GKMATLSVGKTVSRFRKATSILEFYRE LGLPPKQTVKIFNITDAAIKPGTPLYA AHFRPGQYVDVTAKTIGKFGQVGMKRWG FKGQPATHGQTKTHRRPGA VATGDIRV WPGTKMPGKMGNIIYRTEYGLKVMRINTK HNIIVYNGSVPGHKNCLVKVKDSLPLAY KDLGNLPFTTYFPGDDEELEDLYDE NVCCPGAPSITFA
13507	27408	A	13658	128	2626	NSHRWTVRRRWRRRGKREQPEDRGV PMKRAAALHSPQYIIPDSFDPENQFF VTPRSSVELPPYSGTVLQCTQAVDKLP GOEYORIEFGVDEVI EPSDTLPRTPSY ISSTLNPQAFELILGCTASKITPDGKITK EASYGSDICQYPGSALALDGSSNVAEV LENDGVSGGLGQRERKKKKRPPGYYSY LKDGDDSDISTEALVNGHANSAPVNSVS AEDAEFMGDMPPSVTPRTCNSPONSTD VSDIVPDSPPFGLGSDTRTAGQPEGGP GADFGQSCFPAERGRDITSLRTAGAPCV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Start codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GTDTTENLGVANGQILESSGEGTATNGV ELHTTES IDLDPTKPESASPPADGTGSA SGTLPVSPQKSWASLFHDSKPSSSSPVA YVETKYSPPAISPLVSEKQVEVKEGLVP VSEDPVAIKIARLLENTVLIHKPVSLQP RGLINKGNWCYINATLQALVACPMPYHL MKFIPLYSKVQRPCTSTPMIDSFVRLMN EFTNMPFVPPKPRQALGDKIVRDIRPGAA FEPTYITRLITVKNSSISEKGRQEDAE YLGFILNGLIEHMLKLLSPSNEKLT TSNQPKHISWIECEQEGSEDEWEQ VGRNKTSVTRQADPVQTEITITFGGHI RSUVYQSSKESATLQPFPTQLDIOGD KIRTVQDALESIVARESVOGYTTKTKQE VEISRRVTLEKLPVPLVLHLKRFVYEKT GGQKLLIKNIEYVVDLEISKELLSPGVK NKNFKCHRTRYLFAVVYHHGNSATGGHY TTDVFQIGLNGWLRIDDQTVKVINQXQV VKPTAERTAYLLYYRRVDLL
13508	27409	A	13659	42	382	TLNLKTIQTYLTITSLGLGSDYGLAGFSA LGCHQAAVKMLTAFILIQGLDLGRSHFO AHSQCWQDSFPCDSIRHGLLLHVQOES FWFQSAERVSCITCNHRSDDTHLCSIL L
13509	27410	A	13660	178	349	DMGPCYVAQTVLKLGGSSDPPTASQEA GTTCHHAHLLSHFPLMIYRNFSFIQCLE T
13510	27411	A	13661	268	2	RQKVILSSGSLMSEMGRTVLPLKSPG MNPSSPLLASGGCWKSLACGHIIPTSSF ILMWPSPLCVSVSSSLPMRKPLLLHLRS TLFO
13511	27412	A	13662	112	483	AGVGALRMVQRILTYYRRISYNTASNKR LSKRTGNRIIVLYITKVKGAPKACGVC PGRLAGVRAVRPKVLMRLSKTKHVSRA YGSGMCAKCVDRIRKRAFLEEGQIVVK VLKQAQSQKAK
13512	27413	A	13663	2	873	SVEEFDRGCTGRGCGADARAGAAWVKIS FQPAVAGIKGDKADKASADAPASATE ILLTPAREEQPPQRHSKRGSSVGGVCYL SMGMVLLMGLVFAVSYYRYFFLAQLA RDNFFRCGVLVEDLSQSVRTQMELEED VKIYLDENYERINVPVPOFGGGDPADII HDFORGLTAYHDISLCKYVIENTTTIV LPPRNFWEMLMNVKRGTYLPQTYIIQEE MVVTEHVSDEKALGSPYIHLCKNGKDTYR LRRRATRRRINKRGAKNCNAIRHFENTF VVETLICGVV
13513	27414	A	13664	118	3	AWSLIPVIPVPREAKAGGLLEPRSLRPT WATWQDPVST
13514	27415	A	13665	1	2876	IRQRINFSRKNKWDNRKLDQAGVSELAT NQKLLVCGRYEGIDERSVIQTEIDEEWS IGDYVLSGGELFAMTLIDSVSRFIPGVL GHEASATEDSFAGLLDCPHYTRPEVLE GMEVPPVLLSGNHAIRRWRLKQSLGRT WLKRPELLENLALTEBOARLLAEFKTEH AQQQKHGDSMAADEAGRTFLRADFNMTIE EGDRIMVCLSGGKDSPTMLEILRNQQS APINFLVAVNLQKQPGFFPEHVPYLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						EKLGVEYKIVENTYGIKVEKIPGKTT CSLCSRLRLGILYRTATELOATKIALGH HRDDILOTLPLAMYPGKMGKPPKILMS DDGKHIVIRPLAYCREKDIQRFADAKAF PIIPCNLCGSPQNLQROVIADMLRDWDK RYPGRITMFSAQNVVPSHLCDTNLFD FKGITHGSEVVNGDLAFDREIPLQPA CWQPEEDENQDLDELRLNVVPEDPGRHRH APDARRFCQYLHQARYLLSVVPLDVA VTEPLANGDGLNLVLIKREVVGRFRANTVE KTGENQYRVNPNEMPADLHKIRPHHPLN RNLDPFFPLDLTNSTFSGGYVHVHKGVL SDDLKLSFQKMGYVRRDSHRLMVTALP PACQLVQVALGCFALRLECEILGEVLAQ LGTSVLPAAELLQARRASGDVASCORLA QDEEFPPLPPRGSPAAYPALDLRYDLQ EDEGSEADSLYGEPSPGPDSPPAEALAYR PPLMEQSAKLWGTGGRAPPEPPEELFQA SSPPYGALEEGLEPEPSAFSLSLRREL SRPGDLATPESSAAAPRRIRAEQVPAS AYRSVSEPPGYQGTQLPVPWRPAHPLLR HLSPAACCPCLSPARLPSRPLAACAAWR RPAALVATACTDGHASALQPPRGFALGQL QPSRSALGRQLPGWGLLGRGLGLWLP PWGSPGHSRGLES PGQPLLEVLGSLVYGR LGGQA
13515	27416	A	13667	76	289	SGTSPASPCLEMDPNCSCSPVSGSCACAGS CKCKECKCTCKKSCSCCPCVCAKCAQ GCICKGTSDKSCCA
13516	27417	A	13669	2	667	GRVDAEQSRLGATERAAAAAMNEFYDYL FKLLIGDQSGVGKSCILLRFADDTYTES YISTIGVDFKIRTIELDGKTIKLQIWDT AGQERFRTITSSYYRGAHGIIIVYDVTD QESYANVQWLQEI DRYASENVNKLVLG NKSDLTKKVVNDNTAKEFADSLGIPFL ETSAKNATNVEQAFMTMAAEIKKRMGPG AASGGERPNLKIDSTVPKPGAGGCC
13517	27418	A	13670	176	398	RYLKTQLQENNPQPTTTNRKQKTRTDTL PKGIYRRHISLWKLGTWLTVPVIALCEA NAGGRLESRRPVWATY
13518	27419	A	13671	149	247	RKGLALSPRLDCSGAITVNCSLNLQGLS NIP
13519	27420	A	13672	257	359	VASLHGWQWLTVPVITLWRKVGEEFE PRCSR
13520	27421	A	13673	142	1	HLKSGSLAKHQWLMFVIFALWEAEVGG LEPRSSRPVWATLQDPIS
13521	27422	A	13674	619	168	MFIESCCTPKIYTSFVLQSHSFAQGV QWLDLGSGLQPLSLGSSNSPASASCIQVL FVIYTSVGLVGGRLGNKVMSSNKKFV CECRGWIILPFSVPFLRFQGGWDHGV SAEKALQAGRTAGHRVGPPLGAPCGGA PCTTPAWRS
13522	27423	A	13675	3	370	ARALLHPRHLQWQCLCHQGTGGCPOQS PSSGRADLLSPALRGVPPGSGFTF HFLGCSIFNCLPPIIRIAHKSFDALLE TLGPCRAWRLMPVITLWEAKVDRILLES RSSRPSWPTW
13523	27424	A	13676	3	281	IGLRPELSVSLGRQRLTAIRLQPLPAR

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						TPCGFLRARVALALMADETDLPLPLRLE YSGMITAYCSLDLFGSSDPPTLGSVAG TTENCCED
13524	27425	A	13677	272	389	YCRQIEKSKKKRCWLGTVAHACNPS*TWG GRGGRITRSRD
13525	27426	A	13678	261	363	NSWGHWRLWLTSPVIALWEAEVGSPEV RSLRPV
13526	27427	A	13679	149	44	SCVMSVSVLKKMYLWGAHACNPS*TLG GQGGRTA
13527	27428	C	13680	118	267	MSHCTWLCVCVCVCVCVGYAYMYTYSF LRNDLFWLSRLCSGYSOQA**
13528	27429	A	13682	16	346	NHHLTPHPHLDINDFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFLKKSPRPAGKKKKKKK KKKPPRFFFLGAP*PLFFFLINFFFF LCKISLVYNRRGGPCLSRFLFKERKS PL
13529	27430	A	13683	244	140	GRVDVFHHVAQAGLKLSSGDLPAWPFK ELRLQV
13530	27431	A	13684	191	777	NSDEHVYRCVLYGHRKLSFLLSKYLRSGLA GVLLPLDAVDMKEIEEQFANLHIVKCS LGTKEPTYLLGIDTSKTVOAGKENLVAV LCSNGSIRIYDKERLNVREFSGYPGLL NGVRFANS CDVSYSACTDGTVCWDARV AREKPVQLFKGYPSNIFISFDINCNDHI ICACTEKVDDALPGFGCDARMEFLQN
13531	27432	A	13685	150	253	VGWGLWLVPVPIAFWEAKRGESLDPRNL LPCWAT
13532	27433	A	13686	500	321	IEMGSHYVAQAGLELLSSSNPPTSVSQS AGIVGMSHHALAAISKSSDASITSHHPM TTP
13533	27434	A	13687	6	424	MSLLQCGGIRCFKMPPEKASAPAPKKGS KKAVTKAQKKDGKKRRKRKESYSVYVY KVLKQVHPDGTIGSSKAMGIMNSVNDIF ERLAGEASRLAHYNKRSITTSREIQTAV RLLLPGELAKHVSSEGTKAVTKYTSSK
13534	27435	A	13688	178	293	TVYSSQAGLMTVLVTATWEAEGGSLQV RSLRPAAWAT
13535	27436	A	13689	663	144	KELSAVSAGLPHSCSGCGCGGSSVACV PAAPAAAGLCSCRAQKVPVPPSLAGWPP GVNAPPPVCCSSVRLHVCQSDRLWVRLA ARRGTLALLRSALKAAATLACQSVRNSV RPSESRLPTSNAASLFRSSVPTVLSHSV PLAASLGKRRACGGRHSAVAVLSVCL SLFT
13536	27437	A	13690	125	3	FAHQGHAPGQAWLRLVPIFVLRFAELGG RPEPRSSRIARA
13537	27438	A	13691	136	24	GGPPPPPPPPPPPPPPPPPPPPPPPPPP FFPGKLQDDFYVVK
13538	27439	A	13692	144	1	MLKIVQSGECLTLKFKNFCLLSLCTLFF TLIALTTLPLPISPFILIL
13539	27440	A	13693	1476	380	NSWSTLASELTLMAATSADPERKSAQAS AAMWATLPLLCAGAWLLGVPCVCAALC VNSLEKPHFKSWMKHKRTYSTEEYHHR LQTFASNWRKINAHNNNGHTFKMALNQF SDMSFAEIKHKYLSWPQNCSATKSNYL RGTGPYPSPVDWRKGNFVSPVKNGQAC GSCWTFSTTGALESATATGKMLSLAE OQLVDCAQDFNNHCGCGGLSPSAFEYIL

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						YNGKMGEDTTPYQGDGYCKFQPGKAI GFVKDVANITIVDEEAMVEAVALYNPVS FAFEVTDQDFMMYRTGIYSSTSCHKTPDK VNHAVLAVGYGKNGIPYIWKNSWGPQ WGMNGYFLIERGKNNMGLAACASYPIPL V
13540	27441	A	13694	87	2	PGWAWWFTPVILALWETREAGGSPEFKSL
13541	27442	A	13696	130	2	CNLTIIYIQVCWAWMLPVI PALWHREP GGSPEVESSRPALV
13542	27443	A	13697	282	107	GLFKCPGTVCRLKRVISYQLSITCLSM MEHSGTILAHCSLKLGLSSDPPTSVSRV AS
13543	27444	A	13698	198	3	CSITVNKVKVMTLFRSSMSLEIVCDIDL AVLRRLDGLSLQDPPFRPTPLCSLSPSS WDYRRPLV
13544	27445	A	13699	2	120	ARGDGVSLWLPRLKNCAGISAHNCNLRPT GSSDKNFKTRF
13545	27446	A	13700	60	341	PDMGLEDERKMLTESGDPEEEEEQEEL VDPLTTVREOCEQLQKCVKARERLELCD ERVSSRSHTDDDCPEELDFLHAKDHCV ALKLFNNLQ
13546	27447	A	13701	6	540	KNSRTLQCGGIRGSLCRPRKPGVGGTQ TRAVRPVAVCSADSRPHILPLRRADKDS LVLLGRVPAPHPSSRCWFLAWPAGTILLA SCGSDRIRIWTEGDSWICKSVLSEGH QRTVRRKVAWSPCGNYLASAFDATTCTIW KKLTIRIYNI LRKLEACTIPLCCALKYG CLEEQQLHS
13547	27448	A	13702	239	346	AKRGWLMEVLPALWEARVGKSLERPI SR PLNATWQN
13548	27449	A	13703	210	300	LMNVISALWEAKARGLLEPRTLRFPAWAT W
13549	27450	A	13704	141	440	PSAFEHFEKINLYFLKFCISOGFFERQN NRDREIHRERYERDRHREYERGLRE LAHVIVEAKPHHRPFITWETLGCWWSG SVQVQKPWEPGLMV
13550	27451	A	13705	204	438	LLNVLLTQLFFFLSLRQSCSVAQARGO WYNHGLSQPSTHGASNPPTSASQSGVTT GMSHDHGLFLHFSTLDIFSSL
13551	27452	A	13706	1707	1821	AKAGGSGHLEILANAVKFLCYWECKMAG PWWCAPVGG
13552	27453	A	13707	167	334	IRKANFKILTEIGTWQLTFVPIALWEA EGGGLLEPGSPSLVFLFILTILMRKK
13553	27454	A	13708	224	344	KDTAMEEEIKDTEKTGKFWLGAHAHACN PSTLDGQGRQIA
13554	27455	A	13709	1476	380	NSWSTLASELTLWAATSADPERKSQAAS AAMWATPLLCAGAWLLGVPVCGAAELC VNSLEKFHFKSWMKHKRTYSTEEYHHR LQTFASNWRKINAHNNHNTFKMALNQF SDMSFAEIKHKYLNSEPNQCSATKSNYL RGTGTPPPSVDWRKKNFVSPVRNCGAC GSCWTFSTTGALSAIAAATGMLSLAE QLLVDCQDFNNHCGSGGLPQAFEXIL YNGKMGEDTTPYQGDGYCKFQPGKAI GFVKDVANITIVDEEAMVEAVALYNPVS FAFEVTDQDFMMYRTGIYSSTSCHKTPDK VNHAVLAVGYGKNGIPYIWKNSWGPQ WGMNGYFLIERGKNNMGLAACASYPIPL

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						V
13555	27456	A	13710	763	257	YEKILKLTADAKFESGDVKATVAVLSFI LSSAAKHSVDGESLSSELQQLGLPKHEA ASLCRCYEEKQSPLQKHLRVCSLRMNR AGVGRVVDYTLSSSLLQIRGKSFWCHCG WKVATCPQGPQAPACLPFPSSKTKFER SSLARTESRPKTLMKLPWAEKEGVRP
13556	27457	A	13711	133	401	VLKSGNPYVGLSTNHEIKGEGCAWOL TVPALWAEAEAGGSLERPSLRPAWATS WLPREIKLDDKNGCOPSKITQGGPMVA SGSLK
13557	27458	A	13712	212	74	RRINLAPPVRLKGPFPFFFFFFF FPAMGNPLFLFNS*FORT
13558	27459	A	13713	324	141	DRVLFRLECSGVITARYRLNLLGRDPP TSASLIAGSTGTCHAWLSFSYLPTYVF FIIL
13559	27460	A	13714	299	431	IRLIWLSAVDHACNSSTLGHHGVQMTKG QDFETNLANTANPHPY
13560	27461	A	13715	133	1	ILVWAWMDPAPVPLWAEETGLLEPRS LRPAWATWNTISTKN
13561	27462	A	13716	18	165	IFLPHTHTHTHTHTHGYLLALSGETFL SVLYMASERECDTYNLMENK
13562	27463	A	13717	119	1	KPNVSQAQNLAPVPLALNEARVGLFEP RSLRPTWATQO
13563	27464	A	13718	271	64	VLRISISTNLEILAKTNPPLQILMKPRK RWGTVVHLRAPVGDQPDHSETPSLLKI TKISWVWNRTPVI
13564	27465	A	13719	21	209	KDGFPGTGGSETNESVENTECCSVTQAG VQWHDLSLQPPPPGPKFRFSLGLPSSW DYSRND
13565	27466	A	13720	391	151	RGFFLKGKKKNFFPIILGKKILGSPGK KGEKKKKRGGKIFFLKKTPLGFFPKKKV LGEKKNPYSGVGGKKRGGPPPH
13566	27467	A	13721	109	2	RRLGVAHACNPFSTLGGEVGGSGGPGNC QQVTKVS
13567	27468	A	13722	69	369	RDILQADGASHLFPPTPSLNAYIIFSSP IGPHTRPHYATPTYLFPPTNNLIKKKK KKKKKKKKKKKKKKKKKKKKGGGPF KKTGGAIPFGGGGK
13568	27469	A	13723	58	1208	FWNENSPASELAENGGGSVTSVPRLEDY LTPQLYKLTGVSGSPRANSRDFHRK TYKTPSANMVLKVELVTGKNGNGBA GEFLPEDFRDGEYEAANTLEKQEDLKITL LAHPVTLGEQWQKSEKQRAELKKKKLE QRSKLENLEDELEIIQLKKKKRYKTKTV PVVKEPEPEIITPVDVPTFLKAALENK LPVVEKFLSDKNNPDVCDYKRTALHRA CLEGHIAIVEKLMAGAQIEFRDMLST AIHWASRGGNLDVLKLLNKGAKISARD KLLSTALHVAVRTGHYCAEHLIACEAD LNAKDREGDTPLEDAVRLNRYKMIRLLI MYGADLNKNCAGKTPMDLVLHWNGTK AIFDLSRENSYKTSRIATF
13569	27470	A	13724	400	135	KWNGKBLNGVDGIGWDNNMYKGLFPH ETEWNELERNGLWNGMSMDGICNGGIK WNGIECSGMLWNGMECIGMECPLEWIR VEWN
13570	27471	A	13726	186	344	SASLGWLRCRDCRRSLVSVLNVQAQGV

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						QWRDLSSLOQPPPSRLWPPKVLRL APFOKKVFSSKFFPGQFFTFAPPNNRKKLFF SPERKIVPPKFFLWAPLFFFTTTTTTTTT TTTTTFFWYSRTDYK RIMFFIFFYTTTTTTTTVFFLFTTTTTTKR PPPPFF RLCEASLSPVPEILGGALPSAKRTSYLL LSTLCLLSETASRGNLTLGLHRSDDY NSVRSQQSLYSACPIVTTIHGTCTYGGK AKCKK AVHRCKKNGRGWRNLTPVITPLWEAEV GGPLEPRSLRPLALAT RKKACVCFMNDLCLPLDNTFKNVLSSQAW WCVHLVPTIWEAEAGGSLEPRSLKLQCP VVAFVNNTCPANAT IFFFFLFFYFFLFTTTTTFRSRHCTLQ GQSETRSQNKQKTKNKQTKNLP GTVTPEEPKMGDQTPRGLPRPERTLGR LSTSESRVDTPRVGGSSGGRTAPWGP PRERGRVAGSSLRACNFTSTNTIISVG LWLTVPITLGRAEAGGSPVRSSTHAS KLYKNNFFFRFTNPPPLLKGFYLYNFF FKKKKKIVKKKKKKKKKKKKKKKKKKKK GRPLAIKNYPRV EGVSLLLPRLECRGTISAHCNLRHRRR CTPASASQILRLKQENHLNLGGGGYRD PIKLQRTAS PDRPALPTRPGGWITWGREVRDQPGQCG ETPSLLKIEKLACDGTCLQNCLQNNN SNNKVGIR WGSNITQALFEHLCSFGHTSLPAVPCP HQACFPPLPLICRGI IAHCNLGLGSS DSFISASPLDGTGLHPHARLFSFLLWY RWGLTWMPPKRSLSLCKLPSILLADAW SQHFGISRAADLSSNVGDEQEHGKNS LYKKKINQGWAWLTPVIPPWEGQVG GSPBEGKELTPLRLNLGKPHL IKKEALSNAWMLTPVIPALWANAGGSP E FFLGSFFLFTTTTTFGGGGKKTKKFFSQD PLGPPKILGGGGFFSFFPGGFPLKKGK KSPQNLFFLLKNPFPFFPPPKPLWGP YRSCVLLQONPPLFYQSWNFS.CVCVC VCVCVCVCCTGSLKKFLLTQKKR TKRKGYKTKNGYAWAWLTPVIPALFI AEGNLILQMQQAQPEAGCGVCVCVCA CMCVCVCVKVFF RTHHTHTHTHTHTHTINPIHVFWLLKY PKIQSHQFHISAFQDPLL VCGWGWLTVPVIALWEAKVGS KNKIEQMKWEMRGEAVHSCNFTLGG QGEFETSLVNMMPKCLYKKMQKISQVCS C FOHPFGLSQSEMAAVKASTSKATRPWYS HPVYARYWQHYHQMANMQSHHNAYRKA VESCFNLPWYLPALLPOSSYDNEAAYP QSFYDHHVWQDYPCSSSHFRSGQHPR YSSRIQASTKEDQALSKEEMETESDAE
13571	27472	A	13727	380	168	
13572	27473	A	13728	324	219	
13573	27474	A	13729	2	270	
13574	27475	A	13730	134	3	
13575	27476	A	13731	429	641	
13576	27477	A	13732	188	32	
13577	27478	A	13733	341	3	
13578	27479	A	13734	208	2	
13579	27480	A	13735	16	212	
13580	27481	A	13736	22	214	
13581	27482	A	13737	386	51	
13582	27483	A	13738	204	431	
13583	27484	A	13739	69	159	
13584	27485	A	13740	32	285	
13585	27486	A	13741	372	213	
13586	27487	A	13742	29	237	
13587	27488	A	13743	322	183	
13588	27489	A	13744	305	373	
13589	27490	A	13745	172	1	
13590	27491	A	13746	285	1045	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VECDLSNMEITEELRQYFAETERHREER RRQOOLDAERLDSYVNADHDLYCNTRRS VEAPTERPGERROAEMKRLYGDSAAKIQ AMEAAVQLSFDKHCDDRQPKYWPVPLK F
13591	27492	A	13747	2	305	GRVGSFVSURDVELSDPARERGERMPVAVG PYGQSQSPSCFDRVVMGFMVGCAGVMAAG ALPGTFSCLRIGMRGRELMMGGIGKTMQ SGGTGTFMAIGMIGIRC
13592	27493	A	13748	2	305	GRVGSFVSURDVELSDPARERGERMPVAVG PYGQSQSPSCFDRVVMGFMVGCAGVMAAG ALPGTFSCLRIGMRGRELMMGGIGKTMQ SGGTGTFMAIGMIGIRC
13593	27494	A	13750	238	423	AVSWDQLTWGTGVOEKRIQAAAGWLMFV IPTLWGEVGVSGPEVKSSRPACPHGKTP FLKKMQ
13594	27495	A	13751	455	248	ISVGFIFGIFOLNFCFLPYGTPFLSEKKFF IMETGSRFVIQAGVQMSYSSPQPFQFG FESSLKPPHSGVK
13595	27496	A	13752	2	98	IPTPTIHTHTSHHTHTHTHTHTSFLYMP PDLK
13596	27497	A	13753	196	2	IWAPPKPIFKKKPPLFFFFFFFFFFFFFFF FFFFFFFFIISFIWPLTRKQLERSWVF FKDSACSA
13597	27498	A	13754	917	379	KYKCKSLQRNLLLVGCKKYSLSYRRHKL HLVTHGRKKPAAVNSFFLFFSFFFFLL LVRNTEITKKRVNLHETKADAESCNDQC TTSSETASELQIRSGKHNSGKWAGEGA AGRRREGERMEWTEMRRGARRRGGRER EMERARVRGGEEREKEIDLYKVTSKIE ETKLGNNLLKL
13598	27499	A	13755	175	21	KKKNFFFPFVILGPPKVFFKRAPLFFF FFFFFFFFFFFFFFFFLKKSWRLAI
13599	27500	A	13757	234	341	EEGHWQWLMFVPAVWEAEVGGLELPRS LEARAI
13600	27501	A	13758	1	365	PAPNRGCHIQDRATNSTELGANQCFFF SPRPPSLEKKTPEINKRPAQPSNPG NLGTREGDSWAGTTRCLRRDEGDTYR TEPPTALSWGQTRAFFFPALPAGKKRH RNLLKTOFF
13601	27502	A	13759	87	181	SHHTHTHTHTHTHTPTLHVHVFDMET LGL
13602	27503	A	13760	1	228	ARGERERERERERERERERERERERE RYREGGRLLIMGEGETERATDLYHTTP PSIKAWRLCEPRPRAGILCGRNIF
13603	27504	A	13761	383	197	RCDPPAWVSQARIIGVSYRAQAPATSVL MGEDFLDPVIAFVRLAPAVLLSKLSE VSVAMT
13604	27505	A	13762	276	57	YAVLGGGGGRKNLFVVFVFLFFFFFFF FKCGGFLMPLGEDRGNMGFFYFEMVG DKTKLPFKKKKKKKR
13605	27506	A	13763	377	209	PRPAYGPAFLFTGFSWNPFFFFQMESE SVAQAGVQVCYLGSLQPPFPWPGTLN MEKYNVHPHSGILHSHKEQAALPTIAK RWRQPSYPSIDWKNIMSIIHTVEYYTAM KRNKQLYSQ
13607	27508	A	13765	390	284	ESGGHFLSLSLSYTYTYTHIYTVVCUYI THTSHTI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
13608	27509	A	13766	350	41	VYVILQENRNTQNRLLPKSTELCMLLQ MLLFILNTINYPLPLWQCYHRCSFFLLK TGSFYVYTOAKVRWLFTGMITVHCSLKL DSSHPKKVLVLQELATVAS
13609	27510	A	13767	330	156	KITQAWWCVHVVPDNRREAEVTGVIRGR MRLPLEGACTNCVPSWEKEQDPVSHNEK K
13610	27511	A	13768	25	292	KCFFLSWRGGSRLOQHFGRPRADHLR PGVPDQPGQHGFLVVKMSDKPDLSEVK FDRSKLKKNTTEENKTLPSKEIFFSLVG VNIQD
13611	27512	A	13769	585	680	KCLGSRTRWLTVPITLWEAAGGSLRP RSS
13612	27513	A	13770	488	359	PSPRERKFLFFKKKGWGPFPFKKNR GRGPQKQKGPQKPKP
13613	27514	A	13771	794	515	PDGLEDQKMLTESGDPEEEEEEEEL VDPLTTVREOCEQLEKCVKARELELCD ERVSSRSHTTEEDCTELDFDLHARDHCV AHKLFNNLK
13614	27515	A	13772	130	397	VVGLTPLCFMCRASLRPHSKPOARKTK KKKKKKKKKKKKGGSLKKKIFGGA GATKKNFPPKRGQKKNPGFFKNEIFF GGGAI
13615	27516	A	13773	376	145	TRVGGGCSQRLCHCTPSWATEPNPVS NNKIPLELFPSSQTFPHFVRNWKRGNN WLSNYSISSTVTRHFPPLFQF
13616	27517	A	13774	1	247	GLQSLADLLSGLLQKVCFLNSGIMDL LLYVLPFTFETGSCSAQARVOWCEHSL OPHTSASDPPTSATTCHHARLIW
13617	27518	A	13775	376	145	TRVGGGCSQRLCHCTPSWATEPNPVS NNKIPLELFPSSQTFPHFVRNWKRGNN WLSNYSISSTVTRHFPPLFQF
13618	27519	A	13776	107	468	EKARSFERARDQGGTERDRNREKRL PKLREELPWVSGGWRCPWPHQGWSHED NPGWGIPTGPSVVGWGEKKGPGGRSHKY GTGRKCELGVSIGNSAFTLLHFFYFKH RKERKQI
13619	27520	A	13777	125	2	NIFFPLFELYFKCHWARLTPVIALW EAKEGGSPVRS
13620	27521	A	13778	166	74	GRICYSLSLKHHTHTHTHTHTSHISF IP
13621	27522	A	13779	1	341	ARGERERERERERERERERERERERE RERERERERERERERERERERERE RERERLSFSLGGGALKKRIFLCVILE GKHLPLTLTGTGFGENTHTLSMKTREGG FICAGDERRSASVMRAYIYRECEPHTH V
13622	27523	A	13780	614	337	RRCSALCYRRHHNRKVIKRSKQASVS PHEHLRLSLLEVRNVGLGHSIFPHSLR MYVCMYVCMYVCISYLSYLSYLSYLSI LSISISSR
13623	27524	A	13781	390	158	VLIRLSWGRICFQAHSGCWQNSGCSHK TEGLCLLLAGSCSWLLGGALKWASKEE FYTMQHSQSDTLPLPYSIH
13624	27525	A	13782	308	163	TKFYLLFFFFFLLFFIFFFFFFLKKKK LFFIQGGKKIKPGTTELG
13625	27526	A	13783	45	277	IASGPRFFFLRLDPFKAPVFGGGGGT PFEYQNFVAYIKQKQNPFLPGCDLFN

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13626	27527	A	13784	413	218	APQLIKQLSQLGQRYPKKPLL PNFPFPLFFSGKFFFAQNLFFGFFPPP GEGKAFPGQGCPCVGGGFGAGPTFFFGPP AFPEILYFF
13627	27528	A	13785	1011	1368	IDWENDLTPMVLCHGSPSYNYSFSQNI FPISANFPPIAHINLTLLQLVSELSHKI ILRHFYIKPKIDILNLYLIPGVWLEDL CKSTAI CRYLCVCYIYHLIYHTHTHIH YTHRL
13628	27529	A	13786	161	425	HWGSCYCPGVPHLYFKLLLLLVLELM CVLPDLLPRLCSGMITVHCNLEFLCTSY PPISVSQTKKKRPFTLPPLNLQICLP LRGE
13629	27530	A	13787	70	311	DLISITLVISPNKFIYLSIYLSIYLS IYLSIIYLIPISTNLNWLISWETLNKT RLNLFLLTQNNINWPKLLVLSALI
13630	27531	A	13788	25	219	RNMAAATLTSKLYLLERTSTFALTYI VGVMFFERAFDQGADAIYDHYNEGLKWK HIKKHYENK
13631	27532	A	13789	279	138	RRLSLALFRWDCLQWRNLGSLQALLPG FTFPSCLSLPSWDYRPP
13632	27533	A	13790	138	28	GGWVRWLTVPVIALWEARVGGLEPGSS KKEGKKKEV
13633	27534	A	13791	133	7	YSCQRCLTHGQAWLITVISAPWEAKAG RLLEPRSVRSAWAT
13634	27535	A	13792	86	290	EHVHRTLEASVSGWGWLTVPVISAWE AEVGGSLGEOEFESILGKCSPTSLTIT TTESLGSFAATS
13635	27536	A	13793	150	37	KIIYPSQARWLMPVIFALCEAEVGRLL PSSRLAWAV
13636	27537	A	13794	216	77	PTQHPTEGYMIKQQTVYHECRMWANS CLLPEGLRAVTPWCHAP
13637	27538	A	13795	251	347	VARAWGLAPVIALWEAEVGGSPGSRSL KPAL
13638	27539	A	13797	177	274	VQWMSVVPATQAEAEVGGSPGPSRLPA WATY
13639	27540	A	13798	307	406	KFKGWNWMLMPVIALWEAKAGGSPES RSLRP
13640	27541	A	13799	194	3	FFFFFFFFFFFEMGSHYIVQARVQWLTDA NIVHCSSLQLLASDPPVSTQVGLQACA DDAQPIE
13641	27542	A	13800	333	198	LPSEVFFFTOTSCSVTQAGVENCDLGS LHSSLGNRRRLCKLIK
13642	27543	A	13801	1	335	ETERGRERETERGRERETERGRERETER GRERERERERERERERDRERERERER GKONDRERERERETERVGDVVCVCPHP NLILNCSFYISHVIREGLKTYINVGGS FPTLCSG
13643	27544	A	13803	14	454	RVFFDRSRYSRTLGSTHASALLGLILVY RSHLISLLCLEGLILSLFIATLITLITL THSLLANIVPIAILVFAACEAAVGLALL VSKKKKKGAPVLKNPNGAQSLRGQARKY FFPYREPNKNLPGNLGKEPFLGGGDILG QPPYKN
13644	27545	A	13804	1474	1661	TDHNSHLLCKCKNCIFSTLNYIYRREH FSIVIFPCYICVVKVYIRRELRCLYF LLYMCC
13645	27546	A	13805	360	3	LWGKRGGPPSPPPPPFFFLFFFLKKMG

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						GGGFFGGFPWGFPGKEIFFFFFWAPQK KKKKKPPFIWGGGPEFFFFPPPKQK KKKKKKKKKKKKKKKKKKKRAARWPA RSRSSA
13646	27547	A	13806	1	425	RLGGVALRISAADQAFVSGEFCGGKLLRW CLVTDPFPPDSCCTTCSYRRSTPGCSPPG SRGLSEGGSSVLSQRVLSAMKHVLN LYLLGVVLLLSIFVRVMESLEGLLES P SPGTSNTTSQLANTEPTKGLPDHPSPS M
13647	27548	A	13807	5	313	EKPYLGGITFTSKTTHLYEFTPTTIIIV KEYSTNYVLLIGNTQITKIYHIVERKFS MTPIYKQDLAQWLTPVIPTLWEAKPGG LLEPRSLQSSYSILILIL
13648	27549	A	13808	182	314	VITOLDKTERAQLMPVILVLYEAEVGG LLEAMSSRPAAWATKW
13649	27550	A	13809	219	1812	LPPPESGAMSGFNFSGTGAPTGSGTFTGT AKTATTTPATGFSFSTSGTGGFNGGAPF QPATSTPSTGLFSLATQTPATQTTGTFT GTATLASGGTGFFLIGAGSKNLNSNTAA TPAMANPSGFLGSSNLNTAISSTVTSS QGTAPTGFVFGPSTTSVAPATTSGGFSF TGGSTAQPSGFNIGSAGNSAQPTAPATL PLTPATPAATTAGATQPAAPTPTATITS TGPSLFASLATAPTSATGSLCSTPTVT TAGATPACTQGFSLAKCAAGSTSTTS TAATATATTTSSSTGPAALMKPLAPA QIPSNATAAVTAPPGGAGAGAAASAM TYAQLESINKNSLELEDOERHFLQQT QVNAWDRTLIEGKEITSLHREVEKVKL DOKRLDQELDFILSQCKELEDLLSPLEE LVKEQSGTIYLOHADEEREKTYKLAENI DAQLKMAQDLKDIIEHLNTSGAFADTS DPLQIQICKILNAHMDSLQWIDQNSALLQ RKVEEVTKVCEGRKREQERSFRITFD
13650	27551	A	13810	134	263	KNSLFKKKNGRPWPLMPVIPALWEAEA GGLLEPRGLRPTWVT
13651	27552	A	13811	210	51	TLSHRKPISPEAYFARVRGFILEVSETR NPPIGWTRWLTVPVIPALWEAAG
13652	27553	A	13812	241	139	LHEAGLAPMIPALWEVKVGGLEPRSPR PAWASW
13653	27554	A	13813	539	256	RTTOMSTAAGFTEAPNWKQPRCPWTEEQ TNKMSLSLHAMECASAMKWEVLIPAVR MARENSRRKPDMDHDIWSVWSAGEWLP LGRSTGKGS
13654	27555	A	13815	63	369	VRETPKTHYLEEISSPASPTAIPQSL FSFFISPPSLATGSGHSGHPVHSLHP PETEPSVCLWAGPKVPPGAAGKGS SNPLVIRSLAPPASL
13655	27556	A	13817	258	3	AESAPFFSTNSLFFTHTHTHTHTHTH THSLRTRWAPSQVCRQTSQRGGECVG PTAFAPSPFTLLKPHPSNVHLPSQPRR
13656	27557	A	13818	516	665	WFKSGSFWLGHVAHICNPSTLGGQGGWI TSGSRSTVTTTTSQTCA
13657	27558	A	13819	295	361	WLTPVIFALREAVTGGSLPRFS
13658	27559	A	13820	166	368	GWATQHSAGYVSSSSIGALCLGESCS VTQAGVQWCDLSSPQSPHGPGRFLCLS LPSSWDHRGDL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
13639	27560	A	13821	133	530	RKYCGQCLNMLNANNVSSGGDQSRVAY RSSHGDRLPRASALAMVSGDGLVSRPE AIHLGPRQAVRPSVRAESRRVDGGGRSP REPDGGRSRQARFSPYPIPAVEPDLRL SVLQQLRIALGGVIAARISV
13660	27561	A	13822	76	1958	ROELIWLCSPPGGDRFLQKSNWIFRPV MADKLTRIAIVNHDKCKPKKCRQBECKS CPVVRMGKLCIEVTPQSKIAMISSETLCI GCGICIRKCPFGALSIVNLPSPNLERETT HRYCANAFKHLRLPPEPSSEVLGLVDTN GIGKSTALKILAGCKPNLKGDDDDPW QEILTYFRGSELQNYFTKLEDDLKAI KPQYVDQIPKAAGTVGSILDRKDETKT QAIVCQQLDLTHLKERNVEDLSGGELQR FACAVVCIQKADIFMDEPSSYLDVKQR LKAATIRSLINDPRYIIIVVEHDLVLD YLSDFICCLYGVPSAYGVVTFPSVREG INIFLDGYVPTENLFRDASLVFKVAET ANEEEVKMCNKYKPGMKKMGFEFLAI VAGEPTDSEIMVLMGENTGKTTFIRML AGRLKPDDEGGEVPLNVSYKPKIISPKS TGSVRQLLHEKIRDAYTHPQVTDVMKP LOIENI IDOEVOTLSGGELQVALALCL GKPADVYLIDEPSAYLDESQLRMAARVV KRFILHAKKTAFVVEHDFIMATYLDVRV IVFDGVPSSKNTVANSPOTLAGMKNFLS OLEITFRDPNNYRPRINKLNSIKDVEQ KSGNYFFLDD
13661	27562	A	13823	3	292	KCNDYVHEPPRPAPMQTYQVDRCCFVS TINLLVCGERASLPVSSELVPSGLAEVW MKAVLAPERSGKLVLOQVPEYAEAIW ARPACRGLVESA
13662	27563	A	13824	245	91	YKNGFGPPGSGFFRPDPFFFEVPHFFF IIPFFFPFFFPFFSFLGCPMYV
13663	27564	A	13825	276	100	PGGKKKTLSPKKKSTIYLIHTHTIYIYT HTHTIYKYIFVCVYICVSIYHTHIVPR IFS
13664	27565	A	13826	202	375	IYNTYIHTHTHTHTHTNYLYIQSGDC IYAVLLGELSFIYIFVPLSSLSILFHL TY
13665	27566	A	13827	278	34	KPRGLSPAGVSAQRAGPHSCPRLPDPR TELQVRQIPALVGSFAFOGRRGRKGPVG GSGPSRPRAPPQPRPGCCQCTLLQI
13666	27567	A	13828	62	307	GGARAIPLNVPHLKRPMFFLELCLSTKC PVGTPEALDSLLRLYNSNTFCWQWLMP TIPALCKAEMGGLLEARSLIPAWAT
13667	27568	A	13829	386	478	NRIGNVSHACNPSFLGGQRRIMRSGDQ DHS
13668	27569	A	13830	364	484	NPNIWLGWANWMPVIPALWEAKAGGSL EVRGSGPAANMV
13669	27570	A	13831	33	486	PARSAEFGTRERERERERERERERERE RERERERERERERERERERERERERG VICVCPCALLCVRESPLSQKKYCVCVF VVRYTESLALSFFCLGRCLALLIFLEGM WRKIWAPSLSLCVGALFFSQHPFFWC LCVLSLVRPLSLSGGVFVSQRALI
13670	27571	A	13832	6	718	YSAVEFAMAGVAGVPLRAMGRQALLLA LCATGAQGLYFAGIGETKRCFIEEIPDE

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						TMVIGNRYTQWMDQKEVFLPSTFGLGM HVEVKDDPDGKMLQVVLSPRYGSEGRFTF TSHTPGDHOICLHNSNTRMALFAGGKLR VHLIDQVGHANNYPETIAAKDKLTQL RARQLLDQVEQIQKEQDYQYRERERFL TSESTNQRLVWNSIAQTIVILILTGINQM RHLKSFPEAKKLIV
13671	27572	A	13833	17	130	RLQEGFTRERERERERERERERERERE RDTHSFLHG
13672	27573	A	13834	283	460	LVLRLAICKNYSLKRETFEGVAHVNP STLGGGGRTARGQEFKTSLDNIARPPS LQK
13673	27574	A	13835	3	435	WPRFCTALQEFGTRERERERERERERE RERERERERERERERERATSLRARPSF LFPSACVSHTPYVGERENLSLTLKHHTH TREKHSLSYTNASARDTRARFSEGRAPP IYSVYLTHGVFFFFFSLCLSVRHAEG AHV
13674	27575	A	13837	351	57	RTLVIHSKFTGNLSDLYYVQSEWQDLGT ADLSIMTSVLHCLPSLESIKNTDSWPSS VAHTCNPSTLGGRCRCRDQHQHSKQPS LLKIQKTARRCGG
13675	27576	A	13838	336	150	TFCYKYLWAGHCFIFRTGLPIKNFYF GQAWCLLPVISARNEAETGGSLERPSLR VAVAS
13676	27577	A	13839	310	454	HCSLGLPQVLLIILYKILGNARWLTPV IPALWEVEAGGLEARSSRP
13677	27578	A	13840	163	297	ITFFLLDLKLQGANITYYSIYLSIYLSI YLSIYLYTHTLWNLQL
13678	27579	A	13841	33	316	LDGHTERSPLLCHSLKRTSSSQGKSE LVKQSLKKPKLPGRFDAPEDSHLEXP LEKFPDDVNFVTKEKGGRGPEPTRYGD WERKGRCIDF
13679	27580	A	13842	4474	2586	DGSGSCVKMEFPFGGNQNYLTITGFSHPF LSGAETFHTPSLGD EEFETPPISLSDSDP SLAVSDVVGHFDDLADPSSSQDGSFSAQ YGVQTLDMFVGMTHTGLMEQGGGLLSGGL TMDLDHSIGTOYSANPPVTITDPMITDMT SGLMGHSQLTITDQSELSSQLGLSLGGG TILPFAQSPEDRLSTTPSPTSSLHEDGV EDFRRLQPLSQKTVVVEAGKKQKAPKKRK KKDPNEPQKPVSAVALFFRDQTAAIKQG NPNATFGEVSKIVASMWDSLGEQKQIY KRKTEAAKKEYLKALAAYKDNQECQATV ETVELDPAPPQTPSPPPMATVDPASPA PASIEPPALSPSIVVNSTLSSYVANQAS SGAGGQPNITKLIITKQMLPSSITMSQG GMVTVIPATVVVTSRGLQGTSTATIOP SQQAQIVTSRVLQAAAAAASMQPLPP PRLQPPPLQMPQPPPTQQQVITLQPPPP LQAMQPPPPQKVRINLQQQPPPLQIKSV PLPTLMQTTLVPTVESSPERMANSP EARTVEAPSETICEMITDVVPEVSEPS QMDVELVSGSFVALSPQPRCVRSGCNE PIVSKDWDNEYSNCEVCVKHCRDVF LAWVASRNSNTVVFVK
13680	27581	A	13843	54	251	EFYRNNSPSLWLCVVCVCACLFMCCLC ALTCMCVWYKSLHLSNLTQVLSSKPYDS

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13681	27582	A	13844	154	26	ISFAENPGK DPHVPTTERSEGSQARNLFVPIPTLWEA EACGSPVEVKSSNST
13682	27583	A	13845	475	225	GHTELYGGALFQLQAAIFEGGGTSCLE NPSSDGGSSAAGGVGGAGDLARSRVP SPTSSRPVSPDPSPPSLYLTPWKETH
13683	27584	A	13846	479	319	RDCRSLTHSVLSGAGVQVRDLGSLQ PPPSRLPWPPKAPRWQPLPGHHPI
13684	27585	A	13847	182	499	LLCVKLCDSCNENKALREQTAAQVQGGH SRAQVQVQGGHSAHTVQVIRSAASRRK AFSTCSHGLGMVLLFYTGGSSTYMRPTT RVSPLRGRLAADVFSILLIPTLN
13685	27586	A	13848	388	494	RDSWRWLEFLIPVLWEAQAGRLLEPR LRLAMAT
13686	27587	A	13849	198	63	HHATTWNLEDIMRNVUSQTKNKKYMI PLINWTKKVLSHREOK
13687	27588	A	13850	555	353	RCFPGAQALPAPSPAPPHVIALSPLSC GVSWPRELTAHPPEPPPPFFKHHPHQ LSVGRKGQMT
13688	27589	A	13851	169	66	LLAGSTGAQRLTPVLPMLKAEVGGSL EIRSSR
13689	27590	A	13853	12	105	IASGLHDFPKKKKKKKKKKKKKGG AL
13690	27591	A	13854	256	363	ICLFIKDSRGTQWLTVPVILT.LWKA GGSLPEKS
13691	27592	A	13856	23	436	IDRLSDSHEERERERERERERERERE RERERERERERERERERERERERE RERESSLLCVRIHTFAPPTYI.FLWETLR VCPTFCVWGALSVFSTERARIFFYTGC GSVARAPVCAHTRI.FSSRARARALCARP PLSRERRAHRVTFI
13692	27593	A	13857	91	428	PDPDTSPLATDRGETPLGATLPSVCYCG QQSFEPKTKTTNQKKKKKKKKFTPOK NPKIFPPKPCPKPGPRGENQPKTQNP KKKKKILGGGPAPNSPLGGGKKNWAGF
13693	27594	A	13859	465	43	KRVITENPOHICSAETAIPWLSQNCNF HILWGHFNPHIYITTSIYIYIYIYIYI GHVYIYTRICMCVCIYVHCITHTHIY IYIHTHTHYMERERTVCSVAQAQVQ WCDLGLQPPNKLKRFSLCLSPSSWDY W
13694	27595	A	13860	290	52	WYKYLPGTRGLIWLNLKICIGRIELLV GVFSFIYLSIYLSIYLSIYSSRSIAQP GVKRCNHSSLOPRTPOGLMHLNS
13695	27596	A	13861	108	22	IFFLFSAVKTRFSYAPKFFPYRMNV S
13696	27597	A	13862	167	33	VFTVPGTVMCVSVRLDGGAWMLTPVIPA LWEAEAGGSLEELFT
13697	27598	A	13863	448	355	FFFFFFFFFFFFFFFFFFFFFFFFFAKN PLN
13698	27599	A	13864	321	445	SQSTQACMLMPVLPALNETKSSSEFEP SLRPAAWATGHNPI
13699	27600	A	13865	380	80	MLSPSPKPFSSFLFSLFALLLWHLCL PFLSNVKGQMNDPVLGLSPTSTPSDLS IYLFCCFVCLFVCFETGFPVQAQVQ WCDPLGLKNFLPPQSP
13700	27601	A	13866	372	264	KMENPEDKNFFIFFMFIIVLFFFLL FCLTQFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
13701	27602	A	13867	161	304	LFIAEMTSHYIAQAGLELLASSNPFTSA SERTGITDGATELIPQLRL
13702	27603	A	13868	230	348	VSPFQNLVFCVERVVRVDFGWERGSK YNNGSTELHKS
13703	27604	A	13869	168	260	EVIAECYNGCFOTLSLCVCVCVCVCV CY
13704	27605	A	13870	140	16	LKYQQWRDLGSLQPPFRFKQPSCLSL SSRNCTMTDRHE
13705	27606	A	13871	143	30	KILKVVVSQAWLIPVIPALWEAEVGS LEPRISRLA
13706	27607	A	13872	158	59	HLHGCTHLLRLDAVSHACNSLTGGQ GGRIA
13707	27608	A	13873	232	115	APFFFKGAPIFFFFFFFFFFIFFFLIR KGPNQDVGVEG
13708	27609	A	13874	1619	1375	KTTWRHLEKLDMSLLRHVRHVDSSQ LFFPFQOQGLPRLCNGDIIIPYCNLKL LGWSNSPASAFAVARTTSLCRHTWL
13709	27610	A	13875	219	84	NPLQSTSTICNRAWDRTCLWSQLLRL RWEDHLSFGVPCSA
13710	27611	A	13876	166	496	KKKKKKKKGGGFLKTPGAKINRGRK KKIFQGGGQKTPGGILKKKFLGGGK KGNPPKKIKGLREKKFKRGKGAQPAQ NPGWKKISPPGFLKFFPRGRGFFI
13711	27612	A	13877	132	348	PSKKKKRGPFKRTPGGPKFNGGKGS FPLMGGGIKPNLGLGNPYLGGGTNGN NPPTIEIKGFGKCKKF
13712	27613	A	13878	287	134	QQGPFISPGPKENRMGPSPGWNGFI RSPPGAGNPGAFQDGMFPSSKKQ
13713	27614	A	13879	333	480	VHFLRSAGPRPESNMLHTLTKSKQWL TPVIPALWEAKAGGSGQGEIE
13714	27615	A	13880	1	227	PKIKCKIQHIVLVVSFFSFFLSFFQGE SCSAAGVQWHDGSLQAPPPGFKWFR FIELLGLGFHSRRMRGDS
13715	27616	A	13881	276	378	QWFWLTPVIPALLAEVGGLEPRSLR LALAT
13716	27617	A	13882	126	389	GSVLGTGCCGSLGTVCRGSLVLTIVLA SATPDYRLRLSSGSLTRITNSDLVFWL TPVIPALWEAEAGVSLPRINRPARETW EDFH
13717	27618	A	13883	414	150	ARQAPKNGNTGSPFGFLNFPKNNFL GPQKKKIFFTPPPPHFFFKGPPPPFF FFFFFSSPHASGILLCHFGRIAVAQSW LTE
13718	27619	A	13884	197	363	DLGVVVNTFMLKFKCLNVSRGHVQWLI IPVIPILWKAEGRSCLKPSRLPAWAT
13719	27620	A	13885	101	236	NIHYANFPYFGLACPEYIVRALQKQYTO THHTHTHTHTTTTSL
13720	27621	A	13887	17	140	TVHLKMWIKGLHMHVHACNPFSTLGGRG PIMRSAGLGNFCL
13721	27622	A	13888	135	1	VLHAGLKLCSSTSPSASKAGTVGTH YHTQLAQFFLFCFLIR
13722	27623	A	13889	411	276	TLYFKHGEHGFHVGGAGLELLASSDPF ALEFETSLHNKVRPL
13723	27624	A	13890	216	54	EFKLCYTLFDHSYFFLELVSGQVQWLR PAIPSFWEAKEGGSLEPRSSKHEIV
13724	27625	A	13891	3	149	SSDPRFSSSLAWGLWSMVRVPPFL PILFLASHVGSPLSPSHF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13725	27626	A	13892	166	1	LFSKIFWLLFPVIALPREAKVGELLEPGSSRPAAWATWKNPVYTKNTKISQAWOCT
13726	27627	A	13893	128	2	FSTTYNFIKLPHPVLPDLLTFLDLSAHLHPSEINSLVAQKKK
13727	27628	A	13894	225	391	HLSTHILTFPFFSLPEQWLVPIIPVLWEVKMGGLLEPRSSRPAAWATQDDPOVSRK
13728	27629	A	13895	192	1	TLVCVSSSVFKNYNNICLACWFMFTIPA LWEVSGSLLELKSSPPAWPTWWVPLKSIGNTKISLA
13729	27630	A	13896	152	245	DQSIADVLMYTHTHTHTHTHTHTLNQVPG
13730	27631	A	13897	270	406	ISTRFFLYRDRASLCHPGWSAGVQSWLPSSNSQQAQAILPQPPE
13731	27632	A	13898	232	73	EAEGRPDVTSSTFHWRLYDQTTNYHECRMWANSRLRLTPGELLKVITPWCHAH
13732	27633	A	13899	107	7	LGGQWLMFPIIPALWEAKAGGSLEPRTSRPAA
13733	27634	A	13900	62	224	FTPLIHLACNLCVLGSDPPASASQSGVTGMSHCWAGNLIHLPSRSTAICTL
13734	27635	A	13901	450	194	KRQVKSHEVKTTHVQWPGIDFGSPAWEARILPLAHQRLSGTTFWRTTEKSNHKLDELTVLGSFFKCRCLKANKDIQTKCVIGNFY
13735	27636	A	13902	300	404	AAPGRAPCKKKKKKKKKKKKKKKKAPFKRGR
13736	27637	A	13903	131	29	ALGSLQPLSPFRKRFSCLSLPSSWNSTA LTTTMM
13737	27638	A	13904	267	74	VWVLVFPFPTSISYGLDKPILINNIYVHVCVCLCMCVCCVCCVCTVIRRHCHWNMI IISQHDQ
13738	27639	A	13905	193	64	IRSHQTHKLHFKKFRILGWTWMLTPVIPAPWEAEGRSPSEPS
13739	27640	A	13906	309	424	QSTDFLENRRVGNWAWLTPVIPALWEAEVGGLEPKNS
13740	27641	A	13907	404	251	SCLISLSRWDYKHVPQPPANFVFFFEMESCVAQSGVQWQEENSISKINK
13741	27642	A	13908	471	59	GPPQAKKGRGFTPGFPQKGGSGQKSGVLGFSPPPLGCPGLPGPKGWGFWGSGFFFFFRKWEHKNLEFPFSKTEKPRRAGEARKGSQSTKYAGLSRGERQASPTLRPGHLAKASAGGWLOYTRWOGKLEPEGN
13742	27643	A	13909	479	231	QRYCMLIFCEHFGDFDLNI VFCLEKRMVGVIADFYLLSSFTGRPQWLMPIPTLWEAEVGGSLKASFTFPAWATWQDPSMF
13743	27644	A	13910	167	19	CIVLGIMLDSLWEFRQWVPSWRWFTFVIFALWEAEAGGSEVRSNS
13744	27645	A	13911	328	446	GSFSKIDLSQTNWYVPVLAQJQSEVGRLEPRSSRLQ
13745	27646	A	13912	145	460	NAFMSTCCVLVSYSELQRNLVWMLFVIPATPOAEAGRLLOPRSRPPWATKGVRALSHKOTNTKTNKLSHSGVSVFTHHHSFGILWRLSQWLLANNLATN
13746	27647	A	13913	319	210	KLGFFKGPLLFFFFFFFVFVFVFPLTVSCNPTL
13747	27648	A	13914	372	10	PNTTCTPITYGKKCCPREISYLLCHEFIRILRTFFDGESCYIAQAGKLLGSRSPPTSASGAGNTDVCCHHTQPIILFYILETG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LALLPRLILNSWSQAILLPQPLRSYFN FWLFFCLYN
13748	27649	A	13915	594	471	PSVIAYMCIQMCVCVYVYINICVCIYTH VHTPVNPVISKI
13749	27650	A	13916	235	3	EANNLIKRTYTSQWGFORTSKRPFAVRMR KVLFFETESCSVAPGVGWHDSLLQPR PPGLNRSSHLSPSSSDYRWA
13750	27651	A	13917	272	184	KTTAWAQWLTPVISTLWEAKVGGSLAEG S
13751	27652	A	13918	46	321	SRVQGTGGHRRGRCIQAGVGQEAQRKT EGPPWRWLTPVISKLWEAKAGGLEEVS SRRTWNLLKRIYYTDEREYLIPLALNT SQGSTFSF
13752	27653	A	13919	387	484	FTEIYGWARWMPVITPILWEAAGGSPE VRSS
13753	27654	A	13920	142	321	FLFSIHPLHSCWGLFSNVQSLSIFSYL KVLRYGQAWWFTPIIALWEAKAGGSLD PRSL
13754	27655	A	13921	270	412	IEDKKIYSILHTETLRRGQARWLTPVIP AFWEVKAGGSPEPRSLRPV
13755	27656	A	13922	304	396	NFGWAQWLTPVIPALWEAAGGSLEPRG LRS
13756	27657	A	13923	305	387	VWMLTPVIPALWEAAGGSPEPRSSRP
13757	27658	A	13924	103	3	NKSPFELGAWWLAAPVIPALWEAAGGSP EVRSS
13758	27659	A	13925	195	400	CLLILSGLVASCIIERHGGQGAWWLMPV IPTLWEAKVGGSLRLNLSAWGTWRNS ISIKYTELAQG
13759	27660	A	13926	294	489	KWARKMTLHKGRYACVCICVCVCVCVYT YTDIYIFYIHWPMTKCSMLLVIGEMK ILSRMWSNQ
13760	27661	A	13927	363	2	NWGPFGFPFPPPLKTPGVFFIFGAPKKK FLSTPRALKFVLLKGGFLFFFFFLKW FLVKTGSHCVAPDLELLSSSNVLSQ GAGITQMSQVQPLDLFFFFSFETGSR SYAHADAW
13761	27662	A	13928	1	218	LRFKKKTKNPKMWSVHTMEVHSALKRK EIRTOTTRWINLEDIVLSEIRVAVTGKR ILYDSTQMRNLEESNL
13762	27663	A	13929	219	408	TFCHFIATLHVYKMFVVFFSFIMFFFP LNCNKAERKKKKKNNKKKKKKKKKIS LSPPAPP
13763	27664	A	13930	161	22	WHPPASASHVAGTGTGACIHERLRQEDHF SLRVQGCSEPRLCHHTFP
13764	27665	A	13931	116	1	INTGWARWLTPVIPAFWEAAVGGSLPR STSQAWATWK
13765	27666	A	13932	181	38	PWFQRATOPKISPLPPATSALEAEAGG ALEPRSSRPAAWAKSDAWVD
13766	27667	A	13933	267	397	TVPDRTLFFIKKIHSAWPLTPVVPAL WEAEVCGSPVRSRG
13767	27668	A	13934	129	12	NIGVGWALWLTSTVIPALWEAAGGPPKV RSSRTARPMs
13768	27669	A	13935	179	1	KTYGGCIPPFGPPKKGERKKPPFFKKFF LFFISFFIFFFFFLRQSLAKMQASVW KVS
13769	27670	A	13936	245	616	DDKKKKEAAQKATEQKIKVFEQIKPSV SOPQPANSNNGTSTATSTNNNAKRATAN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
						NQPPQQQQQQQQPQQQQPQQPQQPQQ QOQQQQQALPRYPREVPPRFHQEHKQ LLKRGQHPFVEF
13770	27671	A	13937	121	292	NTDLALALALIVRLTSDDNFKNWQVQ WLMFVFPAPWAEVGGSSATNLRPAWA T
13771	27672	A	13938	421	202	GPREAPLPFPSTQGISRPLFFFFFETES RTVTRAAQWHNLGSPQPLCSIDLKLT SQSVCMEPAAILVLSQIT
13772	27673	A	13939	205	543	ILSHRRRLGWSEALFENQLLCRASSWES LGPDPDPCLKPPSPAFWGAAGGWAKST SVSEVPVPGTLLVALFLEMVGLLLGLP PCFHSLSGAPHLCEPDPGVSILPAERQS R
13773	27674	A	13940	140	2	LSQHSSEYTLPPFLYLEKXSSRPPPPQH TTPHPPPWHPDIAIDQ
13774	27675	A	13941	47	303	GLIFLIWTCTVKTSTDFRMEDCSQCI HQVTEESNKKMGFLSYANPHHGSRLLL WQHAAPWDDGVRGKPVFLSGFVSFFPP Q
13775	27676	A	13942	1488	1719	PLVSFSKNTYPCLGNNVKQKTTFCSRN KLHLVLSNLSPPAEVTVVASNLVVSQ SPONSQLPAMLCLVHLQMS
13776	27677	A	13943	127	402	QVTHPPNRTMCSMSMFLFLYLCLFLSL PFFSHLSLYAPPKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKAGGGPFFK KKIHPFGGGRIFPFY
13777	27678	A	13944	852	209	EQTVYCTRIDLQKLVFLRLEAFCLLSQ GDPGSPMMCQLQDFDLWVLRGVLPNGGE TCPGLFLYTKVEDYSKWITSKAERAGPP LSSLHHWEKLISFSHHGPNATMTQKTY DSELGHVGSYLQGGRRITITHSLGNSSR DSLDVREKDVKESRSPASVQPLYDYD YGEVGEVGRIFAGQNRLYQPEETILGSL RACFLFAAVSSPGATPPN
13778	27679	A	13945	68	260	INIFWHCVLLVLYLTAISQFLLPFCVKN IASHLGSAHACPNFTLGGQAGSELEPR NLRAWAT
13779	27680	A	13946	420	156	FLFPGVKYGSFKRAPDFFFFFLVET LSCYIAHTGLELDPSSNYPSTASQSAVI TGMSHHTWLEGACLAIPQALRILVLV PLH
13780	27681	A	13947	317	17	AGHGGSTCNPSQPIVAVPILNWRDILL QQWGAQAFIPEQLYSPQSQHTMGEMGV PGMGLEKNLKGKLPLOAQEQNSHQGLG YNFSAQPLLSLQNLVYL
13781	27682	A	13948	55	224	NFRLTSSFSYFLKMSFWLGMWLTFTVTPAL WEAKTGGLPEARSLRLVWQSKKAGSHL
13782	27683	A	13949	1464	805	RATSVRGAGRRSCGAANSFAGTGFPLR RSVLPNHFRSSREGGMAASTDMAGLEE SFRKFAIHGDKPASKGQEMNGKNWAKLCK DCKVADGKSVGTGTDVIVFSKVKGKSAR VINYEEFKALEELATKRFGKSKKEEAF DAICQLVAGKEPANGVTAKTGGAVDR LTDTSRYTSGHKERFDESGKGIAGRQ DLTDDSGVVSAYKNAGTYDAKVKK
13783	27684	A	13950	356	98	NAGPGIYFWGPIKKILFCPPAGVGLKSL KRAPLFFFFVEMGFHHVAQAGLKLLSSR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DSPTFVSQSIRITSTCEPPCLAKIGSSLRL
13784	27685	A	13951	194	48	NFLEGWPCQRLTFVTPALWKAAGGSLEPKTFPRVWAMWRDLRKPQH
13785	27686	A	13952	341	418	DOPGQHGETPSILKYKLAGRGSTCL
13786	27687	A	13953	158	323	TWLKKYFQSTNQLPFAHLLNQVLLPFG LPLPLPKKKKKKKKKKKKKKKKK
13787	27688	A	13954	231	355	VFLPQKQKQNCQFLTKGRWVWNSNIHTL EYVSAVKMKQLI
13788	27689	A	13955	493	39	PAAFSSGWAAPGSSLLKTTTPASWPFPL LPPAPVSSMAAPDLDSFPLPLCWTLFLV LCRVFSSTLAPLSCVSTSGALTPAAS SNIFSISLPHWASPPLPTARLTSAVSPE PLFPPLPSRLQRPGRGAPSHPGMSMPIL DATSNSTTSR
13789	27690	A	13956	497	372	NTKISWASWYAPVVPATWEVNSNRFOAI HSHQPPKRIGLQA
13790	27691	A	13957	438	301	GTTYLDDIMTCDYVSCLCIYICTRQOS YIYTYVYTHTHTHMYI
13791	27692	A	13958	84	466	OPLGRSGKVPQHLWEMQRLPAAFFRSF AAQGLGESVHINTPTSLSLGRFPFSSS GPGARARVTCAPCLHAARILCCFWRLGL RLKCSNVISAHCNLRFSGSSDSPASAQ VAGITGRSSLEQLLE
13792	27693	A	13959	216	28	KYVRNYVLSSIFWMQEIFHNFKKSSRT QWLTPVIPALWEAAGSGPEPRSSRPAS SIQLENS
13793	27694	A	13960	320	943	VLSFSLSDRAQRNCNRMGKQNSKLAPEV MEDLVKSTEFNEHELKQWYKGFLLKDCPS GRNLNLEEPQQLYVFFPYGDASKFAQHA FRTFDKNGDGTDFEFICALSITSRGS FEOKLNWAFNMYDLDGDSKITRVEML IEAIYKMWGTVMKMKNEEDGLTPQRQV KIFSMDKNKDDQITLDEFKAAKSDPS IVLLLOCDIQK
13794	27695	A	13961	191	8	GLFRFRRLSEEVKHCCCCCCCCCCCC CCCCCCCCCYLRLAPQSPAAPAPELH TPLPGSRNRN
13795	27696	A	13962	203	28	VWGNQHFQFVVPVRKKVCFPPFLNKLRL GGFFFFFFFFFFFLVINDSWVFLGEGDLA GS
13796	27697	A	13963	18	171	GIRHEERERERERERERERERERERERH PAREIDMCVSKRDTRGALCALF
13797	27698	A	13964	25	299	HDFTCTRERERERERERERERERERERE RERERERERERERERERERERERERE REREREREREREREHTLSLYIMCV FLYIPLYFSFLYIHTQREAPPPLSATLS LSIL
13798	27699	A	13965	246	410	AYNGQSGRGVTPVIPSLWEAKTGSSELP RSWRSAWATWHTPPVPGSPKEISLYI
13799	27700	A	13966	91	26	FCGCCCCCCCFYCKKETLV
13800	27701	A	13967	158	24	PFCHYIYFLSCFVAMLECSGKILAH YLRLGSSNSLVPSLA
13801	27702	A	13968	129	7	SWAQWLMPITPTLWEHAGRSLEAMSSR PAWATQDDPVSKK
13802	27703	A	13969	445	268	KIQLTKLNASESLPSRINQAEERTSGW AWCLMPVIPVLWEAKAGGSLEPRSLRRG QVT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
13803	27704	A	13970	1628	1309	HRKXKAGYSSLSALLRERERERERERERESVCVCLGTITCFRRQYCVIOGISGVRQNCVQIPALSDPDLFLFLSLVHLNRTWVVRPTLVTRTERNKGMVCV
13804	27705	A	13971	314	140	QCHNCYILTLQVKIKGQDAWNLMPITPALGAKAGGSLEAGSLRSASATWRAPMSTKTF
13805	27706	A	13972	292	482	YKSVTRQDSCAHSVDRLVGKIRYVNLVFIYIQHSDGRTWNLTPVIFPLWETKGGGSEVGRSG
13806	27707	A	13973	502	303	STALGPSSPFLCTHGSFHGLFFFFCFPCFPLVEMGSHYVAPAGLKLGGSDPPASAPSHLGLQV
13807	27708	A	13974	493	289	IPPTALGTSTSPFLCTHGSFHGLFFFFCFPCFPLVEMGSHYVAPAGLKLGGSDPPASAPSHLGLQV
13808	27709	A	13975	405	121	IREAAQGSLEFVRAAPHTGLLSGPCITEIYAVKDTCKMQRRLVRELECAHGLTECLSIDTHTHTHTHTHTHTHTHTHTHTHHGTREAGQSLKGES
13809	27710	A	13976	135	254	TVCTNSSSSLTFTSFLFLPMFGWIQGRRVVCVCCVCCV
13810	27711	A	13977	179	58	VPLSTNSPQRQCFCCCCCCCCFLVLQKIISERSWAEIG
13811	27712	A	13978	97	186	KIIFWLGVVAHACNPSTLGGGQGRIMRGD
13812	27713	A	13979	289	420	ELGLKIHGFSPQAPWFMPITPALWEAEAAGLLESRSSRIANAMW
13813	27714	A	13980	421	106	SGGRNFFFLGGGFYKKKFPFFFLRGK KKKPPLPKKINPTPIFFPPGGGPPSPFPKGGGKIPFFFGGKNFIMQNFGGPPLWGKKKKFLPKKINPLFFFF
13814	27715	A	13981	309	135	KHIYIYLSIYLSIYLSIYLSIYLPAYLPTYLHAFLIHANAYKNIHIDYFPKKGFEY
13815	27716	A	13982	231	21	CHMYCLKSIWHKLSRKPICYITISEYSSMVLKVSLSQVQNLMPVLPALWEAKAGGLKARSSREWAI
13816	27717	A	13983	209	359	HLRTHTHTHTHTHPNVGKIMTQIPILPLTGPLLLEKFLNFKPLSHPGKRD
13817	27718	A	13984	391	249	INFLPCKPIFFFFFETESCVTQARVQWNLGSLQPPNPVPSLAK
13818	27719	A	13985	181	403	YLVLDSPSTLGLISQFKDYITKDOTLFRPVVVAHACNPSTLGSQKKNITSQVEETSLCNTARECLYOKYKN
13819	27720	A	13986	441	358	ETGSKCVILAGAOAORLSSVQPLPFRFKASIPCIYQTKIPNTQTQKNKNTITPAWMTPIAPATQKAEIPPLHSSLDGLRLSPKKKKGGPNWAPPSKFF
13820	27721	A	13987	7	233	PKAPLFFFFFFFVFYETRSWSVAQAKVQRHDHGLS
13821	27722	A	13988	152	44	NVSCHAAETRVWWEKERPLVPFGAYLLDGMPLVWLLSASSILSIWLSIYLSIYLSIYLSIY
13822	27723	A	13989	188	379	SSILPHASKYHFSGRFLSLLSCKRRNIIQLVPHMYSPLYMYIHTKHIIYSEMYVHIYIMNLRNCRILYHSCTPKENQAR
13823	27724	A	13991	296	53	RLGSPASRHHQIQCLIRACKLGDGTGLGW
13824	27725	A	13992	37	290	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, /-possible nucleotide insertion)
						WLLIPIVIALWEARVGGSLPRSSSTPAW ATQGDLLKKDSTLLQCPHAKGHSSHS
13825	27726	A	13993	189	370	SRNAIFKKRWSSSCQSSFNLSGVFPQAA TKGWVRWLTLPVLPALWEAKAGGSLPRSS SRPA
13826	27727	A	13994	179	25	SKINKKNIQICLLCSKRSMFVHVCIHIH ICVYVYRVAYIYIGMCIHIYIHS
13827	27728	A	13995	159	2	EDPLSPGVODQGHGHRKLSGRGKGKISL GQEFKSSMAAMYFGRSGGCKLER
13828	27729	A	13996	307	99	FTNEHFVNYTMFFTYKKPTSQANWMPV VPALWETEAGGSPFVRSPPFPQGHDDVR PLGPSLHVYLQMD
13829	27730	A	13997	218	21	FOHFGRPRVRDHLSLGVODQPGQHGTEP SPLASSILDLPFPFPIDEPVDLAFQSV TLGVQDQTT
13830	27731	A	13998	227	404	GYSVTLLGLTQDQRIAHGTRGERER ERERERERERVCCLMHLELASHLLFFFL FRE
13831	27732	A	13999	400	668	PVGRRWELQGMGLGVRTWQSSLPCQGP SSSVLSLGRGTPGISNTCLPPRSATELG LPAQVPPFNVSQDQDLFSLSGCFPRPY NRQTL
13832	27733	A	14000	225	414	NRVLLCHTGSTVAI LAYCSFKLLGSRD SPTLASRAARTIVKCRNVWLKKKKKK KGGRL
13833	27734	A	14001	397	118	LFSGPFFFDKSCFCEQPTVPFCLLLYNQ MQPYLLRSAPVDSYMYDSFLRDRVSFC QSGWSTVAPSRLLTAALNSLAQVILLPQ LNVLCGR
13834	27735	A	14002	3	173	YVEYKQGMVCFYKIRIKMFMNRRNLNL GQWCVPVTPATQVAEAGGSPPTSLRPI
13835	27736	A	14003	440	290	YHTHTLYIYIYHTHTHTHTIYIYCTYSG QPDLLVLNDKLYKRIYLSVFI
13836	27737	A	14004	2	116	ARLVAMFFKYEIKDPLLTARRDKASV KIKQKSAV
13837	27738	A	14005	279	422	SAKAPLSCLRTNSLLKNGLRGAWNWIT PVIPTLWEAEVGGSPDVTSP
13838	27739	A	14006	3	497	GGIGDSRCGSTKASSSPQLAGRSSVLP AAAQPCPTTMDVFKGFSIAKEGVVGAV EKTQGVTEAAEKKEGVMYGAKTKEN VVQSSTVAEKTKEQANAVSEAVVSSVN TVATKTVEAENIAVTSGVVRKEDLRPS APQQEGEASKEKEVEAEASQGGD
13839	27740	A	14007	1	292	SLGGGGCNDPRSYHCTPAWATEQDVTSL SLSIYMSVRVCIYMYMCVVCIRIYTYI HTHIHIRVYIYITIPYMWGIYIYIVDLV IYMGWCGCPPI
13840	27741	A	14008	57	250	KIFFFLMNHNTWGGVPVVLATWEAEVGS LEPRSLQLQETMNTSLSLRFPQOGEIL SLILKRN
13841	27742	A	14009	184	2	AVPGRWPCQVFGLLPSIQDTLKQGRG QWLTPVTPMPWEAEAGGLDARSIRPAW ATGK
13842	27743	A	14010	123	3	KEPSRFRGRLTSIIIPACWEAEAGGPPEA RSSTREFRTAK
13843	27744	A	14011	403	168	GTGLKASRCISQPVMSGLLSPSEFFPPE TESHLHVSQRETPARLRDRERERERERE RERERGNASSGKPGASVCP

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13844	27745	A	14012	207	422	EIRRGSLAGPLSLNFI LSVMGSHSKYLRL KVIGRAQLMPVVPFALWEAEVGLHELRL RLGHTWAAW
13845	27746	A	14013	200	405	WLCVLGWSLLALSPLRCEYGPISAHNCNL HLHSSSDSPASASQALQEA WYQHLLMM POAASVGVGKK
13846	27747	A	14014	319	176	KPSTTTFLFLILFISSRESRPVTQTEVK WLNHSSPQPTTPPFLSPSS
13847	27748	A	14015	63	401	EGENKNTLNSFGWDGVIHLVLEFLNTRM PLGHLSFSEGVS GSSGRCQAQAGAGR SATAAARPCQCLGLKGLPAVPSGCLG KAPERAGYSASHPHIGCETGNQWVLYVN
13848	27749	A	14016	416	63	VSKVYPKINHTORTVRHETFKIAMPKYV SNLCSILRFNKRDLRFMRHYTKQCSRTS ITEYIAMFFVCLFVLKIGACHPGWNE VVLVCSQVTAASTSRAQAILPQPPKIL GMQQA
13849	27750	A	14017	196	425	SLMFRPPLIFSCCF CIRYPPFVFFSLL CFAPSWCSLLLFTHYLKLFLLLELLFF LPVLLCLDSFLVHDFLLSS
13850	27751	A	14018	3	233	SSRMGRGRTKTIAPFMKRWCEVDRAIRDR RERERERERERERKGAEPQFPVISPW VDRPCLAGILHLKCCGCHRL
13851	27752	A	14019	163	1	AERWHDQTCVERETWGVQWLMFPVIFVL WEAKAXNLLEPKNLKQRRNRPGNSR
13852	27753	A	14020	203	83	LKKKKNKSQAQLTSVVLASQEAAGGS LEPRNSRPAAWAT
13853	27754	A	14021	179	3	VTWORELRQLMELRLICRANWLTVPVIF VPWEAKAGGSPPEPRSSRPAAWETRRNRPG NS
13854	27755	A	14022	358	431	WHKKKNQNLGTGAHACNPSTLGG
13855	27756	A	14023	98	3	GRFAGWLTVPVATLWEAEMGGSLPRSL GHE
13856	27757	A	14024	254	385	RENWAEFSSHSLNIFLQLGTVARACNP STLGGRGWITRSD
13857	27758	A	14025	140	1	KVLLCGRGLCVFCFCFFFLCVCVCVCV CVCVMRSITLSPLQCI
13858	27759	A	14026	579	852	QREWGWAKGEGEGVSHVPASQAQLPAN GGRGPHPSPLGTGCTWAGEGAYCCLS SCSHCCCCSCCCCCPPGCLFPLSGAI CHLYHL
13859	27760	A	14027	30	663	LRIRALRELPA SHIPGSLITTCVPRPPL PCSSTKPDAGYKPLAQKLGSORTGPG LGHAPCYSPLNWRHGGCSYPGSPSGS VSLWQEA MRLPKNTPEEKDRRTAALQEG LRRAVSVPLTLAETVASLWPAQLQELARC GNLACRSDLOVAKALEMGVGFAYFNVL INLRDITDEAFKDQIHHRVSSLLQEAKT QAALVLDCLLETQGE
13860	27761	A	14028	1	267	AVGVHHAFLPHCFASLLESPVSPRLA MDPNCSCAAGVSTCAGSCKCKECKCTS CKKS CCSCCPVCSCKAQQGCVCKGASEK CSCCD
13861	27762	A	14029	46	1746	PAAGAAETMEFRQEEFRKLGRALGKLRH LLEKROGAETLELSADGRPVTTOTRDP PVVDCTCFGLPRYIIAIMSGLGPCISF GIRCNLGVAIVSMVNNSTTRGGHVUVQ KAQFSWDETVGLIHGSPFWGYITQIDP

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						GGFICQKFAANRVFGFAIVATSTLNMILI PSAARVHYGCVIFVRILQGLVEGVITYPA CHGIWSKWAPPLERSRLATTAFCGSYAG AVVAMPLAGVLVQYSGWSSVFVYVGSFG IFWYLFWLLVSYESPALHPSISEERKY IEDAIGESAKLMNPLTKFSTPWRRFFTS MPVYAIIVANFCRSWTFYLLISQPAYF EEVFGFEISKVGLVSALPHLVMTIIVPI GGQIADFLRSRRIMSTTNVRKLMNCGGF GMEATLLLVGVYSHSGKVAISFLVLAVG FSGFAISGFNVNHLDIAPRIASILMGIS NGVGTLSGMCVPIIVGAMTKHKTREEWQ YVFLIASLVHYGGVIFYGVFASGEKQPW AEPPEMSEKCGFVGHDQLAGSDDSSEME DEAEFPGAPPAPPPSYGATHSTFQPPRP PPFVRDY
13862	27763	A	14030	240	63	VFTAQSNNGVVELNRFNEGFSLAULKGRV AWAQWLTVPVITLMEVKAAGLLEARSLS PA
13863	27764	A	14031	289	414	HAEMGRVQWLTFAIPALCKAEAGGPPEP RSLRPAWNTY
13864	27765	A	14032	386	1765	LGDARAPEKMSAIQAAMPSTGECTIAKYN FHCTAEQDLFPCKGDVLITIVAVTKDPNW YKAKNKVREGIIIPANYVQKREGVKAGT KLSLMPWFHGKITREQAERLLYPETGL FLVRESTNYPGDYTLVCSDCGKVEHYRI MYHASKLSIDEVYFENLMQLVEHYTSD ADGLCTRLIKPKVMEGTVAQDEFYRSG WALNMKELKLLQTIGKGFGDVMGLDYR GNKVAVKCIKNATAQAFLAEASVMTOL RHSNVLQVLGVIIEKGGLYIVTEYMAK GSLVDYLRSGRSLVGGDCLLKFSLDVDC EAMEYLEGNFVHRDLAARNVLVSEDNV AKVDFGLTKEASTQDTGKLPVKWTAP EALREKKFSTKSDVMSFGILLWEIYSFG RVYPRIPLKDVVPRVEKGKYMADPDGC PPAVYEVMNKCHLDDAMRPSFLQLREQ LEHIKTHELHL
13865		A	14033	619	414	EQARCLQHAQTSFRQPRFQLQCSELKG HSLGMEHQGHVPLCHLPCSPCPPVKASPA CWSSNPAPLCPH
13866	27767	A	14034	2	614	LESRPDGRPSSTHDSPSFAFSGPKPHF PEAKMSSKRAKAKTKKIPORATSNVFA MFDQSOIQEFKEAFNMIDQNRDGFIDKE DLHDLASLGNKPTDEYLEGMMSEAPGP INFTMFLTMFGEKLNGTDPEDVIRNAFA CFDEASGFIHEDHLRELLTMGDRFTD EEVDMEYREAPIDKKGNFYVEPTRILK HGAKKDD
13867	27768	A	14035	1	254	AVEFGPAGPGSLGRRAAMIIPVRCFTCG KIVGNKNEAYLGLLQAEYTEGDALDALG LKRYCCRRMLLAHVLDLIEKLLNTAPLEK
13868	27769	A	14036	494	148	FRFLSDCGVFAEGHIELQVESGVPLGFS TMAEDMETKIKNYKTAFPPDSFRPNQNT RNCQWNYLDFHRCQKAMTAKGGDISVCE WYQRVYQSLCPTSVWTDWDEORAEGETF GKI
13869	27770	A	14037	130	3969	IMGDVKNFLYAWCGKRMTPSYEIRAVG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond- ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NKNROKPMCEVQVEGYNITGMGNSNKK DAQSNAAARDFVNYLVRINEIKSEEVAF GVASPPPLTDTPTDTANAEGDLPTTMGG PLPPHIALKAENNSEVGASGVPGPTW DRGANLKDYYSRKEEQVQATLESEED LNAGLHGNWTLNNAKARNLQYFQKEKIQ GEYKYTVQVGDHNRSTFAEMTIIYKQLG RRIIPAREHGSNKKLAAGSCALSIVRQLY HLGQVVEAYSGLTRKKEGEIVFPYKNLS QDLHQLQNTIQIEMLEILPEPDSVP VALNIGKLAQFPSPQRQNGCVGVWSP QSNMNPWTSSNIDEGPLAFATPEQISMD LKNNLMWOLEQDHDQLAILQERELLPVK KPFESEILEATISQNSVVIIRGATCGCKTT QVPQFILDFFIQNDRAAECNIVVTQPRR ISAVSVAERVAFERGEEPGKSCGYSVRF ESVLPRPHASIMFCTVGVLLRKLKLEAGIR GISHVIVDEIHERDINTSFLLVLRDVV QAYPEVRIVFMSATIDTSMFCYFFNCP SLKLWRTYVPQVEFLDCIQMTHFVPPP KDKKKDKDDGGEDDANCNLICGDEY GPETRLMSQLNEKETFPFELIALLKYI ETLNVPGAVLVFLPGWNLIYTMQKHLE NPHFGSHRYQIPLPHSQIPREEQKRVFD PVPVGVTKVILSTNIAETSIITINDVVVY IDSCKQKVKLFTAHNNMNYSTVWASKT NLEQRKGRAGRSTAGFCFHLCSRARFER LETHTPEMFRTPHEIALSIKLLRLGG IQQLAKAIEPPLDVAIEARFTLRELD ALDANDELTPGLRILAKLPIDEPFGDM IMGCIIFYGDAICTIAAATCEPPEFVNE GKQLGYIHRNFAGNRFSDDHALLSVFOA WDDARMGGEAEIRFCEHKRLNMTALRM TWEAKVOLKEILINSGFPEDCLLTQVFT NTGPDNNLDVVISLAFGVVFNVCYHKE KRKILTTEGRNALIHKSSVNCFFSSQDM NYPSFFVFGEKIRTRAIASAKGMTLVFP LQLLLPAKQVSGDQIVLVDWIKLQI SHEAAACITGLRAAMEALVVEVTQKPAI ISQLDPVNERMLNMIQISEPSSAAGINL MIGSTRYGDGPRPKMARYDNGSGYVRG GSSYSGGGYGGCYSSGGYSGGYGGSAT PSGRIACVGGYRGVSRGGFRGNSGGD YRGPSGGYRGSGGFRGGGRGAYGTCLY DIEEEVAALKGYVSVSCRO EGITPGWARLTPVTPLGLEEEAGSGP REIDIGLAN RRCITFLSFRMLAPRVYSVVGKRAFSPV CVRAHGKCDYSYS FRAAGSSSTNSGRICPLPSGALLYQSEG LLARPHGKGSFCVGRQHQHVRVGSAAHA SSAGYVCSAEPFVFLRCPVGGGPGTISR VVALPYGECNPTREHNVSELSPSPOQC NKMNKVEQKSQESVSFKDVTGFTQEW QHLDPQRALYRDVMLENYSNLVSVGYC VHKPEVIFRLQCGEBPWKEEFEPQSQF PEVWTADHLKERSQENQSKHLWEVVFIN NEMLTKEQGDVIGIPFNVDSSPSRKM
13870	27771	A	14038	431	542	
13871	27772	A	14040	238	362	
13872	27773	A	14041	6290	3514	

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						PCQCSGMSFNTVSELVTSIKNYLGKK SDEFNACGKLLLNIXDQETHTREKNEVL KNRNTLSHRENTLQHEKIOTLDHNFYS ICQETLLEKAVFNTRKRENAEENCDYN EFGRTFCDSSSLLFHQISPSRDNHYEFS DCEKFLVCVSTLSKPHGVSMKHYDCGES GNNFRRLCLSHLQKGDGKGEKHFECNEC GKAFWEKSHLTHQORVHTGQKPPQCNEC EKAFWDKSNLTKHQRSHTGKPFECNEC GKAFSHKSALTLLHQRTHTGKPPQCNAC GETFYQKSDLTQKQRTHTGKPPYECYEC GKSFCMNSHLTVHQRTHHTGKPFECLEC GKSFCQKSHLTQQRTHIGDKPPYECNAC GKTIFYHKSVLTRQI IHTGLKPPYECYEC GKTFLKSDLTQHQRTHHTGKPFACPEC GKPFYHKSSTLSQYRTHHTGKPFECHEC GKIFYNKSYLTKHNRTHHTGKPPYECNEC GKTFCQKSQLTQQRTHIGKPPYECNEC GKAFCHKKSALIVHQRTHHTGKPPYKNEC GKSFCVKSGLIFHRKHTHTGKPPYKNEC GKFFRHSSTLVHQRTHHTGKPPYKNEC GKIFYRKSSELAHQQRSHHTGKPPYECNAC RKTFSQKSNLIVHQRTHHTGKPPYECNAC RNFPQVSLHNASEYSHCGESPDILNV Q
13873	27774	A	14043	187	422	LTIPLKLSAQEPAGPVSPPPPPSPTFOI GGRSRAEPNRQYCPQVAPVAPALRGCLPL SPGEPPHDTSSPRHLTCGIVF
13874	27775	A	14044	340	442	NKFLSWVRLLMPVIPTFWKAVGGWLEA RSLRMQ
13875	27776	A	14045	3	1240	LVEGAAGQGVSDGARLRKCGTRSPGSE EVLSSMARGSAFPAALMLWSILLCLLA LRAEAGPPQESLYLWIDAHOARVLIGF EEDILIVSEGMAPPTHDFRKAQQRMPA ISVNIHSMNFTWQAAGQAEYFIEFLSLR SLDKGIADPTVNVPLGLTVPHKASVVQ VGFFCLGQDGVAAFEVDVIVMNSGNT ILQTPQNAIFFKTQQAECPPGCRNGGF CNERRICECPDGFHGHCEKALCTPRCM NGGLCVTPGFCICPPGGFYGVNCDKANC TTCFNGGTCTFYPGKCI CPPGLEGEQCEI SKCPQPCRNGGKICGSKCKCSRGYQGD LCSRFPVCEPGCGAHGTCHEPNKQCQEG WGRHCHKRYEASLIHALRPAGAQLRQH TPLSKKABERDPPBSNYIW
13876	27777	A	14046	18	274	YSQEVLCEMNRSGVSNIKRGNWNLTF TTPALNEAEVCGLLLEPSRLRLASPOPP QHEDYSMSYCAQPRFSLCIRGFIYFSLW F
13877	27778	A	14047	177	441	GGSYVAMPNITFIETPLLAQFCFFEMO SCSEVARLECRGAISAHCNHLHPGSSNSP VMAQILNKQRKSNFDEDATLLGLSYTLL GEI
13878	27779	A	14048	136	319	DVFLLLFHNSYVLFETGSHSVSQAGVK WCDLSSILQPPPLGGSDPPTASRVPALE FFLEF
13879	27780	A	14049	388	128	ELKLFPSYKGQSPQLSLRRYFADLIAVS NRFTLCPSARHLAVYLLDLFMEDYDISI

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						QQHLVALSCLLASKYESDLHDWKF LMF I
13880	27781	A	14050	262	3	VIYNYISVRFPFNHYHTFYTLSEFLYLS THTHTHTHTHTHTHQRETHGVCVCIYTYM YMCMYAKWYKFTFLISGKARIHTHLHP CI
13881	27782	A	14051	149	423	YPHLC AFLLLPSISSFRAGVFFFSYLSL TAYPLTWKPPPEPATQPTTPNPPGHPA TRGPKSALLDHSYACASAPPLGTGTGTA TSPSFLI
13882	27783	A	14052	2	1440	FVAVTAAAFCLLLQGRGAGALKTLQEA QVFRGLASTVSLAESCKSEKGPQNSK KQSPFKNVPEPERGKLLATQTAELSK NLSSPSSYPAPVANKGRKVASPSGSLV FTDEGVPKPLSRKTLVEFPQKVLSPFRK QGSDSEARQVGRKVTSPSSSSSSSSDS ESDDEADVSEVTPRVVSGRGGRLKPEA SHSFENAFRVTSAKEKTLQKPHVDI TDPEKPHQPKKKGPAKPSGRENARPK TTMPRSQVDEEFLKQSLKEKQLQKTFRL NEIDKESQKPFVKGPLPVHTKSGLSAP PKGSPAPVLAEEARAEGLQASPPGAA EGHLEKVPPEPQRKAAPLPKRKETSQT GIEGHLKGGQAIVEDQIPPSNLETVPVE NNHGFHEKTAALKLEAEGEAMEDAAAPG NDRGGTQEPAPVPAEPFDNTTYKNLQHH DYSTYTFDLNLNLSKFRMPQPSGSGRES PRH
13883	27784	A	14053	177	1253	EKKRTLPVRSVTGELQGSLSLDAAGTM DSEKKRTTSEATKYFRERVSPVHLQILL TNEAWKRVTAELPRDEADALYEAL KLRITYAAIEDEVQKQDFREWFLEKF PQVKRKIQESIEKLRALANGIEEVHRC TISNVSSSTGAASGMSIAGLVLPFT AGTSLALTAAVGLGAASAVTGTITSIV EHSYTSAAEAESRLTATSIDRLKVFKE VMRDI TPNNLLSLNNYEAQTITGSEIR AIRQARARARLPVTTWRISAGSGGQAE RTIAGTTRAVSRGARILSATTSGIFLALD VVNLVYESKHLHEGAKSASAEELRRQAO ELEENIMELTQIYQRINPCHTH
13884	27785	A	14054	1585	2099	ICVKTFFPPLALQVRMAAAEHHSGLPY WPLYLTAETLKNRMGHGPPPTQQHSITD NSLSLKTPSERLLYLP.PPSAPPSADDNL KTPPECLLTPLPSPALPSADDNLKTPAE CLLYPLPPSADDNLKTPECLFTPLPPS APPSVDNDLKTPECVCSLPFHPQRMII SRN
13885	27786	A	14055	2	2865	ALPDGGASVSDRAEGRPAKPSKTAARE KTEGAVAAVGGPSSFRCCYGCCHEARL GRTSLPRGVIMLTAEASLSINGWGLGIV LFLITFGPFVIFVLYLTFYILCFVGGGLVV TLLPGKTNSEKYLEQCEHSLFPPTSPGV PKCLEBMKREARTIKIDRLTGANLIDE PLQQVITQFSLRDVQVWYLYLSDDESL LEIROTILQNALIQFATRSKEIDWQPYFT TRIVDDFGTHRVFRAAPQKRIKEDDQV KGTAEDLVDTFFFEVEMEKEVCRDLVC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						TSFKDEEGFLRDLCEVLLYLLPFGDFQ NKIMRYFVREILARGILLPLINQLSDPD YINQYVIMIRDSNCNVEAFMNI IKLSD NIGELAEVRDKAAELOYLRSLDTAGDD INTIKNQINSILLFVKVCDSRIQLQSG KEINTVKLAANFGKLCITVPLDSILVDNV ALQFFMDYMQQTGGQAHLPFWMTEGYR VTAQQQLEVLRLSRORDGKHQTNQTKGLL RAAAVGIYEQLSEKASPRVTVDYDLVA KLADTLNHEDPTPEIFDDIQRVYVELML RDERFYPSFRQNALYVRMLAELDMKDP SFRGSDDDGSGFNPGSPTGSINLSLDDL SNVSSDDSVQLHAYISDTVYADYDPYAV AGVCNDHGKTYALYATVHRRNLNSEEM WKTYRRYSDPHDFHMRITEQFESLSSIL KLPEKTKFNMDRDFLEKRRKDLNAYLQ LLLAPEMMKASPALAHYVYDFLENKAYS KGKGDFAKMDTFVNPLRNSMRNVLSQD KSLPDSLAEGMTKMSDNMGKMSERLQD IKQSFKVPELIPKTDSDPEHRRVSAQL DNVDNDNIPLRVMLLLMDEVFDLKERNQ WLRHRIKMLLQQLIRATYQDTINRKIVD HYDWMTSPEQVADSVKRFDAFWEGILL AEAVPCRDKSIKMRTRVAGTKLLAIMP GE
13886	27787	A	14057	311	150	FLCFKYRRGFATLHSGGLKLGSSDPSS TSQIPGITGTSGHCQVPTHLFFPLALS
13887	27788	A	14058	53	211	RQHITCLDIFFTIHNNYKYKYNLYLSIY LSIYLSIYLYLSISHSXYTERA
13888	27789	A	14059	1	1642	RDGRKMATATIALQVNGQGGSEPA AAVVAAGDKWKPPQGTDSIKMEGQSTA AKLGLPPLTPQQEALQKAKYAMEQSI KSVLVKQTIHAHQOQLTNLMAAQRORA LAIMCRVYVGSIIYELGEDTIRQAFAPF GPIKSIDMSWDSVTMKHKGFAFVEYEV EAAQLALEQMNSVLMGGRNKIVGRPSNI GOAQPIIDQLAEERAFNRIYVASVHOD LSDDDIKSVFEAFGKIKSCTLRDPTTG KHKGYGFIEYEKAQSSQDVA SSMNLFDL GGQYLRVGKAVTPMPLLTPTATPGGLP AAVAAAAATAKITAQEA VAGAAVLGTL GTPGLVSPALTLAQPLGTLFQAVMAAQA PGVITGTVPARPIPIVTPISVGVVNPIL ASPPITGLLEPKKEKEEELFPESERPE MISGEHMSISGSSARHVMQKLLRKQF STVVLNRMWDPKIDDLDECFWTECG KFGAVNRVIIYQEKQGEEDAII VKT VEFSIASETHKATQALNGRWPAGRKVVA EYVDQERFONSDLSA
13889	27790	A	14060	1238	1474	VIALQEGRPWRKRPASIDACRLAFQRL RCKFSNVLPGLAQEALYSGGYHLKPAD ELMGGNLLKKTADASGSRGHQ
13890	27791	A	14061	266	400	GQWARFVPIPALWEAKAGGSLEPSMLRPA GQHITKTPSVLITSKTK
13891	27792	A	14062	2178	1881	VLOAPSTILLDAFRTDGGDMGRANVARLG LWLLLLALLLPQIYSSSETTTGTSNNS QSTNTGLAPNPTNATTKAAGGALQSTA SLFVVSLSLLHLYS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13892	27793	A	14063	261	1	NSVLTLLALLFSLVHLVPPPPSGVTDTAG ALSTGGPPSPSTVTGRGPAHSHASQLPP APGEFAPLNECSRGNAGEAFLEFPDPAW VDP
13893	27794	A	14064	2384	1115	QHFSRRGLCVVQRRSSVTSSTSGAWS PCFPSSNASCNTLHTRDWSAPDGGQSSL GESPGAPPQGQLHTLDTLHSLAQIGGK SPVAGVNGGSLWRPESPGTANGHSPHE TPPGGPPGPCCTHRRLLPAGEAPDVSS EEGFPAPRRRRSLGHTTAMSDAKAT PFWSHLLPGPKPVLDPDTDCGPGWRALK GARRLLKSLPLRSRLKPGQLLSPFRASPV PTAVSRTLGNFEESLLRGRFAPSCHI EGFTAEGISAGSGYCPQHVTLPTVTTFD VSEONAPAPFLGIVDNLPLGRKGYSVPK VGTVQVTLFPNPQTVVKMFLVTFDPSDM PAAHMTFLRHRLFLVPGVEGNANPTHR LLCYLLHLFRSSRSRGLSLHGDIRLLF SRRSLELDTGLPYELQAVTEAPHNPRYS PLP
13894	27795	A	14065	232	416	GWAVQLGIGTEGKEGTSSSERQREGRGD GNRKTGRRREGRRSTKTAPSPYPAPHRP RSKLI
13895	27796	A	14067	238	45	IQTGSSHSFCIPSTWEAKAGLLEPRSL SPACPTQKDPISHLGSLELPQSFRLLIHL VPLFLSAC
13896	27797	A	14068	3	1705	SCESKATPWRVASASQELHPPQGGQRSP LPGLDITPARPNPAYPLTVEQCRSCSRPV PAPLPHPHTHPGSSCFYSFSFITKATA PGAQRRAVTAERGRMGFLGTGTWILVL VLP IQAPFPKGGQSKSLHRELSAERP LNEQIAEAEDEKIKTYPPENKPGQSGY SFVDNMLLKAITEKEKIEKESRGS PLDNKLAVEDVDSTKNRKLDDYDSTKS GLDHKFODDPDLHQLDGTPLTREDIVH KIAARIYEENDRAVFPKIVSKLLNLGLI TESQAHTEDEVAEVLQKLSKEANNYE EDPNKPTSWTENQAGKIEKVTMPAAIQ DGLAKGENDETIVSNTLTLTNGLERTKT YSEDNFEEQLQYFPNFYALLKSIDSEKEA KEKETLITIMKTLIDFVKMMVYGTISF EEGVSYLENLDEMIALQTKNLEKNATD NISKLPAPSEKSHETDSTKEAANKME KEYGSLKDSSTKDDNSNPGKTDPEPKGKT EAYLEAIRKNIWLKKHDKGNKENDYDL SKMRDFINKQADAYVEKGILDKAEAEAI KRIYSSL
13897	27798	A	14069	1	140	NTSVAIQTI EYSAFKRKETLTHVPLWM NLKDTMLREISQSQKDTV
13898	27799	A	14071	212	104	HTNHQCTVLPAGQALATPQGLAPSVEF PQSCLRMV
13899	27800	A	14072	358	112	PFLTVMNLVFLWQNLKHCFWIEQELM FFFFFLRTGSHYVQAGLELLGSTNLP ASVSRVAGTTGIHNCOTFNPPLHTLHL
13900	27801	A	14073	3	151	YMGFHSVGYAGLELLTSSDLPWPFPKCV DYRIEPLCLAMPFYFALTADE
13901	27802	A	14074	8	1493	VTTHHLFVQQAADTLKKKSPSCCLLCI VFIDVPRIDLNTIDQVAIVFKHHFPVGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GDAVLKTPAPQCLCSRMGPANLWLLGT GILASVHCOPLLAHGDKSLQGQP ^{PR} HQ LSEFAPAYHRTPTITN ^F ALRLYKELAA DAPGNI ^{FF} SPVSI ^{TT} LALLSLGAQANT SALILEGLGFNL ^{TET} PEADI ^{HQ} GFRSLL HTLALPSPKLELKVGN ^{SL} FLDKRLKPRQ HYLD ^{SI} KELYGAFAFSAN ^{FT} DSVTTGRQ INDYLRRQTYGQV ^{VD} CLPFSQ ^{DT} FMVL ANYIFFKAKWKHPFSRYQTQKQ ^{ES} FFVD ERTSLQVPMMHKEMH ^{RF} LYDQDLACTV LQIEYRGNALALLVLPDPGKMKQVEAAL QPQTLRKWGQLLPSLLDLHL ^{PR} FSISG TYNLEDILPQIGL ^{TN} ILNLEAD ^{FS} GVGTG QLNK ^{TI} SKVSHKAMVDMSEK ^{GT} EAGAAS GLLSQPPSLNTMSDP ^{HA} FNRPFL ^{LL} LLW EVTTQSL ^{LL} FLGKVNVFVAG

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-13901, a mature protein coding portion of SEQ ID NO: 1-13901, an active domain of SEQ ID NO: 1-13901, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-13901.
11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-13901, a mature protein coding portion of SEQ ID NO: 1-13901, an active domain of SEQ ID NO: 1-13901, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-13901, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 13902-27802, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NOS: 1-13901.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

5 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

10 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

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(71) Applicant (for all designated States except US): HYSEQ, INC. [US/US]: 670 Almanor Avenue, Sunnyvale, CA 94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): TANG, Y., Tom [US/US]: 4230 Ranwick Court, San Jose, CA 95118 (US). LIU, Chenghua [CN/US]: 1125 Ranchero Way #14, San Jose, CA 95117 (US). DRMANAC, Radoje, T. [YU/US]: 850 East Greenwich Place, Palo Alto, CA 94303 (US).

(74) Agents: ELRIFI, Ivor, R. et al.: Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).

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PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rule 13ter.1(c) and 39)

Applicant's or agent's file reference 21272-042	IMPORTANT DECLARATION	Date of mailing (day/month/year) 9 ? AUG 2001
International application No. PCT/US01/04927	International filing date (day/month/year) 26 February 2001 (26.02.2001)	(Earliest) Priority date (day/month/year) 28 February 2000 (28.02.2000)
International Patent Classification (IPC) or both national classification and IPC IPC(6): C07H 21/04 and US Cl.: 536/23.1		
Applicant HYSEQ, INC.		

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
 - a. ☐ scientific theories.
 - b. ☐ mathematical theories
 - c. ☐ plant varieties.
 - d. ☐ animal varieties.
 - e. ☐ essential biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. ☐ schemes, rules or methods of doing business.
 - g. ☐ schemes, rules or methods of performing purely mental acts.
 - h. ☐ schemes, rules or methods of playing games.
 - i. ☐ methods for treatment of the human body by surgery or therapy.
 - j. ☐ methods for treatment of the animal body by surgery or therapy.
 - k. ☐ diagnostic methods practised on the human or animal body.
 - l. ☐ mere presentations of information.
 - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:

☐ the description
☐ the claims
☐ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out:

☐ the written form has not been furnished or does not comply with the standard.
☒ the computer readable form has not been furnished or does not comply with the standard.

4. Further comments:

A text search of key words would not be meaningful. A copy of the CRF problem report is attached.

Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer Marjorie A. Moran Telephone No. (703) 305-3388
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